SEQUENCE LISTING

<110> CODEXIS, INC.
ALVIZO, OSCAR
ELGART, DAVID
ORR, ROBERT KEVIN
RIGGINS, JAMES NICHOLAS
FRYSZKOWSKA, ANNA
LEXA, KATRINA W.
YI, XIANG
DUAN, DA
MOFFETT, COURTNEY DIANNE
DELLAS, NIKKI
MITCHELL,VESNA

<120> PENICILLIN-G ACYLASES

<130> CX2-161USP2

<140> TO BE ASSIGNED
<141> 2017-03-16

<160> 202

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

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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<210> 2
<211> 846
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 2

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Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala Asp
        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
65                  70                  75                  80
Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile Arg
                85                  90                  95
Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu Ser
            100                 105                 110
Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn Ala
        115                 120                 125
Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln Gln
    130                 135                 140
Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp Val
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145                 150                 155                 160
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Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys Tyr
            180                 185                 190
Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu Val
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Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr Pro
    210                 215                 220
Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala Ala Leu Leu Pro Arg
225                 230                 235                 240
Tyr Asp Gln Pro Ala Pro Met Leu Asp Arg Pro Ala Lys Gly Thr Asp
                245                 250                 255
Gly Ala Leu Leu Ala Leu Thr Ala Asp Gln Asn Arg Glu Thr Ile Ala
            260                 265                 270
Ala Gln Phe Ala Gln Ser Gly Ala Asn Gly Leu Ala Gly Tyr Pro Thr
        275                 280                 285
Thr Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys
    290                 295                 300
Ala Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Tyr
305                 310                 315                 320
Thr Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn
                325                 330                 335
Thr Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile
            340                 345                 350
Ser Trp Gly Ser Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala
        355                 360                 365
Glu Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu
    370                 375                 380
Trp Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly
385                 390                 395                 400
Gln Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile
                405                 410                 415
Lys Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp
            420                 425                 430
Asp Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys
        435                 440                 445
Ala Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu
    450                 455                 460
Thr Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val
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His Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu
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Pro Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe
            500                 505                 510
Asp Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn
        515                 520                 525
Trp Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala
    530                 535                 540
Phe Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu
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Asp Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg
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Gln Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu
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Lys Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu
        595                 600                 605
Val Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp
    610                 615                 620
Gly Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu
625                 630                 635                 640
Thr Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe
                645                 650                 655
Gly Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro
            660                 665                 670
Thr Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala
        675                 680                 685
Leu Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly
    690                 695                 700
Gly Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp
705                 710                 715                 720
Gln Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr
                725                 730                 735
Pro Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro
            740                 745                 750
Gln Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg
        755                 760                 765
Gly Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg
    770                 775                 780
Pro Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile
785                 790                 795                 800
Ala Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met
                805                 810                 815
Tyr Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val
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Asp Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Arg
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<210> 3
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 3

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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
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acgcaaacgg cgtaa 2295

<210> 4
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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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 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
            100                 105                 110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
        115                 120                 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130                 135                 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145                 150                 155                 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
                165                 170                 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225                 230                 235                 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr 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
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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
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<210> 5
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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acgcaaacgg cgtaa 2295

<210> 6
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 6
Ser Asn Met Trp Val Ile Gly 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

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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 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> 7
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 7
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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 tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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> 8
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 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> 9
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 9
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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 tctgatgtgt gggcgttcct 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
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> 10
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 10
Ser Asn Met Trp Val Ile Gly 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
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
```

```
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 11
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 11
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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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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> 12
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 12
Ser Asn Met Trp Val Ile 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 Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln 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> 13
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 13
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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
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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> 14
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Val Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr 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 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
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile 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> 15
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 15
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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 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
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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> 16
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 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

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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
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
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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> 17
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 17

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

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 18
Ser Asn Met 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

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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
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln 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 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> 19
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 19
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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
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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
gataaaagga ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca 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> Variant of Penicillin G Acylase From Kluyvera 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
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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
        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
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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> 21
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 21
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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
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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 aattaggaac 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> Variant of Penicillin G Acylase From Kluyvera 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
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly 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
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser 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 Arg Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser 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> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 23
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt atgggtgatg 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
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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 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> 24
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 24
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 Met Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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

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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 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
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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> 25
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 25
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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 ttgcggttct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
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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> 26
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 26
Ser Asn Met Trp Val Ile Gly 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 Val
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 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
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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> 27
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 27
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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 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 gaacatcgca 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 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> 28
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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

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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 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 Ala Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val 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
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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> 29
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 29
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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 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 gaacatcaga 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 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 atggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

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

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 30
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 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 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 Arg Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val 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
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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> 31
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 31
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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 ttgcgttgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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> 32
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 32
Ser Asn Met Trp Val Ile Gly 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe 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 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> 33
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 33
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cttggtgatg 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
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gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 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
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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> 34
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 34
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 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 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

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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 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> 35
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 35
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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 ttgcgaaact gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
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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> 36
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 36
Ser Asn Met Trp Val Ile Gly 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 Lys
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 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> 37
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 37
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acgattaacg 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 cgtctggttt 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 38

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Asp 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 Ile 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 39
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 39
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 40

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 40
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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 41
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 41
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagcg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca 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 cgtctggttt 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 42

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 42
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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Ala 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Asp 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 43
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 43
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 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
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 44

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Asp 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 Ala
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 45
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 45
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagca ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 46

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Asp 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 Gln Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 47
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca 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 aggtacagtc ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 1860
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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 48

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 48
Ser Asn Met Trp Val Ile Gly 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Asp 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 Ser Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 49
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 49
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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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 cgtctggttt 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
ttctctgacg ctaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 50

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 50
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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Asp 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 Ala
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 51
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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ggctatgacg tcaccggcaa tacgccgttt gccctaccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat gaagcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgcataccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcggt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgatg ggtggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgtcgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgata gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 52

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 52
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 Leu Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Glu Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
    130   135   140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145   150   155   160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala His Thr
                165   170   175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro Arg 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys 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 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
Ser Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 53
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 53
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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
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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 tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagaag tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 cgtctggttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 54

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 54
Ser Asn Met Trp Val Ile Gly 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Lys Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 55
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 55
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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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 ttgcgctgct gtggggcggt 780
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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 56

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 56
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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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 57
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 57
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 58

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 59
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 59
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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
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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
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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
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gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 60

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
            20   25   30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35   40   45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 61
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 62

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 62
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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 63
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 64

<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 64
Ser Asn Met Trp Val Ile Gly 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 65
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 65
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgata acgtcgatat 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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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> 66

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

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 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 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 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> 67
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 67
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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
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca 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> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 68
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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 Asn Ala Trp Leu 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
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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
        755                 760
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<210> 69
<211> 2295

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 69
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
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca 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> Variant of Penicillin G Acylase From Kluyvera 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 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
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu

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

<400> 71
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca 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 ttcgcatgaa 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> 72
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 72
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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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

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

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 73
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 tgtcaggtcg ctacggtaac 1320
gacgtcgaca 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 cgtctggttt 1860
gataaagata ttcgcatgaa 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> 74
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 74

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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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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
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            420                 425                 430
Thr Leu Ser Gly Arg Tyr Gly Asn Asp Val Asp 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg Met 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> 75
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila
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<400> 75
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca 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 cgtctcgttt 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 gcaccagcaa aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgacc 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> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
            20                  25                  30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35                  40                  45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys 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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Asp 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 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 Lys 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> 77
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 77
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc gaccgccggt cagggtgatg 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 tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca 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> 78
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 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 Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys 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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Asp Asn 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 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> 79
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 79
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

ggcaccattt catggggagc gaccgccggt atgggtgatg 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 ttgcgaggct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 gaacatcgca gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaggtcg ctacggtaac 1320
gacgtcgaca 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 cgtctggttt 1860
gataaagata ttcgcgagaa 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> 80
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala 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 Ala Thr Ala Gly Met Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys 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 Ala Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Gly Arg Tyr Gly Asn Asp Val Asp 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
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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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg Glu 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> 81
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 81
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca 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 cgtctggttt 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
tacggcaaac 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> Variant of Penicillin G Acylase From Kluyvera 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 Thr Ala Pro Ala Tyr Thr
20 25 30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Asp 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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> 83
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 83
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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 catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
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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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcacta 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 cgtctggttt 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
tacggcaaac 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> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 84
Ser Asn Met Trp Val Ile Gly 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 Ala Thr Ala Gly Gln 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 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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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
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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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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> 85
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 85
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

tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 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> 86
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 86
Ser Asn Met Trp Val Ile 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

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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
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln 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> 87
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 87
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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 catggggagc gaccgccggt cagggtgatg 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
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 cagcgagctt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca actggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca ctatgattgt 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 cgtctcgttc 1860
gataaactta 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 agttgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcg 2220
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 88
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 88
Ser Asn Met Trp Val Ile Gly 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Phe Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Ser 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Thr 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
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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 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 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 89
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 89
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc taccgccggt cagggtgatg 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
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 cgtctggttt 1860
gataaactta 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 90
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Phe Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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
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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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 91
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 91
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttggtctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct 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 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 cgtctggttt 1860
gataaactta 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 92
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 92
Ser Asn Met Trp Val Ile Gly 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Phe Gly Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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
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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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 93
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 93
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact tggcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc 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 ccggcgggct 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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gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 94
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Leu Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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
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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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 95
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 95
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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
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ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatccag 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 acgtcgggtg accgcccggt tcttgcctgg 1500
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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 96
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Phe Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Gln Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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
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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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 97
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 97
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgttca tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 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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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg 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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tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa                              2313
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<210> 98
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 98

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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 His Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys 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 Phe Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
```

<210> 99
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 99
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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 cgtctggttt 1860
gataaactta 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 100
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 100
Ser Asn Met Trp Val Ile Gly 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 Cys Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Phe Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu 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 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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
```

<210> 101
<211> 2298
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 101
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atgagcaata tgtgggtgat tggcaaaaac aaagcccagg atgcgaaggc cattatggtc 60
aatgggccgc agtttggttg gtatgtgccg gcgtacacct acggtatcgg cctgcacggc 120
gcgggctatg acgtcaccgg caatacgccg tttgcctatc cgggcctcgt ttttggtcac 180
aacggcacca tttcatgggg atccaccgcc ggtgggggtg atgatgtcga tatctttgcc 240
gaaaaacttt ccgccgagaa gccgggctat taccagcata acggcgagtg ggtgaagatg 300
ttgagccgca aggagactat tgcggtcaaa gacggccagc cggagacctt taccgtttgg 360
cgcacgctgc acggcaacgt cattaaaacc gatactgcga cgcagaccgc ctatgccaaa 420
gcgcgcgcct gggatggcaa agaggtggcg tccctgctgg cgtggacgca ccagatgaag 480
gccaaaaact ggccggagtg gacgcagcag gcggccaaac aggcgctgac cattaactgg 540
tactacgccg atgtgaacgg caatatcggc tatgtgcata ccggcgccta tccggatcgc 600
cagcccggcc acgacccgcg tttgccggtt cccggcactg gaaaatggga ctggaaaggg 660
```

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ttgctgtcgt ttgatttgaa tccgaaagtg tataacccgc agtcgggcta tatcgccaac 720
tggaacaact cgccgcaaaa agactacccg gcctctgatc tgttcgcgtt cctgtggggc 780
ggtgcggatc gagttactga gatcgacacg atcctcgata agcaaccgcg cttcaccgcc 840
gatcaggcgt gggatgtgat ccgccaaacc agccgtcggg atctcaacct gcggttgttc 900
ttaccggcgc tgaaggacgc caccgcgaac ctggcggaaa acgatccgcg ccgccaactg 960
gtggataaac tggcgagctg ggacggcgaa aaccttgtca acgatgacgg aaaaacctat 1020
cagcaaccgg gatcggcgat tcttaacgcc tggctgacca gcatgctcaa gcgcacggtg 1080
gttgccgcgg tcccagcgcc gtttggtaag tggtacagcg ccagtggcta tgaaaccacc 1140
caggacgggc caaccggctc gctgaacatc agcgtggggg cgaaaatcct ctacgaagct 1200
ctgcagggtg ataagtcgcc aatcccgcag gcggtcgatc tgtttggcgg gaaaccgcag 1260
caggaagtaa tactggcggc gctggacgac gcttggcaga cgctgtcaaa acgctacggt 1320
aacgacgtca ccggctggaa aacccctgcc atggcgctta ccttccgggc caataacttc 1380
ttcggcgtgc cgcaggcggc agcaaaagag gcgcgtcatc aggcggagta ccagaaccgc 1440
ggtacggaaa acgacatgat tgtcttctca ccgacgtcgg gtaaccgccc ggttcttgcc 1500
tgggatgtgg tggcgccggg gcaaagcggt tttatcgcgc cggatggcaa agccgataag 1560
cactatgacg atcagctgaa aatgtacgag agctttggcc gtaaatcgct gtggttaacg 1620
cctcaggacg ttgacgagca ccaagagtct caggaagtgc tgcaggtaca gttggatcag 1680
accgaggtta agatcgttcg cgatgaatac ggcatgccgc atatttacgc cgatgatacc 1740
tatcgactgt tttacggcta tggctacgtg gtggcgcagg atcgcctgtt ccagatggaa 1800
atggcgcgcc gcagtactca ggggaccgtc tccgaggtgc tgggcaaagc attcgtcagt 1860
tttgataaac gtattcgcca gaactactgg ccggattcta ttcgcgcgca gatagcttcc 1920
ctctccgctg aggataaatc cattctgcag ggctatgccg atggcatgaa tgcgtggatc 1980
gataaagtga acgccagccc cgataagctg ttaccccagc agttctccac ctttggtttt 2040
aaacccaagc attgggaacc gtttgatgtg gcgatgattt ttgtcggcac catggcgaac 2100
cgtttctctg acagcaccag cgaaattgat aacctggcgc tgctgacggc gctaaaagac 2160
aaatacggca agcagcaggg catggcggtc tttaaccagc tgaaatggct ggttaatcct 2220
tccgcgccaa ccaccattgc ggcgcgggaa agcgcctatc cgctgaagtt tgatctgcaa 2280
aacacgcaaa cggcgtaa                                                2298


<210> 102
<211> 765
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 102
Met Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys
1               5                  10                  15
Ala Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr
            20                  25                  30
Thr Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn
        35                  40                  45
Thr Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile
    50                  55                  60
Ser Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala
65                  70                  75                  80
Glu Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu
                85                  90                  95
Trp Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly
            100                 105                 110
```

```
Gln Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile
        115                 120                 125
Lys Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp
    130                 135                 140
Asp Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys
145                 150                 155                 160
Ala Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu
                165                 170                 175
Thr Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val
            180                 185                 190
His Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu
        195                 200                 205
Pro Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe
    210                 215                 220
Asp Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn
225                 230                 235                 240
Trp Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala
                245                 250                 255
Phe Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu
            260                 265                 270
Asp Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg
        275                 280                 285
Gln Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu
    290                 295                 300
Lys Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu
305                 310                 315                 320
Val Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp
                325                 330                 335
Gly Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu
            340                 345                 350
Thr Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe
        355                 360                 365
Gly Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro
    370                 375                 380
Thr Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala
385                 390                 395                 400
Leu Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly
                405                 410                 415
Gly Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp
            420                 425                 430
Gln Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr
        435                 440                 445
Pro Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro
    450                 455                 460
Gln Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg
465                 470                 475                 480
Gly Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg
                485                 490                 495
Pro Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile
            500                 505                 510
Ala Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met
        515                 520                 525
Tyr Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val
```

```
    530                 535                 540
Asp Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln
545                 550                 555                 560
Thr Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr
                565                 570                 575
Ala Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala
            580                 585                 590
Gln Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly
        595                 600                 605
Thr Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Arg
    610                 615                 620
Ile Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser
625                 630                 635                 640
Leu Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met
                645                 650                 655
Asn Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro
            660                 665                 670
Gln Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe
        675                 680                 685
Asp Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp
    690                 695                 700
Ser Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp
705                 710                 715                 720
Lys Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp
                725                 730                 735
Leu Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala
            740                 745                 750
Tyr Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760                 765


<210> 103
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 103
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 tcgcgcgtct gtggggcggt 780
```

gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 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> 104
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 104
Ser Asn Met Trp Val Ile 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 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 Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        355                 360                 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
    370                 375                 380
Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
                405                 410                 415
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 495
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
            500                 505                 510
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
        515                 520                 525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr 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> 105
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 105
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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
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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
ttctctgaca gcaccagcga aattaaaaac 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> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 106
Ser Asn Met Trp Val Ile 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
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
    530                 535                 540
Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
```

```
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Lys Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
        755                 760
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<210> 107
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 107
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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
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
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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
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 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> 108
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 108
Ser Asn Met Trp Val Ile Gly 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

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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 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
```

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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> 109
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 109

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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
gacgtcgaca 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
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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 cgtctggttt 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 110
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 110
Ser Asn Met Trp Val Ile Gly 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 Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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

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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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Asp 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
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```
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 111
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 111

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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 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 tcccgttcct 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 aaccaccccg 1140
```

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gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca gctggaaaac ccctgccatg gcgcttacct tccgggccac caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc 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> 112
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 112
Ser Asn Met Trp Val Ile 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 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
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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 Pro Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn 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
        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 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 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 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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> 113
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 113

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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 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 tcccgttcct 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 aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa accgcagcag 1260
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccac caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc 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> 114
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 114
Ser Asn Met Trp Val Ile 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 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

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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 Pro Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn 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
        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 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 Ala Leu Thr Trp 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 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 Gln 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 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 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> 115
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 115

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agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tcccgttcct 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 aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccaa 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 acgagcacca 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
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> 116
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 116
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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 Ile 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
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 Pro Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn 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
        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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser 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> 117
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 117
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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 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 tcccgttcct 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 aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa accgcagcag 1260
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gacgtcgatg gctggaaaac ccctgccatg gcgcttacct ggcgggccac caacttcttc 1380
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc 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> 118
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 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
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 Pro Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn 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
        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 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 Ala Leu Thr Trp 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 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln 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> 119
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 119

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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 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 tcccgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca aatggaaaac ccctgccatg gcgcttacct tccgggccac caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca 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> Variant of Penicillin G Acylase From Kluyvera 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 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
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe 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 Pro Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        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 Lys 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 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr 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> 121
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 121
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 atccgcgcag ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa 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 atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca 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 gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc 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> 122
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 122
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
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn 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 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
        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 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 Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp 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> 123
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 123
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 tcccgttcct 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 aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcatgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

gataaagata ttcgccagaa ctactggccg gattctattc 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> 124
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 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
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser 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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Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn 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
        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 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 Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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> 125
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 125
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tctgatagct tcccgttcct 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 tgacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccac caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtagggcc cgatcagggc 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> 126
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 126
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 Ile 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
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Pro Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile 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 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 Asp Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        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 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 Ala Leu Thr Trp Arg Ala Thr Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln Glu Ser Gln Glu Val Leu Gln Val Gly Pro 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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> 127
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 127
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tctgatagct tcccgttcct 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 tcatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 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> 128
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 128
Ser Asn Met Trp Val Ile 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 Ile 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
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Pro Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile 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 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 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 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 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 Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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
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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> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 129
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatagct tcccgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgcag ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgtggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccaa taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg 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
tacggcaaac 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> Variant of Penicillin G Acylase From Kluyvera 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 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 Ile 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 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 Ser 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
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn 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

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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 Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Val Val Pro Ala Pro Phe Gly
        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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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
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<210> 131
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 131
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat ttggaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatagct tcccgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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caaccgggat cggcgattct tcacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
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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
tacggcgaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                                  2295
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<210> 132
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 132
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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 Ile 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 Glu Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Pro Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn 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

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Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His 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 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 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 Ala Leu Thr Trp Arg Ala Thr Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln Glu Ser Gln Glu Val Leu Gln Val Gly Gly 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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 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 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> 133
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 133
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatagct tcccgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgtggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttgggggggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 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
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tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac 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> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 134
Ser Asn Met Trp Val Ile 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 Ile 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 Glu Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Pro Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
340 345 350

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Ser Met Leu Lys Arg Thr Val Val Ala Val Val Pro Ala Pro Phe Gly
        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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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> 135
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 135
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tctgatagct tcccgttcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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caaccgggat cggcgattct tgatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 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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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> 136
<211> 764

<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 136
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 Ile 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
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Pro Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp 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 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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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> 137

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

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 137
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatagct tcccgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgtggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc 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> 138
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 138
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 Ile 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 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 Ser 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
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Val Val Pro Ala Pro Phe Gly
355 360 365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Pro 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 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 Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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> 139
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 139
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gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tctgatagct tcccgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc 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 cgcaccatca ccatcaccat taa 2313

<210> 140
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 140

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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 Ile 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
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Pro Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        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
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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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln 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 Ala Phe Val Ser Phe Asp Lys Asp Ile
    610                 615                 620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625                 630                 635                 640
Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
                645                 650                 655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
            660                 665                 670
Gln Phe Ser Thr Phe Gly Phe 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 His His His His
        755                 760                 765
His His
    770
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<210> 141
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 141
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt 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 tctgatagct tcccgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgatgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgcctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt gcaccatcac 1680
catcaccatg atcagggcga ggttaagatc gttcgcgatg aatacggcat gccgcatatt 1740
tacgccgatg atacctatcg actgttttac ggctatggct acgtggtggc gcaggatcgc 1800
ctgttccaga tggaaatggc gcgccgcagt actcagggga ccgtctccga ggtgctgggc 1860
aaagcattcg tcagttttga taaagatatt cgccagaact actggccgga ttctattcgc 1920
gcgcagatag cttccctctc cgctgaggat aaatccattc tgcagggcta tgccgatggc 1980
atgaatgcgt ggatcgataa agtgaacgcc agccccgata agctgttacc ccagcagttc 2040
tccacctttg gttttaaacc caagcattgg gaaccgtttg atgtggcgat gatttttgtc 2100
ggcaccatgg cgaaccgttg gtctgacagc accagcgaaa ttgataacct ggcgctgctg 2160
acggcgctaa aagacaaata cggcaagcag cagggcatgg cggtctttaa ccagctgaaa 2220
tggctggtta atccttccgc gccaaccacc attgcggcgc gggaaagcgc ctatccgctg 2280
aagtttgatc tgcaaaacac gcaaacggcg taa   2313

<210> 142
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 142

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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 Ile 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
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Pro Phe
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
            340                 345                 350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
        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
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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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Ala Leu Thr Trp Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Ala Ala Lys Glu Ala Arg Pro Gln Ala Glu Tyr Gln Asn Arg Gly
465                 470                 475                 480
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
                485                 490                 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 Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu His His His
545                 550                 555                 560
His His His Asp Gln Gly Glu Val Lys Ile Val Arg Asp Glu Tyr Gly
                565                 570                 575
Met Pro His Ile Tyr Ala Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr
            580                 585                 590
Gly Tyr Val Val Ala Gln Asp Arg Leu Phe Gln Met Glu Met Ala Arg
        595                 600                 605
Arg Ser Thr Gln Gly Thr Val Ser Glu Val Leu Gly Lys Ala Phe Val
    610                 615                 620
Ser Phe Asp Lys Asp Ile Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg
625                 630                 635                 640
Ala Gln Ile Ala Ser Leu Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly
                645                 650                 655
Tyr Ala Asp Gly Met Asn Ala Trp Ile Asp Lys Val Asn Ala Ser Pro
            660                 665                 670
Asp Lys Leu Leu Pro Gln Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys
        675                 680                 685
His Trp Glu Pro Phe Asp Val Ala Met Ile Phe Val Gly Thr Met Ala
    690                 695                 700
Asn Arg Trp Ser Asp Ser Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu
705                 710                 715                 720
Thr Ala Leu Lys Asp Lys Tyr Gly Lys Gln Gln Gly Met Ala Val Phe
                725                 730                 735
Asn Gln Leu Lys Trp Leu Val Asn Pro Ser Ala Pro Thr Thr Ile Ala
            740                 745                 750
Ala Arg Glu Ser Ala Tyr Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln
        755                 760                 765
Thr Ala
    770
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<210> 143
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 143
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt gggggtgatg atgtcgatat 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 tctgattatt ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgatgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 ggatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 144
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 144

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp 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 Gly 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 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 145
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 145
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt gggggtgatg gtgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat ttggactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 146
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 146

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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 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 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
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 147
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 147
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt gggggtgatg atgtcgatat 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 tctgattatt ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcatgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 ggatcagaca 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 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
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 148
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 148

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 149
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 149
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt atgggtgatg gtgtcgatat 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 aaccaccccg 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaggccg ctacggtaac 1320
gacgtcgaca 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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tccgctgagg ataaagatat 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 cgcaccatca ccatcaccat taa 2313

<210> 150
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 150
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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala Thr Ala Gly Met Gly Asp Gly Val Asp Ile Phe Ala Glu
65                  70                  75                  80
Lys 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Pro Asp Gly Pro Thr
    370                 375                 380
Gly Gly 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 Gly Arg Tyr Gly Asn Asp Val Asp 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 Phe Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 151
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 151
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt atgggtgata gtgtcgatat 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 aaccaccccg 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 cgtctggttt 1860
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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 152
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 152

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala Thr Ala Gly Met 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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Pro Asp Gly Pro Thr
    370                 375                 380
Gly Gly 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 Asp 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 153
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 153
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt tttggtgatg acgtcgatat 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 ttgcgctgct 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 ccggcggcct gaacatcctg gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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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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ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 154
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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
                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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Leu Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 155
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 155
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt tttggtgatt ccgtcgatat 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
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gacgggccaa ccggcggcct gaacatcctg gtgggggcga aaatcctcta cgaagctctg 1200
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 156
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 156

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Ser Asn Met Trp Val Ile Gly Lys Asn 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala Thr Ala Gly Phe 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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Val 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 Gly Leu Asn Ile Leu 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 Asp 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 Gly Leu Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 157
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 157
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaacggtt cgtctggttt 1860
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tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 158
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 158

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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 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 Glu Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp 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 Arg Thr Gly Tyr Glu Thr Thr Pro Asp Gly Pro Thr
    370                 375                 380
Gly Gly Leu Asn Ile Leu 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 Gly Arg Tyr Gly Asn Asp Val Asp 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 Arg Phe Val Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 159
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 159
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat 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
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tacgccgatg tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattatt ttgcgctgct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 160
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 160

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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
                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 Glu Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
            340                 345                 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 Gly Leu Asn Ile Ala 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 161
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 161
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 162
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 162

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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
                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 Glu Gly Asn Ile Gly Tyr Val His
            180                 185                 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195                 200                 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210                 215                 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Trp Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
            340                 345                 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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Gly Gly Leu Asn Ile Ala Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
385                 390                 395                 400
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            420                 425                 430
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
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<210> 163
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt gggggtgatg acgtcgatat 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
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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gacgtcgaca 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 ggatcagact 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 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
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 164
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 164

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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 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 Trp Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp 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 Pro
    370                 375                 380
Gly Gly Leu Asn Ile Ala 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 165
<211> 2313
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 165
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt gggggtgatg acgtcgatat 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 tctgattctt ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccac cgggcggcct gaacatcgca gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 ggatcagggg 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 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 cgcaccatca ccatcaccat taa 2313

<210> 166
<211> 770
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 166

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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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 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 Ser Phe Ala Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
            340                 345                 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 Pro
    370                 375                 380
Gly Gly Leu Asn Ile Ala 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 Asp 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 167
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 167
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat 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 gccagacagg cgctgaccat taactggtac 540
tacgccgatg tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattatt ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa cgggcggcct gaacatcgca gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaaca cgatgattgt cttctcaccg acgtcgggtg 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 cgtctggttt 1860
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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 168
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala 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
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 Arg Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Glu Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
340 345 350
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 Gly Leu Asn Ile Ala Val Gly Ala Lys Ile Leu 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 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 Thr 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 169
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 169
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat 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
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 170
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala 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
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 Glu Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Thr Asp Tyr Phe Ala Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
340 345 350
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 Gly Leu Asn Ile Ala Val Gly Ala Lys Ile Leu 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 171
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 171
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat 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 tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattatt ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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tacggcgaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 172
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 172
Ser Asn Met Trp Val Ile Gly 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala 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
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 Glu Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
340 345 350
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 Gly Leu Asn Ile Ala Val Gly Ala Lys Ile Leu 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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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 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 Met Ala Lys Glu Thr Arg His Gln 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 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 Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 173
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 173
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ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 174
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 174
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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50                  55                  60
Trp Gly Ala 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
                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 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 Leu
                245                 250                 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260                 265                 270
Lys Gln Pro Arg Phe Thr Pro Asp Gln Ala Trp Asp Val Ile Arg Gln
        275                 280                 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290                 295                 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305                 310                 315                 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325                 330                 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
            340                 345                 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 Pro Asp Gly Pro Thr
    370                 375                 380
Gly Gly Leu Asn Ile Ala Val Gly Ala Lys Ile Leu 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 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 Met Ala Lys Glu Ala Arg His Gln 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 175
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat 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 tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattatt gggcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa cgggcggcct gaacatcgca gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
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ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 176
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 176
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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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala 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
                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 Glu Gly Asn Ile Gly Tyr Val His
            180   185   190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
        195   200   205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
    210   215   220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Trp Ala Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
                325   330   335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
            340   345   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 Gly Leu Asn Ile Ala Val Gly Ala Lys Ile Leu 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 177
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 177
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat 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 tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattatg ctgcgctgct 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 tgacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa cgggcggcct gaacatcgca gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca gctggaaaac ccctgccatg aaacttacct tccgggccaa caacttcttc 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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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 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
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 178
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala 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
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 Glu Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Ala Ala Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
340 345 350
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 Gly Leu Asn Ile Ala Val Gly Ala Lys Ile Leu 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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 179
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 179
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat ctttgccgaa 240
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agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 180
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Ile Val Phe Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala 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
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 Glu Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr
340 345 350
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 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

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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 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 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 Trp Phe Asp Lys Asp Ile
    610                 615                 620
Arg 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 His His His His
        755                 760                 765
His His
    770
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<210> 181
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 181
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtgtg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttggcctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 tggtaaatgg tacagcagga ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 aggtacaggg tgatcagacc 1680
cccgttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaaacttt cgtctggttt 1860
gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tcgaaacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 182
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 182
Ser Asn Met Trp Val Ile Gly 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 Cys Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Gly Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp 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 Gly Asp Gln Thr
545                 550                 555                 560
Pro Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Thr Phe Val Trp 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 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 Glu Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 183
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 183
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtgca tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 tctgattacc acggcctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 tggtaaatgg tacagcagga ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca 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 aggtacaggg tgatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaaacttt cgtctggttt 1860
gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctcaacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 184
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 184
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 His Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 His Gly Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp 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 Gly Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Thr Phe Val Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 185
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 185
agcaatatgt gggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtgca tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttggcctgct 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
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gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 186
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 His Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Gly Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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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Lys Pro Gln Gln Glu 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 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 Thr Phe Val Trp 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 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 Glu Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 187
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 187
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtgca tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttggcctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 tggtaaatgg tacagcagga ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct 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
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tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 188
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 188
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 His Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Gly Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp 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 Gly Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
        595                 600                 605
Val Ser Glu Val Leu Gly Lys Thr Phe Val Trp 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 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 Glu Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 189
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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caggacgttg acgagcacaa agagtctcag gaagtgctgc aggtacaggt ggatcagacc 1680
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acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 190
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 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 Cys Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp 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 Val Asp Gln Thr
545                 550                 555                 560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
                565                 570                 575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
            580                 585                 590
Asp Arg 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 Trp 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 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 191
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 191
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgttgt cggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcgacc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 192
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 192
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr 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 Val Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp 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 Trp 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 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 193
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 193
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtgtg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttggcctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 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 tggtaaatgg tacagcagga ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatccaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaaacttt cgtctggttt 1860
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tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 194
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 194
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 Cys Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Gly Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Gln Val Gly Ala Lys Ile Leu 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 Asp 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 Thr Phe Val Trp 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 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 Glu Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
        675                 680                 685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
    690                 695                 700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 195
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 195
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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
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gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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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 cgtctggttt 1860
gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgaaaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 196
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 196
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 Cys Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys Leu Thr Phe Arg Ala Thr Asn Phe Phe Gly Val Pro Gln
    450                 455                 460
Ala Met Ala Lys Glu Ala Arg His Gln 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 Trp 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 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 Glu Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 197
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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 ttgcgctcct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaatg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgtggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 198
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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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 Cys Gly His Asn Gly Thr Ile Ser
    50   55   60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65   70   75   80
Lys 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 Leu
                245   250   255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
            260   265   270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
        275   280   285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
    290   295   300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305   310   315   320
Asp Lys Leu Ala Ser Trp 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 Val 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp Ser Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys 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 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 Trp 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 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 His His His His
        755                 760                 765
His His
    770
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<210> 199
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 199
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gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg 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
tatgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctcct 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 caggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcgaca gctggaaaac ccctgccatg aaacttacct tccgggccac caacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg 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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aaagtgaacg ccagccccga taagctgtta ccccagcagt tctccacctt tggttttaaa 2040
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ttctctgaca gcaccagcga aattgaaaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgcaccatca ccatcaccat taa   2313

<210> 200
<211> 770
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera 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 Cys Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Ala 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 Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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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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 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 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 Thr Phe Val Trp 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 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 Glu Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705                 710                 715                 720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
                725                 730                 735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
            740                 745                 750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
        755                 760                 765
His His
    770
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<210> 201
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 201
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ggcaccattt catggggagc gaccgccggt cagggtgatg 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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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaaacttt cgtctggttt 1860
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<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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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 Cys Gly His Asn Gly Thr Ile Ser
50 55 60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65 70 75 80
Lys 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 Leu
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Ala 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 Val 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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Gly Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu 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 Asp Asn Trp Lys Thr Pro
        435                 440                 445
Ala Met Lys 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 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
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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 Thr Phe Val Trp 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 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 His His His His
        755                 760                 765
His His
    770
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