SEQUENCE LISTING

<110> CODEXIS, INC.

<120> PENICILLIN-G ACYLASES

<130> CX2-154WO1

<140> To Be Assigned
<141> 2017-05-05

<150> US 62/332,103
<151> 2016-05-05

<160> 1902

<170> PatentIn version 3.5

<210> 1
<211> 2541
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates from K. citrophila

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<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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35 40 45
Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln Asp
50 55 60
Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr Val
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Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile Arg
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145                 150                 155                 160
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Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu Val
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Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala Ala Leu Leu Pro Arg
225                 230                 235                 240
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                245                 250                 255
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        275                 280                 285
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Ala Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Tyr
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Thr Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn
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Thr Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile
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Ser Trp Gly Ser Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala
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Glu Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu
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Gln Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile
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Gly Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro
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Thr Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala
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Leu Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly
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<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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<212> PRT
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<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
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115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
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225 230 235 240
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245 250 255
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260 265 270
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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<210> 5
<211> 2295
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<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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<210> 6
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<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Ala Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
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130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Lys Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 7
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 7

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 8
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 8
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 9
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 9
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gatgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 10
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 10

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 11
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 11
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gatgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccct ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 12
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 12

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Phe Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 13
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 13

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 14
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 14
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 15
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 15
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca ataccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 16
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 16
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 17
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 17
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgaa aaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 18
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 18
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Lys Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 19
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 19
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 20
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 20
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 21
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 21

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaacaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 22
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 22
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

```
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 23
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 23
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 24
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 24
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 25
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 25
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagcaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 26
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 26

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 27
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 27
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctga atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680

gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 28
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 28
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 29
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 29
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggcggtct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 30
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 30
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Gly Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 31
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 31
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 32
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 32

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 33
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 33
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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acgcaaacgg cgtaa 2295

<210> 34
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 34

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 35
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 35

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgcg taacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 36
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 36
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Arg Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 37
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 37
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 38
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 38
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 39
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 39
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattatt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 40
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 40

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 41
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 41
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gggccgcagt ttggttggac agtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 42
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 42
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 43
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 43

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 44
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 44
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
```

```
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 45
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 45
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggcgcact gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 46
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 46
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ala Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 47
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 47
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcatg gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 48

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 48

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
```

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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Trp Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 49
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 49

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccaccga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 50
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 50
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Thr Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 51
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 51
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctga aagcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 52
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 52
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Lys Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 53
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 53
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 54
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 54
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 55
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 55
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gccgcggtcc cagcgccgtt tggtaagtgg taccttgcca gtggctatga aaccacccag 1140
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 56
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 56
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Leu Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 57
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 57

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggaa cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 58
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 58
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 59
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 59
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatcatt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 60
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 60
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 61
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 61
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccgc aaacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 62
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 62
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Ala Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 63
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 63
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 64
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 64

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 65
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 65

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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 66
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 66
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 67
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 67
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacctat 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccct taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 68
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 68
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Tyr Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Leu Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 69
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 69
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggccatct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 70
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 70
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly His Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 71
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 71
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcaaaa gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 72
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 72
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

```
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Lys Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
```

```
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 73
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 73

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct tcatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 74
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 74
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

```
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 75
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 75
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 76
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 76
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 77
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 77
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 78
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 78
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 79
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 79

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgagtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 80
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 80
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Ser
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 81
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 81

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagt gtgagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 82
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 82
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Cys Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 83
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 83

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccatg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 84
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 84
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Met Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 85
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 85
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 86
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 86

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75						80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155						160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235						240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 87
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 87

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 88
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 88
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
```

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 89
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 89

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 90
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 90
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

```
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
```

```
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 91
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 91
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 92
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 92

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Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 93
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 93
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 94
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 94
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 95
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 95

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 96
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 96
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 97
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 97

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctacaaaac 2280
acgcaaacgg cgtaa 2295

<210> 98
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 98
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 99

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 99
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 100
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 100
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 101
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 101

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 102
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 102
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 103
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 103
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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acgcaaacgg cgtaa 2295

<210> 104
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 104
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 105
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 105
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 106
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 106

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 107
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 108
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 108
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 109
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 109

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 110
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 110
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 111
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 111

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 112
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 112
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 113
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 113
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 114
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 114
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
```

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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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CX2-154WO1_ST25

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 115
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 115
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 116
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 116
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 117
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 117

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 118
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 118
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 119
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 119
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 120
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 120
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 121
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 121
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 122
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 122
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 123
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 123

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 124
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 124
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 125
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 125

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 126
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 126
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
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            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 127
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 127
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 128
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 128

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 129
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 129
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 130
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 130
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

```
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 131
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 131

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 132
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 132
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 133
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 133

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 134
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 134
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

```
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
```

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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 135
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 135
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 136
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 136
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340   345   350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 137
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 137
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 138
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 138
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 139
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 139
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 140
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 140
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 141
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 141
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 142
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 142
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 143
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 143
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 144

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 144

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 145
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 145

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 146
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 146
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 147
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 147
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 148
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 148
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 149
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 149
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 150
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 150
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 151
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 151
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 152
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 152
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
260 265 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 153
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 153

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 154
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 154
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 155
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 155
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 156
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 156
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 157
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 157
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 158
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 158
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 159
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 159
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840
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ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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acgcaaacgg cgtaa 2295

<210> 160
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 160

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Ser	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Ala	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Lys	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
				245					250					255	

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            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 161
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 161

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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acgcaaacgg cgtaa 2295

<210> 162
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 162
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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 163
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 163

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 164
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 164
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 165
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 165
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggatatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacaggatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 166
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 166
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 167
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 167
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
caagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 168
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 168
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Gln Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 169
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 169

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 170
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 170
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 171
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 171
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
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ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 172
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 172
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 173
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 173
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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acgcaaacgg cgtaa 2295

<210> 174
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 174
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 175
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 175
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 176
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 176
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 177
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 177

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 178
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 178
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 179
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 179

agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacaggatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 180
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 180
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
290 295 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 181
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 181
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 182
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 182
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 183
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 183

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
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gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 184
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 184
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 185
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 185

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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acgcaaacgg cgtaa 2295

<210> 186
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 186
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 187
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 187
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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acgcaaacgg cgtaa 2295

<210> 188
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 188

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 189
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 189
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acgcaaacgg cgtaa 2295

<210> 190
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 190
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 191
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 191

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 192
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 192
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 193
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 193
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 194
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 194
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 195

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 195
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ccggcgctga aagacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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acgcaaacgg cgtaa 2295

<210> 196
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 196
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 197
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 197

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
gcggatcgag ttactgagat cgacaggatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 198
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 198
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 199
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 199

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 200
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 200
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 201
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 201
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggc 780
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<210> 202
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 202

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 203
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 203
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acgcaaacgg cgtaa 2295

<210> 204
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 204

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Ser	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 205
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 205

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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acgcaaacgg cgtaa 2295

<210> 206
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 206
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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Arg Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 207
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 207

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaaccgat gatgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 208
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 208
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1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Asp Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 209
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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acgcaaacgg cgtaa 2295

<210> 210
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 210
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 211
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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<210> 212
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 212
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 213
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 213

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 214
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 214
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 215
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 215
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgatgctc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 216
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 216
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Ala Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 217
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 217
agcaatatgt gggtgattgg caaaagcaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcacagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 218
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 218
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
```

```
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 219
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 219

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agcaatatgt gggtgattgg caaaagcaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 220
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 220
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 221
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 221

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctgc aagacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagacat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 222
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 222
Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Gln
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
```

```
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 223
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 223
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gctgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggcaaacg atccgcgccg ccaactggtg 960
gataaactga ccagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tgggaaacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagcat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 224
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 224

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Ser Asn Met Trp Val Ile Gly Lys Ser Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Ala Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Thr Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Glu
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 225
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 225
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 226
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 226
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 227
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 227

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccag taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 228
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 228
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Ser Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 229
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 229

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagcta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 230
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 230
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 231
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 231
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 232
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 232
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340   345   350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 233
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 233
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 234
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 234
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 235
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 235
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 236
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 236
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 237
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 237
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 238
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 238
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 239
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 239
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 240

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 240

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 241
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 241

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 242
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 242
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 243
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 243
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 244
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 244
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 245
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 245
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 246
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 246
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 247
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 247
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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acgcaaacgg cgtaa 2295

<210> 248
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 248

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 249
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 249

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acgcaaacgg cgtaa 2295

<210> 250
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 250
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20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 251
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 251
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 252
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 252

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 253
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 253
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 254
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 254
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 255
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 255
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 256
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 256

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
```

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu Tyr Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 257
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 257

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 258
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 258
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 259
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 259
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 260
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 260
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 261
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 261
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 262
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 262
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 263
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 263
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 264
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 264
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 265
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 265

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
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acgcaaacgg cgtaa 2295

<210> 266
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 266
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1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 267
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 267
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 268
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 268
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 269
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 269
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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acgcaaacgg cgtaa 2295

<210> 270
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 270
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 271
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 271
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 272
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 272
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 273
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 273

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 274
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 274
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 275
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 275

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 276
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 276
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

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Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 277
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 277
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 278
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 278
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 279
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 279

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcttgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagcta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 280
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 280
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 281
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 281
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 282
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 282
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 283
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 283
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 284
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 284

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 285
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 285
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 286
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 286
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 287
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 287

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 288
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 288
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 289
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 289
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 290
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 290
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 291

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 291
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 292
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 292
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 293
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 293

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 294
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 294
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 295
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 295

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 296
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 296
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 297
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 297
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 298
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 298

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 299
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 299
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

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acgcaaacgg cgtaa 2295

<210> 300
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 300
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 301
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 301

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 302
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 302
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 303
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 303
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 304
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 304
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 305
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 305
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 306
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 306
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr

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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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               725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 307
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 307

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 308
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 308
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 309
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 309

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 310
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 310
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 311
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 311
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaacaga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 312
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 312
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 313
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 313
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaggtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 314
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 314
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 315
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 315

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 316
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 316
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 317
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 317

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgagtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 318
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 318
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Glu Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 319
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 319
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtttct gtggggcggt 780
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 320
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 320

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 321
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 321
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 322
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 322
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 323
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 323

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 324
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 324
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 325
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 325

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 326
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 326
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 327
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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acgcaaacgg cgtaa 2295

<210> 328
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 328

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 329
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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acgcaaacgg cgtaa 2295

<210> 330
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 330
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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<210> 331
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 331
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 332
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 332
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
```

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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 333
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 333
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 334
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 334
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 335
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 335
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaaaaca ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 336

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 336
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320

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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 337
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 337
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 338
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 338
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 339
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 339
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
ccaggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 340
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 340
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 341
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 341
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 342
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 342
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 343
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 343
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 344
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 344
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 345
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 345

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 346
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 346
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 347
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 347
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatctct ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 348
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 348
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 349
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 349
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 350
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 350
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 351
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 351
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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acgcaaacgg cgtaa 2295

<210> 352
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 352
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 353
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 353

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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 354
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 354
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 355
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 355
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 356
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 356
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 357
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 357
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 358
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 358
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 359
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 359
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 360
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 360
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 361
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 361

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 362
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 362
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 363
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 363
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 364
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 364
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 365
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 365
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 366
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 366
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 367
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 367

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggatatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 368
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 368
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 369
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 369
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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acgcaaacgg cgtaa 2295

<210> 370
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 370
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ser Pro Ala Tyr Thr
20 25 30
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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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<210> 371
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 371

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<210> 372
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 372
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20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
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225 230 235 240
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 373
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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<210> 374
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 374
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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675 680 685
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690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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<223> Penicillin-G Acylates Variant from K. citrophila

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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 376
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 376
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 377
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 377
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcccttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 378
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 378
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

```
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 379
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 379
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 380
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 380

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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<210> 381
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 381
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acgcaaacgg cgtaa 2295

<210> 382
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 382
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 383
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 383

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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acgcaaacgg cgtaa 2295

<210> 384
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 384
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 385
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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acgcaaacgg cgtaa 2295

<210> 386
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 386
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1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 387

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 387
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 388
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 388
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 389
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 389

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 390
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 390
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 391
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 391
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 392
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 392
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 393
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 393
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 394
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 394

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 395
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 395
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtatct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 396
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 396
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Tyr
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 397
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 397

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaaca ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 398
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 398
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 399
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 399
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctca acgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 400
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 400
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 401
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 401
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 402
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 402
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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CX2-154WO1_ST25

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 403
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 403
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta gcggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 404
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 404
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 405
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 405

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 406
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 406
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 407
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 407
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gcggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcccttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 408
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 408
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 409
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 409
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
gataaacaga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 410
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 410
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Gln Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 411
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 411

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcact ttgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca ccggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcctt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 412
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 412
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp His Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Thr Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 413
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 413

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccctg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 414
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 414
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Leu Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Gln Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 415
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 415
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 416
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 416

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 417
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 417
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 418
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 418
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 419
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 419

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggatggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 420
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 420
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
```

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Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 421
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 421

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 422
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 422
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln

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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 423
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 423
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 424
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 424
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340   345   350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 425
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 425
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 426
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 426
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 427
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 427
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgggttgta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 428
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 428
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Gly Cys Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 429
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 429
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagtgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 430
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 430
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 431
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 431
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 432

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 432

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 433
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 433

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggt 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 434
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 434
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

```
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 435
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 435
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 436
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 436
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
```

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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 437
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 437
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc aatggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 438
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 438
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 439
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 439
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc gttggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 440
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 440
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

```
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 441
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 441

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 442
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 442
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 443
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 443
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa                                                  2295


<210> 444
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 444
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 445
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 445
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 446
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 446
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 447
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 447
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 448
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 448

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 449
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 449

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc taaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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ttctctgaca acaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 450
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 450
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
```

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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
    690                 695                 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 451
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 451
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 452
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 452
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
```

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 453
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 453
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 454
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 454
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 455
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 455
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctga aagcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca acaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 456
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 456
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Lys Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 457
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 457

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tactcggcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca acaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 458
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 458
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
    690                 695                 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 459
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 459
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccatg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc taaagaggaa cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 460
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 460
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Met Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 461
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 461
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc taaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 462
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 462
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 463
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 463

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 464
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 464
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 465
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 465

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 466
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 466
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
    690                 695                 700
Thr Thr Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 467
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 467

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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 468
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 468
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

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Lys Trp Tyr Leu Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 469
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 469
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380
ggcgtgccgc aggcggcagc taaagagtgc cgtcatcagt gcgagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 470
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 470
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Cys Arg His Gln Cys Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 471
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 471
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc taaagaggaa cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca acaccaccga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 472
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 472
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
    690                 695                 700
Thr Thr Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 473
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 473

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tactcggcca gtggctatga aaccaccatg 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc taaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 474
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 474

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
```

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    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Met Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
```

```
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 475
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 475
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggcagtct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcatg gaaagagtgc cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca acaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 476
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 476

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Trp Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Asn
    690                 695                 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 477
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 477
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacttggcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccca gaacttcttc 1380
ggcgtgccgc aggcggcagc taaagaggaa cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcact aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 478
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 478
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

```
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Leu Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Glu Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
```

```
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 479
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 479

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 480
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 480
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

```
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
```

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 481
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 481

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaacagat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tactcggcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc taaagagtgc cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga acttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 482
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 482
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Cys Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Leu Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 483

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 483
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggca cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 484
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 484
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 485
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 485

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 486
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 486
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 487
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 487

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 488
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 488
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 489
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 489
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 490
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 490

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 491
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acgcaaacgg cgtaa 2295

<210> 492
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 492

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asp	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 493
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 493

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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acgcaaacgg cgtaa 2295

<210> 494
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 494
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 495
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 495
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 496
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 496
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1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
        435                 440                 445
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 497
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 497
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 498
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 498
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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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               725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 499
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 499

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 500
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 500
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 501
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 501

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 502
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 502
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 503
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 503
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 504
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 504
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 505
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 505
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 506
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 506
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 507
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 507

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 508
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 508
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 509
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 509

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 510
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 510
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 511
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 511
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
gacaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 512
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 512

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Asp Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 513
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 513
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 514
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 514

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 515
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 515

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 516
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 516
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
```

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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 517
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 517

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acgcaaacgg cgtaa 2295

<210> 518
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 518
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 519
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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acgcaaacgg cgtaa 2295

<210> 520
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 520
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340   345   350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 521
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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acgcaaacgg cgtaa 2295

<210> 522
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 522
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 523
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 523
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagacccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 524
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 524
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Arg Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 525
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 525
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 526
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 526
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 527
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 527
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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acgcaaacgg cgtaa 2295

<210> 528

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 528

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 529
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 529

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 530
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 530
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 531
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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acgcaaacgg cgtaa 2295

<210> 532
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 532
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 533
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 533
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 534
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 534
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Asn Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 535
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 535
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 536
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 536

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 537
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 537

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 538
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 538
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 539
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 540
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 540
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 541
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
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tacggcaagc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 542
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 542
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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 543
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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acgcaaacgg cgtaa 2295

<210> 544
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 544
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 545
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 545

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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acgcaaacgg cgtaa 2295

<210> 546
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 546
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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545                 550                 555                 560
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 547
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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acgcaaacgg cgtaa 2295

<210> 548
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 548
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 549
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 550
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 550
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 551
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 551
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 552
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 552
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 553
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 553

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 554
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 554
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 555
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 555
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 556
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 556
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 557
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 557
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 558
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 558
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 559
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 559
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 560
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 560
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 561
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 561

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agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
```

```
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 562
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 562
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 563
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 563

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 564
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 564
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

```
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 565
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 565
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 566
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 566
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 567
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 567

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 568
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 568
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 569
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 569
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 570
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 570
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
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        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 571
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 571
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 572
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 572

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 573
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 573
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 574
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 574
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
```

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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 575
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 575

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 576
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 576
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 577
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 577
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 578
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 578
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 579

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 579
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 580
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 580
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 581
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 581

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 582
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 582
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 583
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 583

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 584
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 584
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 585
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 585
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 586
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 586

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 587
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 587
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 588
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 588

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 589
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 589

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 590
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 590
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 591
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 591
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 592
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 592
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 593
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 593
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 594
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 594
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 595
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 595
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 596
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 596
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 597
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 597

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 598
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 598
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 599
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 599
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 600
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 600
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 601
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 601
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acacaaacgg cgtaa 2295

<210> 602
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 602
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 603
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 603

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 604
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 604
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 605
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 605

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 606
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 606
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 607
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 607
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca attggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 608
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 608

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 609
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 609
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 610
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 610
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 611
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 611

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 612
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 612
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
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Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 613
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 613
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 614
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 614
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 615
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 615
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 616
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 616

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 617
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 617
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 618
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 618
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 619
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 619
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 620
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 620
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
```

```
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 621
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 621
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 622
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 622
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 623
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 623
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 624

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 624

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 625
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 625

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 626
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 626
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 627
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 627
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 628
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 628
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 629
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 629
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 630
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 630
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 631
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 631
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 632
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 632

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 633
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 633

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gacgtcgata gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 634
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 634
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 635
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 635
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 636
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 636
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 637
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 637
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gacgtcgata gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 638
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 638
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 639
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 639
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 640
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 640

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 641
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 641

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 642
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 642
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
```

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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 643
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 643
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 644
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 644
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
```

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 645
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 645
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 646
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 646

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 647
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 647
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 648
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 648
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 649
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 649

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 650
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 650
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 651
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 651
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 652
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 652
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 653
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 653
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 654
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 654
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 655
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 655

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 656
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 656
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 657
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 657
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 658
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 658
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Met Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 659
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 659

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 660
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 660
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 661
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 661
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 662
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 662

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asp	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25				30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75						80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155						160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235						240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 663
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 663

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 664
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 664
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
```

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
```

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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 665
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 665
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 666
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 666
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

```
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
```

```
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 667
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 667
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 668
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 668

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 669
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 669
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 670
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 670
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
```

```
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 671
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 671

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 672
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 672
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 673
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 673
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 674
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 674
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
```

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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 675

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 675
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 676
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 676
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Glu Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 677
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 677

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 678
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 678
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 679
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 679

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 680
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 680
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 681
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 681
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 682
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 682

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 683
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 683
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 684
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 684

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asp	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 685
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 685

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcagtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 686
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 686
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
```

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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 687
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 687

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 688
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 688
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 689
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 689
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 690
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 690
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
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```
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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CX2-154WO1_ST25

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 691
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 691
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 692
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 692
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 693
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 693

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 694
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 694
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 695
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 695
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 696
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 696
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 697
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 697
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 698
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 698
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser

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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 699
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 699

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 700
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 700
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 701
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 701

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 702
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 702
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
```

```
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 703
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 703
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 704
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 704

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 705
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 705
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 706
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 706

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

```
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

```
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 707
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 707

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 708
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 708
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

```
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
```

```
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 709
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 709

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 710
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 710
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

```
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 711
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 711
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 712
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 712

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 713
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 713
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 714
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 714
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 715
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 715
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 716
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 716
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 717
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 717
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 718
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 718
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 719
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 719
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 720

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 720

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 721
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 721

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 722
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 722
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 723
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 723
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 724
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 724
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 725
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 725
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 726
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 726
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 727
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 727
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 728
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 728

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asn Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 729
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 729

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 730
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 730
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 731
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 731
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 732
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 732
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
```

```
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 733
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 733
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 734
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 734
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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 735
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 735
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 736
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 736

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asp	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Phe
				245					250					255	

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 737
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 737

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 738
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 738
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 739
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 739
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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 740
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 740
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 741
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 741
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 742
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 742

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 743
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 743
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 744
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 744
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
```

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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 745
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 745

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agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 746
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 746
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 747
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 747
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 748
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 748
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
```

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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 749
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 749
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 750
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 750
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 751
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 751
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 752
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 752
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 753
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 753

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 754
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 754
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 755
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 755

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 756
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 756
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
```

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 757
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 757
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 758
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 758
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 759
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 759

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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```
gacgtcaccc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 760
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 760
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
```

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
```

```
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 761
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 761

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 762
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 762
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 763
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 763
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 764
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 764

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 765
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 765
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gacgtcgata catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 766
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 766
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 767
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 767

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 768
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 768
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 769
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 769

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 770
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 770
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
```

```
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 771

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 771
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 772
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 772
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 773
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 773

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 774
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 774
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
```

```
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 775
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 775

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 776
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 776
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 777
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 777
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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acgcaaacgg cgtaa 2295

<210> 778
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 778

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 779
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 779
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acgcaaacgg cgtaa 2295

<210> 780
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 780

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asp	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 781
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 781

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
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acgcaaacgg cgtaa 2295

<210> 782
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 782
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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 783
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 783
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 784
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 784
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1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 785
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 785
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 786
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 786
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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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CX2-154WO1_ST25

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 787
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 787
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 788
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 788
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 789
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 789

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 790
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 790
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 791
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 791
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 792
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 792
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 793
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 793
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 794
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 794
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 795
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 795

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 796
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 796
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 797
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 797

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 798
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 798
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 799
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 799
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 800
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 800

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 801
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 801
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 802
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 802

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 803
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 803

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 804
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 804
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 805
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 805
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 806
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 806
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 807
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 807
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc agtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 808
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 808

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gln Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 809
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 809
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 810
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 810

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
```

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 811
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 811
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 812
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 812
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 813
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 813
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggatgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 814
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 814
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Asp Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 815
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 815
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 816

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 816

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 817
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 817

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 818
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 818
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1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 819
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 819
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 820
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 820
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 821
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 821
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 822
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 822
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 823
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 823
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 824
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 824

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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
```

```
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 825
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 825

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcggcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 826
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 826
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Arg Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 827
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 827
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatc gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 828
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 828
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Arg Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 829
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 829
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 830
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 830
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Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 831
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 831
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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acgcaaacgg cgtaa 2295

<210> 832
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 832

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asp	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asp	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Phe
				245					250					255	

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 833
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 833

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gagcgaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 834
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 834
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Lys Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Ser Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 835
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 835
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggagggaa accgcagcag 1260
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gacgtcaccg gttggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc tgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 836
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 836
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
```

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 837
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 837
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca catggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa ggataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 838
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 838
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Thr Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Lys Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 839
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 839
agcaatatgt gggtgattgg caaagacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccc tgtggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgatc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc ggaagaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 840
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 840
Ser Asn Met Trp Val Ile Gly Lys Asp Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe His Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Leu Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Gly
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Glu Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 841
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 841

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 842
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 842
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 843
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 843
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 844
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 844
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 845
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 845
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 846
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 846
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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```
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
```

```
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 847
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 847
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 848
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 848
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 849
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 849

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 850
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 850
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 851
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 851

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 852
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 852
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 853
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 853
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 854
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 854

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75						80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130				135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155						160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210				215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235						240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 855
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 855

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa                                                  2295


<210> 856
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 856
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 857
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 857

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 858
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 858
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
```

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        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 859
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 859
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 860
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 860

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 861
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 861
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 862
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 862
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 863
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 863

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 864
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 864
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 865
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 865
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 866
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 866
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 867

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 867
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaatggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 868
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 868
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 869
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 869
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 870
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 870
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
```

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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 871
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 871

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 872
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 872
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
```

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 873
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 873
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 874
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 874

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 875
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 875
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 876
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 876
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 877
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 877

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 878
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 878
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 879
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 879
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 880
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 880
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 881
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 881
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 882
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 882
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 883
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 883
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 884
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 884
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 885
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 885

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 886
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 886
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 887
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 887
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 888
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 888
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 889
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 889
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 890
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 890
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 891
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 891

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 892
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 892
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

```
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
```

```
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 893
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 893

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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```
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 894
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 894
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
```

```
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

```
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 895
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 895
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 896
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 896

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 897
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 897
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 898
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 898

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

```
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

```
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 899
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 899

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
```

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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 900
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 900
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
```

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 901
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 901
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 902
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 902
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 903
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 903
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 904
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 904

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 905
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 905
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 906
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 906
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Arg

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 907
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 907
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 908
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 908
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 909
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 909
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 910
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 910
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 911
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 911
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 912

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 912

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 913
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 913

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 914
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 914
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
```

595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 915
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 915
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 916
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 916
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 917
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 917
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 918
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 918
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
435 440 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 919
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 919
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 920
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 920

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 921
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 921

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 922
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 922
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 923
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 923

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 924
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 924
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
```

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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 925
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 925
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 926
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 926
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

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        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 927
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 927
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 928
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 928

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
1				5				10						15	
Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	His	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Trp	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Asn	Ala	Phe
				245					250					255	

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 929
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 929

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 930
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 930
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
```

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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 931
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 931
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 932
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 932
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 933
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 933
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 934
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 934

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 935
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 935
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 936
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 936
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 937
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 937

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 938
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 938
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 939
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 939
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgtttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 940
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 940
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 941
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 941
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 942
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 942
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
```

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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 943
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 943

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccca aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 944
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 944
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

```
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 945
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 945

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaatgggat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattaca atgcgttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 946
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 946
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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Trp Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Asn Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Gln Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 947
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 947

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg aaacttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 948
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 948
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

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Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 949
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 949
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 950
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 950

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
```

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 951
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 951

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaaagtat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 952
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 952
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Lys
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 953
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 953
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct cgccagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 954
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 954
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60

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Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Arg Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 955
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 955
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ctgtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 956
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 956
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Leu Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 957
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 957
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
gcgtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 958
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 958
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Ala Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 959
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 959

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 960
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 960
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

```
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

```
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 961
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 961
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gtgggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 962
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 962
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Val Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 963
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 963
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aaaggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 964
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 964
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Lys Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 965
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 965

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gaaggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 966
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 966
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Glu Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
```

```
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 967
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 967
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 968
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 968
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 969
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 969
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccct ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 970
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 970

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 971
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 971
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccac taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 972
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 972

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Thr Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 973
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 973

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctactggcgt ttacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc cgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 974
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 974
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Pro Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 975
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 975
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 976
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 976
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Asp Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 977
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 977
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
gtttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 978
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 978
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340   345   350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Val Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 979
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 979
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 980
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 980

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Phe	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 981
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 981
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tgttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 982
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 982
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Cys Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 983
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 983
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
atttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 984
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 984
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

```
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Ile Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 985
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 985
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
atgtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 986

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 986

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
```

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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Met Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 987
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 987

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt tgcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 988
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 988
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Phe Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 989
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 989
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccgg ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 990
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 990
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Gly Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 991
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 991
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gggccgcagt ttggttggta tgcgccggcg tttacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 992
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 992
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Phe Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 993
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 993
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gggccgcagt ttggttggta tgcgccggcg ttgacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 994
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 994

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Leu Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 995
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 995

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gggccgcagt ttggttggta tgcgccggcg gtgacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 996
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 996
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Val Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

```
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 997
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 997
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 998
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 998
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Thr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 999
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 999
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gggccgcagt ttggttggta tgcgccggcg tgtacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1000
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1000
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Cys Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1001
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1001
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gggccgcagt ttggttggta tgcgccggcg aatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1002
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1002

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Asn Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1003
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1003

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gggccgcagt ttggttggta tgcgccggcg atgacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1004
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1004
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Met Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
```

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    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1005
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1005
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgcgccggcg aagacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1006
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1006
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Lys Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1007
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1007
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gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cataa 2295

<210> 1008
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1008
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1009
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1009
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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1010
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1010
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1011
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1011

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gggccgcagg ctggttggta tgtgccggcg tgtacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggcccgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1012
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1012
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Cys Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Pro Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1013
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1013
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1014
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1014
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1015
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1015
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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atgtgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1016
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1016
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Val Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1017
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1017
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgtg ctactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaggc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1018
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1018
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Gly Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1019
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1019

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1020
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1020
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1021
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1021

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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctacaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1022
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1022
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1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1023
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1023
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1024
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1024
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1025
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1025

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1026
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1026
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1027
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1027

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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt tcacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacggtc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1028
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1028
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Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Val Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1029
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1029
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg ttaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcagaaaacg atccgcgccg ccaactggtg 960
gataaactgg ctagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1030
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1030

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Phe Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1031
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1031
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1032
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1032
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

```
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1033
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1033

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg tggacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1034
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1034
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Trp Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1035
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1035
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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1036
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1036
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
```

```
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1037

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1037
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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cacgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccgcccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1038
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1038
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Thr Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Ala Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
```

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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1039
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1039

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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
aataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1040
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1040
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asn Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
```

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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1041
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1041

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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccta taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1042
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1042
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Tyr Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
```

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1043
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1043
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1044
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1044

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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1045
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1045
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcgttcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1046
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1046

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Tyr	Gly	Trp	Cys	Thr	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Phe	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210				215					220						
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260					265					270			

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Phe Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1047
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1047

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1048
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1048
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1049
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1049
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctatg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac tgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100
tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 1050
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1050

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
```

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Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Tyr Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1051
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1051
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gcggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1052
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1052
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
```

```
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Arg Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1053
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1053
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
atctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1054
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1054
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

```
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
```

```
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Ile Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1055
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1055

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcagccg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattccattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt tgcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1056
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1056
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Pro Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Phe Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1057
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1057
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gatagactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100
gtctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1058
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1058
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Arg Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Val Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1059
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1059
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttactt tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1060
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1060
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1061
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1061

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gggccgcagt ttggttggta tgtgccggcg tgtacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1062
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1062
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Cys Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1063
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1063

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1064
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1064
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1065
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1065
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaagccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt ttcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1066
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1066

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Ala Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Phe Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1067
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1067
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac caggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1068
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1068

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Gln Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1069
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1069

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaacac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1070
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1070
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Thr Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1071
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1071
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt tcacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1072
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1072
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1073
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1073
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgttaggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcgaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1074
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1074

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Arg Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Glu Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1075
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1075
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaagat gtacgagagc tttggccgta aatcgctgtg gttaacgccc 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcacctt agcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1076
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1076
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
```

625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Leu Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1077
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1077
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tatggtgata aggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1078
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1078
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Tyr Gly Asp Lys Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1079
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1079
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gggccgcagt ttggttggta tgtgccggcg gcaacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1080
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1080
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Ala Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1081
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1081
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aagggtgatc ttgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1082

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1082

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Lys Gly Asp Leu Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1083
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1083
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aagggtgata atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaccagat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1084
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1084
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Lys Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Pro Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1085
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1085
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gggccgcagt ttggttggta tgtgccggcg taccgttacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1086
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1086
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Arg
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

```
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
```

```
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1087
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1087
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccttgggt ggtggtgata cagtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1088
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1088
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Leu Gly Gly Gly Asp Thr Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1089
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1089
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atcatgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1090
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1090

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp His Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1091
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1091

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
gcagcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1092
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1092
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Ala Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1093
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1093
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggtgtcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1094
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1094
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Cys Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1095
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1095
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttg gggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1096
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1096
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Trp Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1097
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1097
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gaaggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1098
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1098

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Glu Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1099
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1099

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gagggtgata cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1100
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1100
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Glu Gly Asp Thr Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
```

```
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1101
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1101
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tggggtgata ctgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1102
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1102
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Trp Gly Asp Thr Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1103
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1103
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tggggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1104
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1104

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Trp Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1105
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1105
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tggggtgatt cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1106
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1106
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Trp Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1107
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1107

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gatggtgatc atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1108
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1108
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Asp Gly Asp His Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1109
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1109
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gatggtgata tggtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1110
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1110
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Asp Gly Asp Met Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1111
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1111
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gatggtgatc ttgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1112
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1112
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Asp Gly Asp Leu Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1113
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1113
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gagggtgata ctgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggtg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1114
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1114
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Glu Gly Asp Thr Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Val Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1115
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1115

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1116
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1116
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Trp Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1117
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1117

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gatggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1118
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1118
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Asp Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1119
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1119
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcgt atatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1120
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1120
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Tyr Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1121
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1121

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt catggtgata tggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1122
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1122
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1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Met Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1123
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1123
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ggcaccattt catggggatc caccgccggt attggtgatc aggtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atagcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1124
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1124
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly Ile Gly Asp Gln Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Ser Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1125
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1125
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt catggtgatc atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1126
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1126

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp His Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1127
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1127
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgtgg gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1128
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1128
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Trp Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1129
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1129

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt attggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggtgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1130
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1130
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Ile Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Val Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1131
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1131
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aatggtgatc aggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1132
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1132
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Asn Gly Asp Gln Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1133

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1133
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aatggtgatg cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1134
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1134
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Asn Gly Asp Ala Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
```

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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1135
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1135

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt catggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1136
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1136
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1137
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1137
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gggccgcagt ttggttggta tgtgccggcg ttgacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac caccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccgcccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac caggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaggc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1138
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1138
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Leu Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

```
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Thr Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Ala Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
```

```
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Gln Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Gly Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1139
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1139
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aatggtgatg ttgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctgcccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1140
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1140

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Asn Gly Asp Val Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Cys Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1141
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1141
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt catggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1142
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1142
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1143
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1143

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt catggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacacacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1144
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1144
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
```

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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1145
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1145
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt aatggtgatt ctgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 1146
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1146

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
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Trp Gly Ser Thr Ala Gly Asn Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1147
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1147
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg aggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1148
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1148
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Glu Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
```

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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1149
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1149
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tatggtgatt tggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1150
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1150
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Tyr Gly Asp Leu Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1151
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1151

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt catggtgatt ctgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1152
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1152
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1153
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1153
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt catggtgatg ctgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1154
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1154
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly His Gly Asp Ala Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1155
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1155
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cttggtgata tggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1156
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1156

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Leu Gly Asp Met Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1157
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1157

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt actggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1158
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1158
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Thr Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1159
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1159
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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1160
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1160
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1161
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1161
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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgataatt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1162
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1162

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Asn Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1163
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1163
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcagtttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1164
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1164

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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ser Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1165
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1165

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1166
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1166
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Glu Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1167
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1167

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tccatttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1168
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1168
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe His Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1169
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1169
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatatgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1170
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1170
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Met Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340   345   350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1171
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1171
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccat atggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1172
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1172
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Tyr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1173
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1173
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcaat tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1174
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1174
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Gln Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1175
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1175
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact taaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1176
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1176
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

```
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1177
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1177
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tctatttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1178

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1178

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Tyr Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
```

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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
```

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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1179
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1179

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttctat 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1180
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1180
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Tyr Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1181
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1181
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1182
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1182
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1183
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1183
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgtgtat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1184
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1184
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Cys
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1185
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1185
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacatg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1186
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1186

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1187
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1187

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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggccg tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1188
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1188
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Arg Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

```
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1189
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1189
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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgaaatg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1190
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1190
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80

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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Lys Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1191
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1191
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgaggtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1192
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1192
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Arg Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1193
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1193
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1194
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1194

Ser	Leu	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
1				5				10					15		
Ile	Met	Val	Asn	Gly	Pro	Gln	Tyr	Gly	Trp	Tyr	Ala	Pro	Ala	Tyr	Thr
			20					25				30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Cys	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
				245					250					255	

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1195
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1195

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agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1196
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1196
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1197
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1197
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1198
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1198
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1199
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1199
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1200
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1200

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Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1201
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1201
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1202
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1202
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
```

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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1203
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1203

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agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
```

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1204
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1204
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

```
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1205
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1205
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1206
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1206
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1207
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1207
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ggaccgcagt atggttggta tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1208
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1208
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1209
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1209

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1210
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1210
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1211
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1211

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1212
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1212
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Thr Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1213
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1213

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1214
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1214
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1215
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1215
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1216
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1216

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Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1217
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1217
agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320

gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1218
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1218
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1219
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1219

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agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1220
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1220
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

```
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
```

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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1221
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1221
agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1222
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1222

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Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
```

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1223
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1223
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1224
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1224
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1225
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1225

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ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1226
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1226
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1227
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1227
agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gtgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1228
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1228
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1229

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1229
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1230
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1230
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1231
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1231

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1232
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1232
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

```
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1233
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1233

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agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1234
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1234
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1235
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1235
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1236
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1236

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Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
```

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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1237
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1237
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 1238
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1238

Ser	Leu	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Ala	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Tyr	Gly	Trp	Tyr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Cys	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75						80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Ala	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155						160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210				215					220						
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Lys	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235						240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260					265					270			

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1239
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1239

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1240
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1240
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1241
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1241

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1242
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1242
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

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Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1243
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1243
agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1244
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1244
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Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
```

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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
```

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1245
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1245
agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcact gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1246
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1246
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1247
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1247

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agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgacctg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1248
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1248
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1249
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1249
agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

acgctgcacg gcaacgtcat taaaaccgat gcggcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggtgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1250
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1250
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Ala Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1251
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1251
agcttgatgt gggtgattgg caaaaacaaa gccgcggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgaaat cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg atcgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1252
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1252
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Ala Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Lys Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1253
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1253

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agcttgatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga tgagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1254
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1254
Ser Leu Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Glu Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1255
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1255

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa aaggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1256
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1256
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Lys
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
```

```
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1257
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1257
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcatt gaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1258
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1258
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Leu Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1259
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1259
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
ggaccgcagt atggttggta tgcgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1260
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1260

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Ile Met Val Asn Gly Pro Gln Tyr Gly Trp Tyr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
```

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Thr Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
```

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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1261
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1261

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1262
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1262
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

```
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1263
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1263

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggcaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtgatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagataaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1264
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1264
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

```
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1265
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1265

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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tattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 1266
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1266
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Tyr Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1267
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1267
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ggcaccattt catggggatc caccgccggt ctgggtgatg gtgtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1268
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1268

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr
			20					25				30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Leu	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130				135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210				215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1269
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1269

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ggcaccattt catggggatc caccgccggt tgtggtgatg gtgtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1270
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1270
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

```
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
```

```
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1271
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1271

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cgtggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1272
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1272
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

```
    50                  55                  60
Trp Gly Ser Thr Ala Gly Arg Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
```

```
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1273
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1273
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1274
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1274

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1275
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1275
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1276
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1276
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1277
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1277

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctgtt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1278
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1278
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1279
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1279
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctactggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1280
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1280
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1281

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1281
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctactggcgt ttacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1282
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1282
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Phe Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1283
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1283

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1284
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1284
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

```
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
```

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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1285
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1285
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cagggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggt cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1286
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1286
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gln Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Ser Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1287
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1287
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1288
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1288

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1289
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1289
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1290
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1290

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Phe	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210				215					220						
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260					265					270			

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1291
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1291

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
gtttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1292
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1292
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
```

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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Val Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1293
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1293

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgtcggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgtccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaagcg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1294
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1294
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Ser Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
    50 55 60

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Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Ser
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Ser Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1295
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1295
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcgg 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gggggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1296
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1296
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Arg Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Gly Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
```

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1297
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1297
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg cacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcatctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttctctc 1920

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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 1298
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1298

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala His Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Ile Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
```

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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1299
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1299

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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaaccgt 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggtaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1300
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1300
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Arg
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1301
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1301
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gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tgcggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgtgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctattcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1302
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1302
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Cys Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1303
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1303
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagg ctggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1304
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1304
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Ala Gly Trp Tyr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Leu Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
```

```
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1305
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1305

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctctt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatac ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1306
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1306
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Thr Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1307
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1307

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1308
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1308
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Cys Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1309
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1309
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
aatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1310
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1310

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asn Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1311
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1311
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcacatt tggtcacaac 180
ggcaccattt catggggatc caccgccggt tttggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1312
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1312

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Thr Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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```
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Trp Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1313
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1313

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
```

<210> 1314
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1314

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1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
```

```
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
```

```
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1315
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1315

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
```

ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1316
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1316
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

```
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
```

```
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1317
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1317
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1318
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1318
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1319
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1319
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1320
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1320
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1321
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1321
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1322
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1322
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1323
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1323
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1324
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1324
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1325
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1325
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1326

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1326

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1327
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1327

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1328
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1328
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1329
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1329
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1330
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1330
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
```

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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1331
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1331
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1332
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1332
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1333
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1333
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1334
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1334

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
```

```
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1335
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1335

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
```

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1336
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1336
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1337
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1337

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
```

```
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1338
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1338
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
```

```
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1339
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1339
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1340
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1340
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1341
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1341
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1342
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1342

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1343
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1343

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1344
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1344
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1345
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1345

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1346
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1346
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1347
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1347
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1348
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1348

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1349
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1349
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1350
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1350
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
```

```
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1351
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1351

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1352
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1352
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1353
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1353
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1354
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1354
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1355
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1355
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1356
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1356
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1357
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1357
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560

tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1358
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1358
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1359
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1359

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
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```
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1360
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1360
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
```

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1361
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1361

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1362
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1362
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1363
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1363
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1364
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1364

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Trp	Gly	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1365
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1365

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1366
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1366
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
```

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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1367
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1367

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacggaccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1368
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1368
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1369
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1369
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1370
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1370

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
```

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1371
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1371
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1372
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1372
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

```
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1373
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1373

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1374
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1374
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1375
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1375
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1376
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1376
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1377

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1377
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1378
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1378
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
```

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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1379
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1379

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
```

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1380
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1380
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1381
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1381
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1382
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1382
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1383
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1383
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
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acgcaaacgg cgtaa 2295

<210> 1384
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1384

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1385
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1385
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ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acgcaaacgg cgtaa 2295

<210> 1386
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1386

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Ser	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210				215					220						
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260					265					270			

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 1387
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1387

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acgcaaacgg cgtaa 2295

<210> 1388
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1388
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35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
```

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1389
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1389
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1390
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1390
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1391
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1391
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1392
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1392
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1393
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1393
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1394
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1394
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1395
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1395

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1396
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1396
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1397
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1397
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1398
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1398
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1399
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1399
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1400
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1400
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1401
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1401

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1402
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1402
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1403
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1403

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1404
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1404
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1405
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1405
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1406
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1406

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1407
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1407
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1408
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1408
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1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1409
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1409
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440

acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1410
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1410
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

```
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
```

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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1411
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1411

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1412
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1412
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu

```
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1413
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1413
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1414
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1414

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
```

```
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1415
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1415
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1416
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1416
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1417
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1417
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1418
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1418
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1419
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1419
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1420
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1420
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1421
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1421
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1422

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1422

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
```

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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1423
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1423

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1424
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1424
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
```

595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1425
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1425
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1426
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1426
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1427
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1427
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1428
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1428
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1429
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1429
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1430
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1430
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1431
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1431

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1432
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1432
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1433
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1433
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

```
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgtcatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1434
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1434
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Val Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1435
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1435
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1436
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1436
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

```
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
```

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1437
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1437
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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acgcaaacgg cgtaa 2295

<210> 1438
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1438

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Val	Phe	Gly	Phe
				245					250					255	

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 1439
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1439

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1440
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1440
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1441
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1441

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1442
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1442
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
```

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1443
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1443
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1444
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1444

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1445
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1445
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1446
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1446
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

```
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1447
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1447

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1448
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1448
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1449
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1449
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1450
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1450
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1451
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1451
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1452
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1452
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
```

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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1453
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1453

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1454
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1454
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

```
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1455
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1455

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 1456
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1456

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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```
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

```
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1457
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1457

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1458
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1458
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1459
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1459
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tgggttgatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1460
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1460
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Leu Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
```

```
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1461
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1461

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1462
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1462
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
```

```
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1463
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1463

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1464
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1464
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
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    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1465
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1465
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1466
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1466

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
```

```
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1467
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1467

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1468
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1468
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

```
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
```

```
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1469
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1469

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1470
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1470
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

```
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1471
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1471
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1472
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1472
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
```

405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1473

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1473
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1474
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1474
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
```

```
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1475
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1475

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1476
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1476
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
```

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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1477
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1477

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1478
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1478
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1479
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1479
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1480
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1480

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1481
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1481
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1482
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1482
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1483
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1483

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1484
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1484
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
```

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545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1485
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1485
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1486
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1486
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1487
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1487
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1488
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1488
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1489
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1489
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1490
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1490
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1491
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1491

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1492
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1492
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1493
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1493
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1494
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1494
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1495
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1495
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1496
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1496
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
```

```
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1497
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1497

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1498
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1498
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
```

```
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1499
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1499

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
```

```
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1500
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1500
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
```

```
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

```
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1501
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1501
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1502
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1502

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1503
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1503
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1504
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1504
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1505
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1505

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1506
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1506
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1507
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1507

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1508
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1508
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1509
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1509
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgt ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1510
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1510

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Val Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1511
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1511
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1512
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1512
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1513
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1513
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1514
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1514
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1515
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1515
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1516
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1516
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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```
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1517
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1517
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1518

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1518

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1519
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1519

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1520
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1520
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1521
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1521
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1522
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1522
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
```

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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1523
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1523
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1524
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1524
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1525
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1525
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1526
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1526

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
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Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1527
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1527

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1528
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1528
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1529
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1529
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720

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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 1530
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1530

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
```

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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
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Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1531
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1531
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1532
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1532
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
```

```
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1533
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1533
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1534
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1534

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
```

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1535
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1535

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1536
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1536
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
```

```
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1537
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1537

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1538
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1538
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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```
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1539
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1539
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1540
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1540

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
```

705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1541
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1541
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1542
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1542
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
```

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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1543
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1543

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
```

caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1544
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1544
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1545
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1545
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1546
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1546
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1547
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1547
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1548
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1548
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1549
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1549

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1550
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1550
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

```
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

```
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1551
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1551

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
```

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1552
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1552
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1553
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1553

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1554
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1554
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1555
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1555
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1556
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1556
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
```

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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1557
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1557

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1558
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1558
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
```

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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1559
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1559
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1560
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1560
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

```
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
```

```
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1561
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1561
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1562
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1562

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
```

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1563
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1563
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1564
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1564
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
```

```
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1565
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1565

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1566
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1566
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

```
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1567
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1567
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1568
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1568
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1569

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1569
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1570
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1570
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
```

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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1571
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1571

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1572
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1572
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

```
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
```

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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1573
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1573
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1574
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1574
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

```
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
```

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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1575
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1575
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1576
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1576

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1577
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1577
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggctgt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1578
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1578

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
1				5				10						15	
Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Val	Trp	Gly	Phe
				245					250					255	
Leu	Trp	Gly	Cys	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1579
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1579

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1580
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1580
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1581
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1581
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1582
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1582
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1583
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1583
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1584
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1584
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1585
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1585
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1586
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1586
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1587
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1587

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1588
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1588
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

```
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1589
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1589
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1590
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1590
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1591
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1591
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1592
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1592
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1593
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1593

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1594
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1594
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1595
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1595

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
```

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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1596
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1596
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
```

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1597
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1597
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1598
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1598

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1599
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1599
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1600
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1600
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1601
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1601

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1602
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1602
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1603
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1603

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1604
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1604
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1605
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1605
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1606
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1606

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1607
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1607
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1608
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1608
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1609
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1609
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1610
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1610
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
```

```
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1611
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1611
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1612
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1612
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

```
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

```
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1613
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1613
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1614

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1614

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1615
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1615

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1616
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1616
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1617
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1617
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1618
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1618
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1619
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1619
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1620
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1620
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
```

385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1621
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1621
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1622
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1622

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
```

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
```

```
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1623
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1623

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
```

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1624
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1624
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1625
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1625

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
```

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aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1626
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1626
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65                  70                  75                  80
```

```
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1627
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1627
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1628
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1628
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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           740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1629
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1629

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1630
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1630

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Trp	Ala	Phe
				245					250					255	

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1631
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1631

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1632
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1632
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

```
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
```

```
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1633
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1633
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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1634
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1634
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

```
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
```

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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1635
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1635
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1636
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1636

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1637
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1637
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1638
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1638
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

```
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
```

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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1639
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1639

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
```

caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1640
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1640
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1641
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1641
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
aatgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1642
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1642
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asn Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1643
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1643
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1644
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1644
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1645
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1645

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1646
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1646
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1647
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1647
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1648
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1648
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1649
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1649

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1650
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1650
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340   345   350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355   360   365

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Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1651
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1651
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1652
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1652
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1653
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1653

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1654
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1654
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
```

```
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
```

```
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1655
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1655

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
```

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1656
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1656
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

```
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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```
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1657
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1657
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1658
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1658

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
```

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1659
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1659
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgcatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1660
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1660
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

```
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
```

```
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1661
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1661

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
```

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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 1662
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1662

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                   10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
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```
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
```

```
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1663
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1663
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300

agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1664
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1664
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
```

405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1665

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1665
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1666
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1666
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
```

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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1667
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1667

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1668
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1668
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1669
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1669
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1670
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1670
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
```

```
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1671
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1671
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1672
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1672

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1673
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1673
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1674
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1674

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
1				5				10						15	
Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Val	Phe	Ala	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		

```
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1675
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1675

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1676
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1676
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1677
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1677
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggtg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1678
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1678
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Val Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1679
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1679
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1680
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1680
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
```

725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1681
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1681
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1682
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1682
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1683
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1683

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1684
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1684
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

```
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1685
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1685
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1686
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1686
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1687
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1687
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1688
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1688
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val

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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1689
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1689

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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1690
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1690
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1691
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1691

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1692
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1692
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1693
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1693
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tgggggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1694
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1694

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Trp Gly Pro Pro
    370                 375                 380
```

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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1695
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1695
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1696
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1696

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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```
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
```

```
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1697
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1697

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatc cggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

<210> 1698
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1698
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Pro Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1699
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1699

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1700
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1700
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1701
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1701
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gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt ggggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1702
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1702
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65   70   75   80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85   90   95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100   105   110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115   120   125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225   230   235   240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340   345   350

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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1703
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1703
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt gggcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttgctgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1704
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1704
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Cys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1705
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1705

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgtgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
tttgggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1706
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1706
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1707
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1707
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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcgtgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
aaagggccac cgggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1708
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1708
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Arg Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Pro
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1709
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1709
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggac cgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata gcgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcggcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagatt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1710

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1710

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Ile Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
```

```
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1711
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1711

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1712
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1712
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1713
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1713
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actagtacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1714
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1714
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

```
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ser Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
```

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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1715
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1715
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacga tgaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1716
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1716
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Met Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1717
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1717
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaatgga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1718
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1718

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Trp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
```

```
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1719
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1719

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatcgtt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
```

gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1720
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1720
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

```
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Arg Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1721
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1721
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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
```

```
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagat gtactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1722
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1722
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
```

```
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Met Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1723
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1723
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagcg ttactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1724
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1724
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Arg Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1725
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1725
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1726
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1726

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1727
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1727

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat cttgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1728
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1728
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Leu Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1729
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1729

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcgttgcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1730
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1730
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Val Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 1731
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1731
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
ttggggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1732
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1732

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Leu Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1733
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1733
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
cgtgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1734
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1734
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Arg Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
```

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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1735
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1735

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actggtacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1736
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1736
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Gly Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1737
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1737
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcaag taaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1738
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1738
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ser Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1739
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1739
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc tgatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1740
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1740
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

```
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
```

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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1741
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1741

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgtatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1742
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1742
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

```
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Tyr
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
```

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1743
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1743
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780

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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagtta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 1744
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1744

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
```

```
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

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465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Val Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1745
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1745

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gccatgcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1746
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1746
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly His Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1747
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1747
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagcaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100

ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1748
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1748

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Ala Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1749
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1749

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
caagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1750
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1750
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Gln Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1751
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1751
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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaaggtt tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1752
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1752
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Val Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1753
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1753
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gctgtgcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1754
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1754

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Cys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
```

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1755
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1755
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1756
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1756
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

```
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1757
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1757

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1758
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1758
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
```

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Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1759
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1759

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatatgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1760
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1760
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Met Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1761

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1761
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgcatct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1762
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1762
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala His
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
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Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1763
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1763

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
```

caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaacgttt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1764
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1764
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
```

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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Arg Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1765
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1765
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
cgtgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1766
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1766
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Arg Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
```

```
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1767
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1767
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1768
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1768

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1769
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1769
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ggggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1770
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1770
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1771
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1771

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1772
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1772
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
```

545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Leu Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1773
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1773
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600

cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgctttgtt tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1774
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1774
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1   5   10   15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
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Ala Met Ala Leu Cys Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1775
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1775
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1776
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1776
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Val Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1777
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1777
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
aaagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920

tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1778
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1778
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

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Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Lys Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1779
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1779

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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tttgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta cccaagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1780
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1780
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Phe Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
```

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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Lys
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1781
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1781
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaatata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1782
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1782
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Tyr Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1783
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1783
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1784
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1784

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
```

```
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
```

```
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1785
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1785

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaacgta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1786
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1786
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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```
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Arg Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1787
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1787

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaattta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1788
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1788
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

```
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
```

```
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Phe Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1789
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1789
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaaaa ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1790
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1790

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Lys Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1791
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1791
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1792
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1792

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
```

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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Tyr Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1793
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1793

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
attgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1794
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1794
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Ile Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1795
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1795

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1796
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1796
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1797
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1797
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1798
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1798

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1799
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1799
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaaaata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1800
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1800
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asn Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1801
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1801
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaacgta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1802
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1802
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Arg Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1803
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1803
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
caagggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1804
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1804
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Gln Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1805
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1805
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccac gtggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1806

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1806

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Arg
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1807
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1807
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740

cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1808
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1808
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
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595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ile Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1809
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1809
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatgttt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960

gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1810
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1810
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
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Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1811
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1811
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatagtt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1812
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1812
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Ser Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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385 390 395 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1813
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1813
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280

acgcaaacgg cgtaa 2295

<210> 1814
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1814

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Arg Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
```

```
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1815
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1815

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggctcgct ggaaatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1816
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1816
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Glu Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

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                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1817
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1817

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
```

```
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccac aaacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1818
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1818
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Thr Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
```

```
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1819
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1819
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgcag ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccca 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1820
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1820
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Ser Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
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        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Pro Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
```

740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1821
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1821
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagctata gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040

cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1822
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1822

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
				245					250					255	

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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Tyr Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
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Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1823
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1823

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcaaaa gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1824
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1824
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Lys Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1825
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1825

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccaaaga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1826
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1826
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

```
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
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Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Lys Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1827
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1827
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtcgt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1828
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1828

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1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
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                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Arg Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
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705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1829
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1829
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taaagcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcaac aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800

gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1830
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1830
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

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Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Lys Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Thr Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
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Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1831
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1831

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattggtaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1832
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1832
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
```

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            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Gly Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1833
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1833
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240

aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgcaaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1834
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1834
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Ala Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1835
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1835
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtcgt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1836
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1836
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Arg Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
```

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        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1837
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1837

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattaataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1838
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1838
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

```
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
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Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asn Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1839
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1839

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgaaac agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1840
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1840
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Lys Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
```

```
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1841
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1841

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattcataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1842
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1842
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

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Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile His Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1843
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1843
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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatgc aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acgcaaacgg cgtaa 2295

<210> 1844
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1844

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65				70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
			85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
		100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
130					135					140					
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145				150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225				230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
			245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp

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            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Ala Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
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                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 1845
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1845

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1846
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1846
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Lys Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1847
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1847

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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1848
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1848
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
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        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Arg Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1849
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1849
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattaggaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1850
<211> 764
<212> PRT

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1850

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Arg Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
```

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Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1851
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1851

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcgtcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1852
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1852
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

```
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Arg Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
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    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1853
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1853

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattcaaaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1854
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1854
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Ser Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

```
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
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```
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Gln Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1855
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1855

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtcgt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1856
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1856
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr

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            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
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405 410 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Arg Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1857

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1857
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattagtaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1858
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1858
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
```

```
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
```

```
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Ser Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1859
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1859

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat ttggaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1860
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1860
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
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            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1861
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1861
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcgaaagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1862
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1862
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
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Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Glu Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1863
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1863
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60

gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctga cagcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1864
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1864

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Thr Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
```

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    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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755 760

<210> 1865
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1865
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcccattcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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acgcaaacgg cgtaa 2295

<210> 1866
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1866

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Pro	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		

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Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
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Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<210> 1867
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1867

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1868
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1868
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
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545 550 555 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605
Val Ser Glu Val Leu Gly Lys Ala Phe Cys Ser Phe Asp Lys Asp Ile
610 615 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1869
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1869
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1870
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1870
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50 55 60

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Glu Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
```

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Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```

<210> 1871
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>

<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1871
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccatgggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1872
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1872
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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Met Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
```

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            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
```

```
               725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1873
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1873

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctga cagcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1874
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1874
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

```
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Thr Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
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Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1875
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1875

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctga aagcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1876
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1876
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Lys Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
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        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1877
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1877
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgcaggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg tcgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360

acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1878
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1878
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Val Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
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Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1879
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1879
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
cattctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1880
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1880

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
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305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg His Ser Asp Ser
```

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    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1881
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1881

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggaaaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1882
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1882
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

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Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Lys Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
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Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1883
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1883

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc cacccttggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1884
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1884
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Leu Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
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                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1885
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1885
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120

ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga agttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1886
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1886

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
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Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Val Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1887
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1887
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aatggataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220

gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1888
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1888

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
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            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Met Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1889
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1889

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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcaaattcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1890
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1890
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

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Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Lys Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
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Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1891
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1891

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ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1892
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1892
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu

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65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Thr Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
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    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1893
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1893
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tccgtttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1894
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1894

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Arg Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
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Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1895
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1895
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgttggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980

aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1896
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1896
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Val Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
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625 630 635 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 1897
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1897
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggcgta ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295


<210> 1898
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1898
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
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Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Arg Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
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Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1899
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1899
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420

cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcagtagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1900
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1900
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
```

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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Ser Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 1901
<211> 2295
<212> DNA

<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1901
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcagtagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

<210> 1902

<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Penicillin-G Acylates Variant from K. citrophila

<400> 1902

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1               5                  10                  15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
                85                  90                  95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
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Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
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Ser Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
```