<110> E.I. du Pont de Nemours and Co.
Van Dyk, Tina

<120> Variant Sucrose Transporter Polypeptides That Enable Growth Over a Wide Range of Sucrose Concentrations

<130> CL5509 USNP

<160> 136

<170> PatentIn version 3.5

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<213> Saccharomyces cerevisiae

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ccagaagttt tcgctccaat agtacaaatg tgggtgttcg aagaagagat caatggtgaa 240

aaattgactg aaatcataaa tactagacat caaaacgtga aatacttgcc tggcatcact 300

ctacccgaca atttggttgc taatccagac ttgattgatt cagtcaagga tgtcgacatc 360

atcgttttca acattccaca tcaatttttg ccccgtatct gtagccaatt gaaaggtcat 420

gttgattcac acgtcagagc tatctcctgt ctaaagggtt ttgaagttgg tgctaaaggt 480

gtccaattgc tatcctctta catcactgag gaactaggta ttcaatgtgg tgctctatct 540

ggtgctaaca ttgccaccga agtcgctcaa gaacactggt ctgaaacaac agttgcttac 600

cacattccaa aggatttcag aggcgagggc aaggacgtcg accataaggt tctaaaggcc 660

ttgttccaca gaccttactt ccacgttagt gtcatcgaag atgttgctgg tatctccatc 720

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gatttgatca ccacctgcgc tggtggtaga aacgtcaagg ttgctaggct aatggctact 960

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ttaattacct gcaaagaagt tcacgaatgg ttggaaacat gtggctctgt cgaagacttc 1080

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<212> PRT
<213> Saccharomyces cerevisiae

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Ala Gly Arg Lys Arg Ser Ser Ser Ser Val Ser Leu Lys Ala Ala Glu
            20                  25                  30

Lys Pro Phe Lys Val Thr Val Ile Gly Ser Gly Asn Trp Gly Thr Thr
        35                  40                  45

Ile Ala Lys Val Val Ala Glu Asn Cys Lys Gly Tyr Pro Glu Val Phe
    50                  55                  60

Ala Pro Ile Val Gln Met Trp Val Phe Glu Glu Glu Ile Asn Gly Glu
65                  70                  75                  80

Lys Leu Thr Glu Ile Ile Asn Thr Arg His Gln Asn Val Lys Tyr Leu
                85                  90                  95

Pro Gly Ile Thr Leu Pro Asp Asn Leu Val Ala Asn Pro Asp Leu Ile
            100                 105                 110

Asp Ser Val Lys Asp Val Asp Ile Ile Val Phe Asn Ile Pro His Gln
        115                 120                 125

Phe Leu Pro Arg Ile Cys Ser Gln Leu Lys Gly His Val Asp Ser His
    130                 135                 140

Val Arg Ala Ile Ser Cys Leu Lys Gly Phe Glu Val Gly Ala Lys Gly
145                 150                 155                 160

Val Gln Leu Leu Ser Ser Tyr Ile Thr Glu Glu Leu Gly Ile Gln Cys
                165                 170                 175

Gly Ala Leu Ser Gly Ala Asn Ile Ala Thr Glu Val Ala Gln Glu His
            180                 185                 190

Trp Ser Glu Thr Thr Val Ala Tyr His Ile Pro Lys Asp Phe Arg Gly
        195                 200                 205

Glu Gly Lys Asp Val Asp His Lys Val Leu Lys Ala Leu Phe His Arg
    210                 215                 220

Pro Tyr Phe His Val Ser Val Ile Glu Asp Val Ala Gly Ile Ser Ile
225                 230                 235                 240

Cys Gly Ala Leu Lys Asn Val Val Ala Leu Gly Cys Gly Phe Val Glu
                245                 250                 255

Gly Leu Gly Trp Gly Asn Asn Ala Ser Ala Ala Ile Gln Arg Val Gly
            260                 265                 270
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Leu Gly Glu Ile Ile Arg Phe Gly Gln Met Phe Phe Pro Glu Ser Arg
275 280 285

Glu Glu Thr Tyr Tyr Gln Glu Ser Ala Gly Val Ala Asp Leu Ile Thr
290 295 300

Thr Cys Ala Gly Gly Arg Asn Val Lys Val Ala Arg Leu Met Ala Thr
305 310 315 320

Ser Gly Lys Asp Ala Trp Glu Cys Glu Lys Glu Leu Leu Asn Gly Gln
325 330 335

Ser Ala Gln Gly Leu Ile Thr Cys Lys Glu Val His Glu Trp Leu Glu
340 345 350

Thr Cys Gly Ser Val Glu Asp Phe Pro Leu Phe Glu Ala Val Tyr Gln
355 360 365

Ile Val Tyr Asn Asn Tyr Pro Met Lys Asn Leu Pro Asp Met Ile Glu
370 375 380

Glu Leu Asp Leu His Glu Asp
385 390

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<213> Saccharomyces cerevisiae

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ttacaaacac aactgcactc aaagatgact gctcatacta atatcaaaca gcacaaacac 180

tgtcatgagg accatcctat cagaagatcg gactctgccg tgtcaattgt acatttgaaa 240

cgtgcgccct tcaaggttac agtgattggt tctggtaact gggggaccac catcgccaaa 300

gtcattgcgg aaaacacaga attgcattcc catatcttcg agccagaggt gagaatgtgg 360

gtttttgatg aaaagatcgg cgacgaaaat ctgacggata tcataaatac aagacaccag 420

aacgttaaat atctacccaa tattgacctg ccccataatc tagtggccga tcctgatctt 480

ttacactcca tcaagggtgc tgacatcctt gttttcaaca tccctcatca atttttacca 540

aacatagtca aacaattgca aggccacgtg gcccctcatg taagggccat ctcgtgtcta 600

aaagggttcg agttgggctc caagggtgtg caattgctat cctcctatgt tactgatgag 660

ttaggaatcc aatgtggcgc actatctggt gcaaacttgg caccggaagt ggccaaggag 720

cattggtccg aaaccaccgt ggcttaccaa ctaccaaagg attatcaagg tgatggcaag 780

gatgtagatc ataagatttt gaaattgctg ttccacagac cttacttcca cgtcaatgtc 840

atcgatgatg ttgctggtat atccattgcc ggtgccttga agaacgtcgt ggcacttgca 900

tgtggtttcg tagaaggtat gggatggggt aacaatgcct ccgcagccat tcaaaggctg 960

ggtttaggtg aaattatcaa gttcggtaga atgtttttcc cagaatccaa agtcgagacc 1020

tactatcaag aatccgctgg tgttgcagat ctgatcacca cctgctcagg cggtagaaac 1080

gtcaaggttg ccacatacat ggccaagacc ggtaagtcag ccttggaagc agaaaaggaa 1140

ttgcttaacg gtcaatccgc ccaagggata atcacatgca gagaagttca cgagtggcta 1200

caaacatgtg agttgaccca agaattccca ttattcgagg cagtctacca gatagtctac 1260

aacaacgtcc gcatggaaga cctaccggag atgattgaag agctagacat cgatgacgaa 1320

tag 1323

<210> 4
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<212> PRT
<213> Saccharomyces cerevisiae

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His Pro Val Leu Tyr Thr Arg Arg Ala Tyr Lys Ile Leu Pro Ser Arg
20 25 30

Ser Thr Phe Leu Arg Arg Ser Leu Leu Gln Thr Gln Leu His Ser Lys
35 40 45

Met Thr Ala His Thr Asn Ile Lys Gln His Lys His Cys His Glu Asp
50 55 60

His Pro Ile Arg Arg Ser Asp Ser Ala Val Ser Ile Val His Leu Lys
65 70 75 80

Arg Ala Pro Phe Lys Val Thr Val Ile Gly Ser Gly Asn Trp Gly Thr
85 90 95

Thr Ile Ala Lys Val Ile Ala Glu Asn Thr Glu Leu His Ser His Ile
100 105 110

Phe Glu Pro Glu Val Arg Met Trp Val Phe Asp Glu Lys Ile Gly Asp
115 120 125

Glu Asn Leu Thr Asp Ile Ile Asn Thr Arg His Gln Asn Val Lys Tyr
130 135 140

Leu Pro Asn Ile Asp Leu Pro His Asn Leu Val Ala Asp Pro Asp Leu
145 150 155 160

Leu His Ser Ile Lys Gly Ala Asp Ile Leu Val Phe Asn Ile Pro His
165 170 175

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Gln Phe Leu Pro Asn Ile Val Lys Gln Leu Gln Gly His Val Ala Pro
            180                 185                 190

His Val Arg Ala Ile Ser Cys Leu Lys Gly Phe Glu Leu Gly Ser Lys
        195                 200                 205

Gly Val Gln Leu Leu Ser Ser Tyr Val Thr Asp Glu Leu Gly Ile Gln
    210                 215                 220

Cys Gly Ala Leu Ser Gly Ala Asn Leu Ala Pro Glu Val Ala Lys Glu
225                 230                 235                 240

His Trp Ser Glu Thr Thr Val Ala Tyr Gln Leu Pro Lys Asp Tyr Gln
                245                 250                 255

Gly Asp Gly Lys Asp Val Asp His Lys Ile Leu Lys Leu Leu Phe His
            260                 265                 270

Arg Pro Tyr Phe His Val Asn Val Ile Asp Asp Val Ala Gly Ile Ser
        275                 280                 285

Ile Ala Gly Ala Leu Lys Asn Val Val Ala Leu Ala Cys Gly Phe Val
    290                 295                 300

Glu Gly Met Gly Trp Gly Asn Asn Ala Ser Ala Ala Ile Gln Arg Leu
305                 310                 315                 320

Gly Leu Gly Glu Ile Ile Lys Phe Gly Arg Met Phe Phe Pro Glu Ser
                325                 330                 335

Lys Val Glu Thr Tyr Tyr Gln Glu Ser Ala Gly Val Ala Asp Leu Ile
            340                 345                 350

Thr Thr Cys Ser Gly Gly Arg Asn Val Lys Val Ala Thr Tyr Met Ala
        355                 360                 365

Lys Thr Gly Lys Ser Ala Leu Glu Ala Glu Lys Glu Leu Leu Asn Gly
    370                 375                 380

Gln Ser Ala Gln Gly Ile Ile Thr Cys Arg Glu Val His Glu Trp Leu
385                 390                 395                 400

Gln Thr Cys Glu Leu Thr Gln Glu Phe Pro Leu Phe Glu Ala Val Tyr
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Gln Ile Val Tyr Asn Asn Val Arg Met Glu Asp Leu Pro Glu Met Ile
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Glu Glu Leu Asp Ile Asp Asp Glu
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<213> Saccharomyces cerevisiae

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gacggtacca tcatcatctc tcaaccagcc attgctgctt tctggagaga tttcggtaaa 180

gacaagcctt acttcgatgc cgaacacgtt attcacatct ctcacggttg gagaacttac 240

gatgccattg ccaagttcgc tccagacttt gctgatgaag aatacgttaa caagctagaa 300

ggtgaaatcc cagaaaagta cggtgaacac tccatcgaag ttccaggtgc tgtcaagttg 360

tgtaatgctt tgaacgcctt gccaaaggaa aaatgggctg tcgccacctc tggtacccgt 420

gacatggcca agaaatggtt cgacattttg aagatcaaga gaccagaata cttcatcacc 480

gccaatgatg tcaagcaagg taagcctcac ccagaaccat acttaaaggg tagaaacggt 540

ttgggtttcc caattaatga acaagaccca tccaaatcta aggttgttgt ctttgaagac 600

gcaccagctg gtattgctgc tggtaaggct gctggctgta aaatcgttgg tattgctacc 660

actttcgatt tggacttctt gaaggaaaag ggttgtgaca tcattgtcaa gaaccacgaa 720

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tacttatacg ctaaggatga cttgttgaaa tggtaa 816

<210> 6
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Ile Gln Thr Ile Ala Met Pro Leu Thr Thr Lys Pro Leu Ser Leu Lys
20 25 30

Ile Asn Ala Ala Leu Phe Asp Val Asp Gly Thr Ile Ile Ile Ser Gln
35 40 45

Pro Ala Ile Ala Ala Phe Trp Arg Asp Phe Gly Lys Asp Lys Pro Tyr
50 55 60

Phe Asp Ala Glu His Val Ile His Ile Ser His Gly Trp Arg Thr Tyr
65 70 75 80

Asp Ala Ile Ala Lys Phe Ala Pro Asp Phe Ala Asp Glu Glu Tyr Val
85 90 95

Asn Lys Leu Glu Gly Glu Ile Pro Glu Lys Tyr Gly Glu His Ser Ile
100 105 110

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Glu Val Pro Gly Ala Val Lys Leu Cys Asn Ala Leu Asn Ala Leu Pro
        115                 120                 125

Lys Glu Lys Trp Ala Val Ala Thr Ser Gly Thr Arg Asp Met Ala Lys
    130                 135                 140

Lys Trp Phe Asp Ile Leu Lys Ile Lys Arg Pro Glu Tyr Phe Ile Thr
145                 150                 155                 160

Ala Asn Asp Val Lys Gln Gly Lys Pro His Pro Glu Pro Tyr Leu Lys
                165                 170                 175

Gly Arg Asn Gly Leu Gly Phe Pro Ile Asn Glu Gln Asp Pro Ser Lys
            180                 185                 190

Ser Lys Val Val Val Phe Glu Asp Ala Pro Ala Gly Ile Ala Ala Gly
        195                 200                 205

Lys Ala Ala Gly Cys Lys Ile Val Gly Ile Ala Thr Thr Phe Asp Leu
    210                 215                 220

Asp Phe Leu Lys Glu Lys Gly Cys Asp Ile Ile Val Lys Asn His Glu
225                 230                 235                 240

Ser Ile Arg Val Gly Glu Tyr Asn Ala Glu Thr Asp Glu Val Glu Leu
                245                 250                 255

Ile Phe Asp Asp Tyr Leu Tyr Ala Lys Asp Asp Leu Leu Lys Trp
            260                 265                 270
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aaaccttatt tcgatgctga acacgttatc caagtctcgc atggttggag aacgtttgat      180

gccattgcta agttcgctcc agactttgcc aatgaagagt atgttaacaa attagaagct      240

gaaattccgg tcaagtacgg tgaaaaatcc attgaagtcc caggtgcagt taagctgtgc      300

aacgctttga acgctctacc aaaagagaaa tgggctgtgg caacttccgg tacccgtgat      360

atggcacaaa aatggttcga gcatctggga atcaggagac caaagtactt cattaccgct      420

aatgatgtca aacagggtaa gcctcatcca gaaccatatc tgaagggcag gaatggctta      480

ggatatccga tcaatgagca agacccttcc aaatctaagg tagtagtatt tgaagacgct      540

ccagcaggta ttgccgccgg aaaagccgcc ggttgtaaga tcattggtat tgccactact      600
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ttcgacttgg acttcctaaa ggaaaaaggc tgtgacatca ttgtcaaaaa ccacgaatcc 660

atcagagttg gcggctacaa tgccgaaaca gacgaagttg aattcatttt tgacgactac 720

ttatatgcta aggacgatct gttgaaatgg taa 753

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<212> PRT
<213> Saccharomyces cerevisiae

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20 25 30

Phe Trp Arg Asp Phe Gly Lys Asp Lys Pro Tyr Phe Asp Ala Glu His
35 40 45

Val Ile Gln Val Ser His Gly Trp Arg Thr Phe Asp Ala Ile Ala Lys
50 55 60

Phe Ala Pro Asp Phe Ala Asn Glu Glu Tyr Val Asn Lys Leu Glu Ala
65 70 75 80

Glu Ile Pro Val Lys Tyr Gly Glu Lys Ser Ile Glu Val Pro Gly Ala
85 90 95

Val Lys Leu Cys Asn Ala Leu Asn Ala Leu Pro Lys Glu Lys Trp Ala
100 105 110

Val Ala Thr Ser Gly Thr Arg Asp Met Ala Gln Lys Trp Phe Glu His
115 120 125

Leu Gly Ile Arg Arg Pro Lys Tyr Phe Ile Thr Ala Asn Asp Val Lys
130 135 140

Gln Gly Lys Pro His Pro Glu Pro Tyr Leu Lys Gly Arg Asn Gly Leu
145 150 155 160

Gly Tyr Pro Ile Asn Glu Gln Asp Pro Ser Lys Ser Lys Val Val Val
165 170 175

Phe Glu Asp Ala Pro Ala Gly Ile Ala Ala Gly Lys Ala Ala Gly Cys
180 185 190

Lys Ile Ile Gly Ile Ala Thr Thr Phe Asp Leu Asp Phe Leu Lys Glu
195 200 205

Lys Gly Cys Asp Ile Ile Val Lys Asn His Glu Ser Ile Arg Val Gly
210 215 220

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Gly Tyr Asn Ala Glu Thr Asp Glu Val Glu Phe Ile Phe Asp Asp Tyr
225                 230                 235                 240


Leu Tyr Ala Lys Asp Asp Leu Leu Lys Trp
                245                 250


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<212>  DNA
<213>  Klebsiella pneumoniae


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1               5                   10                  15

cag gac ggg ctg att ggc gag tgg cct gaa gag ggg ctg atc gcc atg         96
Gln Asp Gly Leu Ile Gly Glu Trp Pro Glu Glu Gly Leu Ile Ala Met
            20                  25                  30

gac agc ccc ttt gac ccg gtc tct tca gta aaa gtg gac aac ggt ctg        144
Asp Ser Pro Phe Asp Pro Val Ser Ser Val Lys Val Asp Asn Gly Leu
        35                  40                  45

atc gtc gaa ctg gac ggc aaa cgc cgg gac cag ttt gac atg atc gac        192
Ile Val Glu Leu Asp Gly Lys Arg Arg Asp Gln Phe Asp Met Ile Asp
    50                  55                  60

cga ttt atc gcc gat tac gcg atc aac gtt gag cgc aca gag cag gca        240
Arg Phe Ile Ala Asp Tyr Ala Ile Asn Val Glu Arg Thr Glu Gln Ala
65                  70                  75                  80

atg cgc ctg gag gcg gtg gaa ata gcc cgt atg ctg gtg gat att cac        288
Met Arg Leu Glu Ala Val Glu Ile Ala Arg Met Leu Val Asp Ile His
                85                  90                  95

gtc agc cgg gag gag atc att gcc atc act acc gcc atc acg ccg gcc        336
Val Ser Arg Glu Glu Ile Ile Ala Ile Thr Thr Ala Ile Thr Pro Ala
            100                 105                 110

aaa gcg gtc gag gtg atg gcg cag atg aac gtg gtg gag atg atg atg        384
Lys Ala Val Glu Val Met Ala Gln Met Asn Val Val Glu Met Met Met
        115                 120                 125

gcg ctg cag aag atg cgt gcc cgc cgg acc ccc tcc aac cag tgc cac        432
Ala Leu Gln Lys Met Arg Ala Arg Arg Thr Pro Ser Asn Gln Cys His
    130                 135                 140

gtc acc aat ctc aaa gat aat ccg gtg cag att gcc gct gac gcc gcc        480
Val Thr Asn Leu Lys Asp Asn Pro Val Gln Ile Ala Ala Asp Ala Ala
145                 150                 155                 160

gag gcc ggg atc cgc ggc ttc tca gaa cag gag acc acg gtc ggt atc        528
Glu Ala Gly Ile Arg Gly Phe Ser Glu Gln Glu Thr Thr Val Gly Ile
                165                 170                 175

gcg cgc tac gcg ccg ttt aac gcc ctg gcg ctg ttg gtc ggt tcg cag        576
Ala Arg Tyr Ala Pro Phe Asn Ala Leu Ala Leu Leu Val Gly Ser Gln
            180                 185                 190
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tgc ggc cgc ccc ggc gtg ttg acg cag tgc tcg gtg gaa gag gcc acc        624
Cys Gly Arg Pro Gly Val Leu Thr Gln Cys Ser Val Glu Glu Ala Thr
        195                 200                 205

gag ctg gag ctg ggc atg cgt ggc tta acc agc tac gcc gag acg gtg        672
Glu Leu Glu Leu Gly Met Arg Gly Leu Thr Ser Tyr Ala Glu Thr Val
    210                 215                 220

tcg gtc tac ggc acc gaa gcg gta ttt acc gac ggc gat gat acg ccg        720
Ser Val Tyr Gly Thr Glu Ala Val Phe Thr Asp Gly Asp Asp Thr Pro
225                 230                 235                 240

tgg tca aag gcg ttc ctc gcc tcg gcc tac gcc tcc cgc ggg ttg aaa        768
Trp Ser Lys Ala Phe Leu Ala Ser Ala Tyr Ala Ser Arg Gly Leu Lys
                245                 250                 255

atg cgc tac acc tcc ggc acc gga tcc gaa gcg ctg atg ggc tat tcg        816
Met Arg Tyr Thr Ser Gly Thr Gly Ser Glu Ala Leu Met Gly Tyr Ser
            260                 265                 270

gag agc aag tcg atg ctc tac ctc gaa tcg cgc tgc atc ttc att act        864
Glu Ser Lys Ser Met Leu Tyr Leu Glu Ser Arg Cys Ile Phe Ile Thr
        275                 280                 285

aaa ggc gcc ggg gtt cag gga ctg caa aac ggc gcg gtg agc tgt atc        912
Lys Gly Ala Gly Val Gln Gly Leu Gln Asn Gly Ala Val Ser Cys Ile
    290                 295                 300

ggc atg acc ggc gct gtg ccg tcg ggc att cgg gcg gtg ctg gcg gaa        960
Gly Met Thr Gly Ala Val Pro Ser Gly Ile Arg Ala Val Leu Ala Glu
305                 310                 315                 320

aac ctg atc gcc tct atg ctc gac ctc gaa gtg gcg tcc gcc aac gac       1008
Asn Leu Ile Ala Ser Met Leu Asp Leu Glu Val Ala Ser Ala Asn Asp
                325                 330                 335

cag act ttc tcc cac tcg gat att cgc cgc acc gcg cgc acc ctg atg       1056
Gln Thr Phe Ser His Ser Asp Ile Arg Arg Thr Ala Arg Thr Leu Met
            340                 345                 350

cag atg ctg ccg ggc acc gac ttt att ttc tcc ggc tac agc gcg gtg       1104
Gln Met Leu Pro Gly Thr Asp Phe Ile Phe Ser Gly Tyr Ser Ala Val
        355                 360                 365

ccg aac tac gac aac atg ttc gcc ggc tcg aac ttc gat gcg gaa gat       1152
Pro Asn Tyr Asp Asn Met Phe Ala Gly Ser Asn Phe Asp Ala Glu Asp
    370                 375                 380

ttt gat gat tac aac atc ctg cag cgt gac ctg atg gtt gac ggc ggc       1200
Phe Asp Asp Tyr Asn Ile Leu Gln Arg Asp Leu Met Val Asp Gly Gly
385                 390                 395                 400

ctg cgt ccg gtg acc gag gcg gaa acc att gcc att cgc cag aaa gcg       1248
Leu Arg Pro Val Thr Glu Ala Glu Thr Ile Ala Ile Arg Gln Lys Ala
                405                 410                 415

gcg cgg gcg atc cag gcg gtt ttc cgc gag ctg ggg ctg ccg cca atc       1296
Ala Arg Ala Ile Gln Ala Val Phe Arg Glu Leu Gly Leu Pro Pro Ile
            420                 425                 430

gcc gac gag gag gtg gag gcc gcc acc tac gcg cac ggc agc aac gag       1344
Ala Asp Glu Glu Val Glu Ala Ala Thr Tyr Ala His Gly Ser Asn Glu
        435                 440                 445

atg ccg ccg cgt aac gtg gtg gag gat ctg agt gcg gtg gaa gag atg       1392
Met Pro Pro Arg Asn Val Val Glu Asp Leu Ser Ala Val Glu Glu Met
    450                 455                 460
```

```
atg aag cgc aac atc acc ggc ctc gat att gtc ggc gcg ctg agc cgc       1440
Met Lys Arg Asn Ile Thr Gly Leu Asp Ile Val Gly Ala Leu Ser Arg
465                 470                 475                 480

agc ggc ttt gag gat atc gcc agc aat att ctc aat atg ctg cgc cag       1488
Ser Gly Phe Glu Asp Ile Ala Ser Asn Ile Leu Asn Met Leu Arg Gln
                485                 490                 495

cgg gtc acc ggc gat tac ctg cag acc tcg gcc att ctc gat cgg cag       1536
Arg Val Thr Gly Asp Tyr Leu Gln Thr Ser Ala Ile Leu Asp Arg Gln
            500                 505                 510

ttc gag gtg gtg agt gcg gtc aac gac atc aat gac tat cag ggg ccg       1584
Phe Glu Val Val Ser Ala Val Asn Asp Ile Asn Asp Tyr Gln Gly Pro
        515                 520                 525

ggc acc ggc tat cgc atc tct gcc gaa cgc tgg gcg gag atc aaa aat       1632
Gly Thr Gly Tyr Arg Ile Ser Ala Glu Arg Trp Ala Glu Ile Lys Asn
    530                 535                 540

att ccg ggc gtg gtt cag ccc gac acc att gaa taa                       1668
Ile Pro Gly Val Val Gln Pro Asp Thr Ile Glu
545                 550                 555
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<210> 10
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<212> PRT
<213> Klebsiella pneumoniae

<400> 10

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Met Lys Arg Ser Lys Arg Phe Ala Val Leu Ala Gln Arg Pro Val Asn
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Gln Asp Gly Leu Ile Gly Glu Trp Pro Glu Glu Gly Leu Ile Ala Met
            20                  25                  30

Asp Ser Pro Phe Asp Pro Val Ser Ser Val Lys Val Asp Asn Gly Leu
        35                  40                  45

Ile Val Glu Leu Asp Gly Lys Arg Arg Asp Gln Phe Asp Met Ile Asp
    50                  55                  60

Arg Phe Ile Ala Asp Tyr Ala Ile Asn Val Glu Arg Thr Glu Gln Ala
65                  70                  75                  80

Met Arg Leu Glu Ala Val Glu Ile Ala Arg Met Leu Val Asp Ile His
                85                  90                  95

Val Ser Arg Glu Glu Ile Ile Ala Ile Thr Thr Ala Ile Thr Pro Ala
            100                 105                 110

Lys Ala Val Glu Val Met Ala Gln Met Asn Val Val Glu Met Met Met
        115                 120                 125

Ala Leu Gln Lys Met Arg Ala Arg Arg Thr Pro Ser Asn Gln Cys His
    130                 135                 140
```

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Val Thr Asn Leu Lys Asp Asn Pro Val Gln Ile Ala Ala Asp Ala Ala
145                 150                 155                 160

Glu Ala Gly Ile Arg Gly Phe Ser Glu Gln Glu Thr Thr Val Gly Ile
                165                 170                 175

Ala Arg Tyr Ala Pro Phe Asn Ala Leu Ala Leu Leu Val Gly Ser Gln
            180                 185                 190

Cys Gly Arg Pro Gly Val Leu Thr Gln Cys Ser Val Glu Glu Ala Thr
        195                 200                 205

Glu Leu Glu Leu Gly Met Arg Gly Leu Thr Ser Tyr Ala Glu Thr Val
    210                 215                 220

Ser Val Tyr Gly Thr Glu Ala Val Phe Thr Asp Gly Asp Asp Thr Pro
225                 230                 235                 240

Trp Ser Lys Ala Phe Leu Ala Ser Ala Tyr Ala Ser Arg Gly Leu Lys
                245                 250                 255

Met Arg Tyr Thr Ser Gly Thr Gly Ser Glu Ala Leu Met Gly Tyr Ser
            260                 265                 270

Glu Ser Lys Ser Met Leu Tyr Leu Glu Ser Arg Cys Ile Phe Ile Thr
        275                 280                 285

Lys Gly Ala Gly Val Gln Gly Leu Gln Asn Gly Ala Val Ser Cys Ile
    290                 295                 300

Gly Met Thr Gly Ala Val Pro Ser Gly Ile Arg Ala Val Leu Ala Glu
305                 310                 315                 320

Asn Leu Ile Ala Ser Met Leu Asp Leu Glu Val Ala Ser Ala Asn Asp
                325                 330                 335

Gln Thr Phe Ser His Ser Asp Ile Arg Arg Thr Ala Arg Thr Leu Met
            340                 345                 350

Gln Met Leu Pro Gly Thr Asp Phe Ile Phe Ser Gly Tyr Ser Ala Val
        355                 360                 365

Pro Asn Tyr Asp Asn Met Phe Ala Gly Ser Asn Phe Asp Ala Glu Asp
    370                 375                 380

Phe Asp Asp Tyr Asn Ile Leu Gln Arg Asp Leu Met Val Asp Gly Gly
385                 390                 395                 400

Leu Arg Pro Val Thr Glu Ala Glu Thr Ile Ala Ile Arg Gln Lys Ala
                405                 410                 415
```

```
Ala Arg Ala Ile Gln Ala Val Phe Arg Glu Leu Gly Leu Pro Pro Ile
            420                 425                 430

Ala Asp Glu Glu Val Glu Ala Ala Thr Tyr Ala His Gly Ser Asn Glu
        435                 440                 445

Met Pro Pro Arg Asn Val Val Glu Asp Leu Ser Ala Val Glu Glu Met
    450                 455                 460

Met Lys Arg Asn Ile Thr Gly Leu Asp Ile Val Gly Ala Leu Ser Arg
465                 470                 475                 480

Ser Gly Phe Glu Asp Ile Ala Ser Asn Ile Leu Asn Met Leu Arg Gln
                485                 490                 495

Arg Val Thr Gly Asp Tyr Leu Gln Thr Ser Ala Ile Leu Asp Arg Gln
            500                 505                 510

Phe Glu Val Val Ser Ala Val Asn Asp Ile Asn Asp Tyr Gln Gly Pro
        515                 520                 525

Gly Thr Gly Tyr Arg Ile Ser Ala Glu Arg Trp Ala Glu Ile Lys Asn
    530                 535                 540

Ile Pro Gly Val Val Gln Pro Asp Thr Ile Glu
545                 550                 555


<210>  11
<211>  585
<212>  DNA
<213>  Klebsiella pneumoniae


<220>
<221>  CDS
<222>  (1)..(585)

<400>  11
gtg caa cag aca acc caa att cag ccc tct ttt acc ctg aaa acc cgc          48
Val Gln Gln Thr Thr Gln Ile Gln Pro Ser Phe Thr Leu Lys Thr Arg
1               5                   10                  15

gag ggc ggg gta gct tct gcc gat gaa cgc gcc gat gaa gtg gtg atc          96
Glu Gly Gly Val Ala Ser Ala Asp Glu Arg Ala Asp Glu Val Val Ile
            20                  25                  30

ggc gtc ggc cct gcc ttc gat aaa cac cag cat cac act ctg atc gat         144
Gly Val Gly Pro Ala Phe Asp Lys His Gln His His Thr Leu Ile Asp
        35                  40                  45

atg ccc cat ggc gcg atc ctc aaa gag ctg att gcc ggg gtg gaa gaa         192
Met Pro His Gly Ala Ile Leu Lys Glu Leu Ile Ala Gly Val Glu Glu
    50                  55                  60

gag ggg ctt cac gcc cgg gtg gtg cgc att ctg cgc acg tcc gac gtc         240
Glu Gly Leu His Ala Arg Val Val Arg Ile Leu Arg Thr Ser Asp Val
65                  70                  75                  80
```

```
tcc ttt atg gcc tgg gat gcg gcc aac ctg agc ggc tcg ggg atc ggc        288
Ser Phe Met Ala Trp Asp Ala Ala Asn Leu Ser Gly Ser Gly Ile Gly
                85                  90                  95

atc ggt atc cag tcg aag ggg acc acg gtc atc cat cag cgc gat ctg        336
Ile Gly Ile Gln Ser Lys Gly Thr Thr Val Ile His Gln Arg Asp Leu
            100                 105                 110

ctg ccg ctc agc aac ctg gag ctg ttc tcc cag gcg ccg ctg ctg acg        384
Leu Pro Leu Ser Asn Leu Glu Leu Phe Ser Gln Ala Pro Leu Leu Thr
        115                 120                 125

ctg gag acc tac cgg cag att ggc aaa aac gct gcg cgc tat gcg cgc        432
Leu Glu Thr Tyr Arg Gln Ile Gly Lys Asn Ala Ala Arg Tyr Ala Arg
    130                 135                 140

aaa gag tca cct tcg ccg gtg ccg gtg gtg aac gat cag atg gtg cgg        480
Lys Glu Ser Pro Ser Pro Val Pro Val Val Asn Asp Gln Met Val Arg
145                 150                 155                 160

ccg aaa ttt atg gcc aaa gcc gcg cta ttt cat atc aaa gag acc aaa        528
Pro Lys Phe Met Ala Lys Ala Ala Leu Phe His Ile Lys Glu Thr Lys
                165                 170                 175

cat gtg gtg cag gac gcc gag ccc gtc acc ctg cac atc gac tta gta        576
His Val Val Gln Asp Ala Glu Pro Val Thr Leu His Ile Asp Leu Val
            180                 185                 190

agg gag tga                                                            585
Arg Glu
```

<210> 12
<211> 194
<212> PRT
<213> Klebsiella pneumoniae

<400> 12

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Val Gln Gln Thr Thr Gln Ile Gln Pro Ser Phe Thr Leu Lys Thr Arg
1               5                   10                  15

Glu Gly Gly Val Ala Ser Ala Asp Glu Arg Ala Asp Glu Val Val Ile
            20                  25                  30

Gly Val Gly Pro Ala Phe Asp Lys His Gln His His Thr Leu Ile Asp
        35                  40                  45

Met Pro His Gly Ala Ile Leu Lys Glu Leu Ile Ala Gly Val Glu Glu
    50                  55                  60

Glu Gly Leu His Ala Arg Val Val Arg Ile Leu Arg Thr Ser Asp Val
65                  70                  75                  80

Ser Phe Met Ala Trp Asp Ala Ala Asn Leu Ser Gly Ser Gly Ile Gly
                85                  90                  95

Ile Gly Ile Gln Ser Lys Gly Thr Thr Val Ile His Gln Arg Asp Leu
            100                 105                 110
```

```
Leu Pro Leu Ser Asn Leu Glu Leu Phe Ser Gln Ala Pro Leu Leu Thr
        115                 120                 125


Leu Glu Thr Tyr Arg Gln Ile Gly Lys Asn Ala Ala Arg Tyr Ala Arg
    130                 135                 140


Lys Glu Ser Pro Ser Pro Val Pro Val Val Asn Asp Gln Met Val Arg
145                 150                 155                 160


Pro Lys Phe Met Ala Lys Ala Ala Leu Phe His Ile Lys Glu Thr Lys
                165                 170                 175


His Val Val Gln Asp Ala Glu Pro Val Thr Leu His Ile Asp Leu Val
            180                 185                 190


Arg Glu



<210>  13
<211>  426
<212>  DNA
<213>  Klebsiella pneumoniae


<220>
<221>  CDS
<222>  (1)..(426)

<400>  13
atg agc gag aaa acc atg cgc gtg cag gat tat ccg tta gcc acc cgc         48
Met Ser Glu Lys Thr Met Arg Val Gln Asp Tyr Pro Leu Ala Thr Arg
1               5                   10                  15

tgc ccg gag cat atc ctg acg cct acc ggc aaa cca ttg acc gat att         96
Cys Pro Glu His Ile Leu Thr Pro Thr Gly Lys Pro Leu Thr Asp Ile
            20                  25                  30

acc ctc gag aag gtg ctc tct ggc gag gtg ggc ccg cag gat gtg cgg        144
Thr Leu Glu Lys Val Leu Ser Gly Glu Val Gly Pro Gln Asp Val Arg
        35                  40                  45

atc tcc cgc cag acc ctt gag tac cag gcg cag att gcc gag cag atg        192
Ile Ser Arg Gln Thr Leu Glu Tyr Gln Ala Gln Ile Ala Glu Gln Met
    50                  55                  60

cag cgc cat gcg gtg gcg cgc aat ttc cgc cgc gcg gcg gag ctt atc        240
Gln Arg His Ala Val Ala Arg Asn Phe Arg Arg Ala Ala Glu Leu Ile
65                  70                  75                  80

gcc att cct gac gag cgc att ctg gct atc tat aac gcg ctg cgc ccg        288
Ala Ile Pro Asp Glu Arg Ile Leu Ala Ile Tyr Asn Ala Leu Arg Pro
                85                  90                  95

ttc cgc tcc tcg cag gcg gag ctg ctg gcg atc gcc gac gag ctg gag        336
Phe Arg Ser Ser Gln Ala Glu Leu Leu Ala Ile Ala Asp Glu Leu Glu
            100                 105                 110

cac acc tgg cat gcg aca gtg aat gcc gcc ttt gtc cgg gag tcg gcg        384
His Thr Trp His Ala Thr Val Asn Ala Ala Phe Val Arg Glu Ser Ala
        115                 120                 125

gaa gtg tat cag cag cgg cat aag ctg cgt aaa gga agc taa                426
```

Glu Val Tyr Gln Gln Arg His Lys Leu Arg Lys Gly Ser
130 135 140

<210> 14
<211> 141
<212> PRT
<213> Klebsiella pneumoniae

<400> 14

Met Ser Glu Lys Thr Met Arg Val Gln Asp Tyr Pro Leu Ala Thr Arg
1 5 10 15

Cys Pro Glu His Ile Leu Thr Pro Thr Gly Lys Pro Leu Thr Asp Ile
20 25 30

Thr Leu Glu Lys Val Leu Ser Gly Glu Val Gly Pro Gln Asp Val Arg
35 40 45

Ile Ser Arg Gln Thr Leu Glu Tyr Gln Ala Gln Ile Ala Glu Gln Met
50 55 60

Gln Arg His Ala Val Ala Arg Asn Phe Arg Arg Ala Ala Glu Leu Ile
65 70 75 80

Ala Ile Pro Asp Glu Arg Ile Leu Ala Ile Tyr Asn Ala Leu Arg Pro
85 90 95

Phe Arg Ser Ser Gln Ala Glu Leu Leu Ala Ile Ala Asp Glu Leu Glu
100 105 110

His Thr Trp His Ala Thr Val Asn Ala Ala Phe Val Arg Glu Ser Ala
115 120 125

Glu Val Tyr Gln Gln Arg His Lys Leu Arg Lys Gly Ser
130 135 140

<210> 15
<211> 1539
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1539)

<400> 15
atg acc aat aat ccc cct tca gca cag att aag ccc ggc gag tat ggt 48
Met Thr Asn Asn Pro Pro Ser Ala Gln Ile Lys Pro Gly Glu Tyr Gly
1 5 10 15

ttc ccc ctc aag tta aaa gcc cgc tat gac aac ttt att ggc ggc gaa 96
Phe Pro Leu Lys Leu Lys Ala Arg Tyr Asp Asn Phe Ile Gly Gly Glu
20 25 30

tgg gta gcc cct gcc gac ggc gag tat tac cag aat ctg acg ccg gtg 144
Trp Val Ala Pro Ala Asp Gly Glu Tyr Tyr Gln Asn Leu Thr Pro Val

```
        35                  40                  45

acc ggg cag ctg ctg tgc gaa gtg gcg tct tcg ggc aaa cga gac atc        192
Thr Gly Gln Leu Leu Cys Glu Val Ala Ser Ser Gly Lys Arg Asp Ile
    50                  55                  60

gat ctg gcg ctg gat gct gcg cac aaa gtg aaa gat aaa tgg gcg cac        240
Asp Leu Ala Leu Asp Ala Ala His Lys Val Lys Asp Lys Trp Ala His
65                  70                  75                  80

acc tcg gtg cag gat cgt gcg gcg att ctg ttt aag att gcc gat cga        288
Thr Ser Val Gln Asp Arg Ala Ala Ile Leu Phe Lys Ile Ala Asp Arg
                85                  90                  95

atg gaa caa aac ctc gag ctg tta gcg aca gct gaa acc tgg gat aac        336
Met Glu Gln Asn Leu Glu Leu Leu Ala Thr Ala Glu Thr Trp Asp Asn
            100                 105                 110

ggc aaa ccc att cgc gaa acc agt gct gcg gat gta ccg ctg gcg att        384
Gly Lys Pro Ile Arg Glu Thr Ser Ala Ala Asp Val Pro Leu Ala Ile
        115                 120                 125

gac cat ttc cgc tat ttc gcc tcg tgt att cgg gcg cag gaa ggt ggg        432
Asp His Phe Arg Tyr Phe Ala Ser Cys Ile Arg Ala Gln Glu Gly Gly
    130                 135                 140

atc agt gaa gtt gat agc gaa acc gtg gcc tat cat ttc cat gaa ccg        480
Ile Ser Glu Val Asp Ser Glu Thr Val Ala Tyr His Phe His Glu Pro
145                 150                 155                 160

tta ggc gtg gtg ggg cag att atc ccg tgg aac ttc ccg ctg ctg atg        528
Leu Gly Val Val Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met
                165                 170                 175

gcg agc tgg aaa atg gct ccc gcg ctg gcg gcg ggc aac tgt gtg gtg        576
Ala Ser Trp Lys Met Ala Pro Ala Leu Ala Ala Gly Asn Cys Val Val
            180                 185                 190

ctg aaa ccc gca cgt ctt acc ccg ctt tct gta ctg ctg cta atg gaa        624
Leu Lys Pro Ala Arg Leu Thr Pro Leu Ser Val Leu Leu Leu Met Glu
        195                 200                 205

att gtc ggt gat tta ctg ccg ccg ggc gtg gtg aac gtg gtc aat ggc        672
Ile Val Gly Asp Leu Leu Pro Pro Gly Val Val Asn Val Val Asn Gly
    210                 215                 220

gca ggt ggg gta att ggc gaa tat ctg gcg acc tcg aaa cgc atc gcc        720
Ala Gly Gly Val Ile Gly Glu Tyr Leu Ala Thr Ser Lys Arg Ile Ala
225                 230                 235                 240

aaa gtg gcg ttt acc ggc tca acg gaa gtg ggc caa caa att atg caa        768
Lys Val Ala Phe Thr Gly Ser Thr Glu Val Gly Gln Gln Ile Met Gln
                245                 250                 255

tac gca acg caa aac att att ccg gtg acg ctg gag ttg ggc ggt aag        816
Tyr Ala Thr Gln Asn Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys
            260                 265                 270

tcg cca aat atc ttc ttt gct gat gtg atg gat gaa gaa gat gcc ttt        864
Ser Pro Asn Ile Phe Phe Ala Asp Val Met Asp Glu Glu Asp Ala Phe
        275                 280                 285

ttc gat aaa gcg ctg gaa ggc ttt gca ctg ttt gcc ttt aac cag ggc        912
Phe Asp Lys Ala Leu Glu Gly Phe Ala Leu Phe Ala Phe Asn Gln Gly
    290                 295                 300

gaa gtt tgc acc tgt ccg agt cgt gct tta gtg cag gaa tct atc tac        960
Glu Val Cys Thr Cys Pro Ser Arg Ala Leu Val Gln Glu Ser Ile Tyr
```

305 310 315 320

gaa cgc ttt atg gaa cgc gcc atc cgc cgt gtc gaa agc att cgt agc 1008
Glu Arg Phe Met Glu Arg Ala Ile Arg Arg Val Glu Ser Ile Arg Ser
325 330 335

ggt aac ccg ctc gac agc gtg acg caa atg ggc gcg cag gtt tct cac 1056
Gly Asn Pro Leu Asp Ser Val Thr Gln Met Gly Ala Gln Val Ser His
340 345 350

ggg caa ctg gaa acc atc ctc aac tac att gat atc ggt aaa aaa gag 1104
Gly Gln Leu Glu Thr Ile Leu Asn Tyr Ile Asp Ile Gly Lys Lys Glu
355 360 365

ggc gct gac gtg ctc aca ggc ggg cgg cgc aag ctg ctg gaa ggt gaa 1152
Gly Ala Asp Val Leu Thr Gly Gly Arg Arg Lys Leu Leu Glu Gly Glu
370 375 380

ctg aaa gac ggc tac tac ctc gaa ccg acg att ctg ttt ggt cag aac 1200
Leu Lys Asp Gly Tyr Tyr Leu Glu Pro Thr Ile Leu Phe Gly Gln Asn
385 390 395 400

aat atg cgg gtg ttc cag gag gag att ttt ggc ccg gtg ctg gcg gtg 1248
Asn Met Arg Val Phe Gln Glu Glu Ile Phe Gly Pro Val Leu Ala Val
405 410 415

acc acc ttc aaa acg atg gaa gaa gcg ctg gag ctg gcg aac gat acg 1296
Thr Thr Phe Lys Thr Met Glu Glu Ala Leu Glu Leu Ala Asn Asp Thr
420 425 430

caa tat ggc ctg ggc gcg ggc gtc tgg agc cgc aac ggt aat ctg gcc 1344
Gln Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg Asn Gly Asn Leu Ala
435 440 445

tat aag atg ggg cgc ggc ata cag gct ggg cgc gtg tgg acc aac tgt 1392
Tyr Lys Met Gly Arg Gly Ile Gln Ala Gly Arg Val Trp Thr Asn Cys
450 455 460

tat cac gct tac ccg gca cat gcg gcg ttt ggt ggc tac aaa caa tca 1440
Tyr His Ala Tyr Pro Ala His Ala Ala Phe Gly Gly Tyr Lys Gln Ser
465 470 475 480

ggt atc ggt cgc gaa acc cac aag atg atg ctg gag cat tac cag caa 1488
Gly Ile Gly Arg Glu Thr His Lys Met Met Leu Glu His Tyr Gln Gln
485 490 495

acc aag tgc ctg ctg gtg agc tac tcg gat aaa ccg ttg ggg ctg ttc 1536
Thr Lys Cys Leu Leu Val Ser Tyr Ser Asp Lys Pro Leu Gly Leu Phe
500 505 510

tga 1539

<210> 16
<211> 512
<212> PRT
<213> Escherichia coli

<400> 16

Met Thr Asn Asn Pro Pro Ser Ala Gln Ile Lys Pro Gly Glu Tyr Gly
1 5 10 15

Phe Pro Leu Lys Leu Lys Ala Arg Tyr Asp Asn Phe Ile Gly Gly Glu
20 25 30

```
Trp Val Ala Pro Ala Asp Gly Glu Tyr Tyr Gln Asn Leu Thr Pro Val
        35                  40                  45

Thr Gly Gln Leu Leu Cys Glu Val Ala Ser Ser Gly Lys Arg Asp Ile
    50                  55                  60

Asp Leu Ala Leu Asp Ala Ala His Lys Val Lys Asp Lys Trp Ala His
65                  70                  75                  80

Thr Ser Val Gln Asp Arg Ala Ala Ile Leu Phe Lys Ile Ala Asp Arg
                85                  90                  95

Met Glu Gln Asn Leu Glu Leu Leu Ala Thr Ala Glu Thr Trp Asp Asn
            100                 105                 110

Gly Lys Pro Ile Arg Glu Thr Ser Ala Ala Asp Val Pro Leu Ala Ile
        115                 120                 125

Asp His Phe Arg Tyr Phe Ala Ser Cys Ile Arg Ala Gln Glu Gly Gly
    130                 135                 140

Ile Ser Glu Val Asp Ser Glu Thr Val Ala Tyr His Phe His Glu Pro
145                 150                 155                 160

Leu Gly Val Val Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met
                165                 170                 175

Ala Ser Trp Lys Met Ala Pro Ala Leu Ala Ala Gly Asn Cys Val Val
            180                 185                 190

Leu Lys Pro Ala Arg Leu Thr Pro Leu Ser Val Leu Leu Leu Met Glu
        195                 200                 205

Ile Val Gly Asp Leu Leu Pro Pro Gly Val Val Asn Val Val Asn Gly
    210                 215                 220

Ala Gly Gly Val Ile Gly Glu Tyr Leu Ala Thr Ser Lys Arg Ile Ala
225                 230                 235                 240

Lys Val Ala Phe Thr Gly Ser Thr Glu Val Gly Gln Gln Ile Met Gln
                245                 250                 255

Tyr Ala Thr Gln Asn Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys
            260                 265                 270

Ser Pro Asn Ile Phe Phe Ala Asp Val Met Asp Glu Glu Asp Ala Phe
        275                 280                 285

Phe Asp Lys Ala Leu Glu Gly Phe Ala Leu Phe Ala Phe Asn Gln Gly
    290                 295                 300
```

Glu Val Cys Thr Cys Pro Ser Arg Ala Leu Val Gln Glu Ser Ile Tyr
305 310 315 320

Glu Arg Phe Met Glu Arg Ala Ile Arg Arg Val Glu Ser Ile Arg Ser
325 330 335

Gly Asn Pro Leu Asp Ser Val Thr Gln Met Gly Ala Gln Val Ser His
340 345 350

Gly Gln Leu Glu Thr Ile Leu Asn Tyr Ile Asp Ile Gly Lys Lys Glu
355 360 365

Gly Ala Asp Val Leu Thr Gly Gly Arg Arg Lys Leu Leu Glu Gly Glu
370 375 380

Leu Lys Asp Gly Tyr Tyr Leu Glu Pro Thr Ile Leu Phe Gly Gln Asn
385 390 395 400

Asn Met Arg Val Phe Gln Glu Glu Ile Phe Gly Pro Val Leu Ala Val
405 410 415

Thr Thr Phe Lys Thr Met Glu Glu Ala Leu Glu Leu Ala Asn Asp Thr
420 425 430

Gln Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg Asn Gly Asn Leu Ala
435 440 445

Tyr Lys Met Gly Arg Gly Ile Gln Ala Gly Arg Val Trp Thr Asn Cys
450 455 460

Tyr His Ala Tyr Pro Ala His Ala Ala Phe Gly Gly Tyr Lys Gln Ser
465 470 475 480

Gly Ile Gly Arg Glu Thr His Lys Met Met Leu Glu His Tyr Gln Gln
485 490 495

Thr Lys Cys Leu Leu Val Ser Tyr Ser Asp Lys Pro Leu Gly Leu Phe
500 505 510

<210> 17
<211> 1440
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1440)

<400> 17
atg tca gta ccc gtt caa cat cct atg tat atc gat gga cag ttt gtt 48
Met Ser Val Pro Val Gln His Pro Met Tyr Ile Asp Gly Gln Phe Val
1 5 10 15

acc tgg cgt gga gac gca tgg att gat gtg gta aac cct gct aca gag 96

```
Thr Trp Arg Gly Asp Ala Trp Ile Asp Val Val Asn Pro Ala Thr Glu
            20                  25                  30

gct gtc att tcc cgc ata ccc gat ggt cag gcc gag gat gcc cgt aag        144
Ala Val Ile Ser Arg Ile Pro Asp Gly Gln Ala Glu Asp Ala Arg Lys
        35                  40                  45

gca atc gat gca gca gaa cgt gca caa cca gaa tgg gaa gcg ttg cct        192
Ala Ile Asp Ala Ala Glu Arg Ala Gln Pro Glu Trp Glu Ala Leu Pro
    50                  55                  60

gct att gaa cgc gcc agt tgg ttg cgc aaa atc tcc gcc ggg atc cgc        240
Ala Ile Glu Arg Ala Ser Trp Leu Arg Lys Ile Ser Ala Gly Ile Arg
65                  70                  75                  80

gaa cgc gcc agt gaa atc agt gcg ctg att gtt gaa gaa ggg ggc aag        288
Glu Arg Ala Ser Glu Ile Ser Ala Leu Ile Val Glu Glu Gly Gly Lys
                85                  90                  95

atc cag cag ctg gct gaa gtc gaa gtg gct ttt act gcc gac tat atc        336
Ile Gln Gln Leu Ala Glu Val Glu Val Ala Phe Thr Ala Asp Tyr Ile
            100                 105                 110

gat tac atg gcg gag tgg gca cgg cgt tac gag ggc gag att att caa        384
Asp Tyr Met Ala Glu Trp Ala Arg Arg Tyr Glu Gly Glu Ile Ile Gln
        115                 120                 125

agc gat cgt cca gga gaa aat att ctt ttg ttt aaa cgt gcg ctt ggt        432
Ser Asp Arg Pro Gly Glu Asn Ile Leu Leu Phe Lys Arg Ala Leu Gly
    130                 135                 140

gtg act acc ggc att ctg ccg tgg aac ttc ccg ttc ttc ctc att gcc        480
Val Thr Thr Gly Ile Leu Pro Trp Asn Phe Pro Phe Phe Leu Ile Ala
145                 150                 155                 160

cgc aaa atg gct ccc gct ctt ttg acc ggt aat acc atc gtc att aaa        528
Arg Lys Met Ala Pro Ala Leu Leu Thr Gly Asn Thr Ile Val Ile Lys
                165                 170                 175

cct agt gaa ttt acg cca aac aat gcg att gca ttc gcc aaa atc gtc        576
Pro Ser Glu Phe Thr Pro Asn Asn Ala Ile Ala Phe Ala Lys Ile Val
            180                 185                 190

gat gaa ata ggc ctt ccg cgc ggc gtg ttt aac ctt gta ctg ggg cgt        624
Asp Glu Ile Gly Leu Pro Arg Gly Val Phe Asn Leu Val Leu Gly Arg
        195                 200                 205

ggt gaa acc gtt ggg caa gaa ctg gcg ggt aac cca aag gtc gca atg        672
Gly Glu Thr Val Gly Gln Glu Leu Ala Gly Asn Pro Lys Val Ala Met
    210                 215                 220

gtc agt atg aca ggc agc gtc tct gca ggt gag aag atc atg gcg act        720
Val Ser Met Thr Gly Ser Val Ser Ala Gly Glu Lys Ile Met Ala Thr
225                 230                 235                 240

gcg gcg aaa aac atc acc aaa gtg tgt ctg gaa ttg ggg ggt aaa gca        768
Ala Ala Lys Asn Ile Thr Lys Val Cys Leu Glu Leu Gly Gly Lys Ala
                245                 250                 255

cca gct atc gta atg gac gat gcc gat ctt gaa ctg gca gtc aaa gcc        816
Pro Ala Ile Val Met Asp Asp Ala Asp Leu Glu Leu Ala Val Lys Ala
            260                 265                 270

atc gtt gat tca cgc gtc att aat agt ggg caa gtg tgt aac tgt gca        864
Ile Val Asp Ser Arg Val Ile Asn Ser Gly Gln Val Cys Asn Cys Ala
        275                 280                 285

gaa cgt gtt tat gta cag aaa ggc att tat gat cag ttc gtc aat cgg        912
```

```
Glu Arg Val Tyr Val Gln Lys Gly Ile Tyr Asp Gln Phe Val Asn Arg
    290                 295                 300

ctg ggt gaa gcg atg cag gcg gtt caa ttt ggt aac ccc gct gaa cgc        960
Leu Gly Glu Ala Met Gln Ala Val Gln Phe Gly Asn Pro Ala Glu Arg
305                 310                 315                 320

aac gac att gcg atg ggg ccg ttg att aac gcc gcg gcg ctg gaa agg       1008
Asn Asp Ile Ala Met Gly Pro Leu Ile Asn Ala Ala Ala Leu Glu Arg
                325                 330                 335

gtc gag caa aaa gtg gcg cgc gca gta gaa gaa ggg gcg aga gtg gcg       1056
Val Glu Gln Lys Val Ala Arg Ala Val Glu Glu Gly Ala Arg Val Ala
            340                 345                 350

ttc ggt ggc aaa gcg gta gag ggg aaa gga tat tat tat ccg ccg aca       1104
Phe Gly Gly Lys Ala Val Glu Gly Lys Gly Tyr Tyr Tyr Pro Pro Thr
        355                 360                 365

ttg ctg ctg gat gtt cgc cag gaa atg tcg att atg cat gag gaa acc       1152
Leu Leu Leu Asp Val Arg Gln Glu Met Ser Ile Met His Glu Glu Thr
    370                 375                 380

ttt ggc ccg gtg ctg cca gtt gtc gca ttt gac acg ctg gaa gat gct       1200
Phe Gly Pro Val Leu Pro Val Val Ala Phe Asp Thr Leu Glu Asp Ala
385                 390                 395                 400

atc tca atg gct aat gac agt gat tac ggc ctg acc tca tca atc tat       1248
Ile Ser Met Ala Asn Asp Ser Asp Tyr Gly Leu Thr Ser Ser Ile Tyr
                405                 410                 415

acc caa aat ctg aac gtc gcg atg aaa gcc att aaa ggg ctg aag ttt       1296
Thr Gln Asn Leu Asn Val Ala Met Lys Ala Ile Lys Gly Leu Lys Phe
            420                 425                 430

ggt gaa act tac atc aac cgt gaa aac ttc gaa gct atg caa ggc ttc       1344
Gly Glu Thr Tyr Ile Asn Arg Glu Asn Phe Glu Ala Met Gln Gly Phe
        435                 440                 445

cac gcc gga tgg cgt aaa tcc ggt att ggc ggc gca gat ggt aaa cat       1392
His Ala Gly Trp Arg Lys Ser Gly Ile Gly Gly Ala Asp Gly Lys His
    450                 455                 460

ggc ttg cat gaa tat ctg cag acc cag gtg gtt tat tta cag tct taa       1440
Gly Leu His Glu Tyr Leu Gln Thr Gln Val Val Tyr Leu Gln Ser
465                 470                 475


<210>  18
<211>  479
<212>  PRT
<213>  Escherichia coli

<400>  18

Met Ser Val Pro Val Gln His Pro Met Tyr Ile Asp Gly Gln Phe Val
1               5                   10                  15


Thr Trp Arg Gly Asp Ala Trp Ile Asp Val Val Asn Pro Ala Thr Glu
            20                  25                  30


Ala Val Ile Ser Arg Ile Pro Asp Gly Gln Ala Glu Asp Ala Arg Lys
        35                  40                  45


Ala Ile Asp Ala Ala Glu Arg Ala Gln Pro Glu Trp Glu Ala Leu Pro
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50 55 60

Ala Ile Glu Arg Ala Ser Trp Leu Arg Lys Ile Ser Ala Gly Ile Arg
65 70 75 80

Glu Arg Ala Ser Glu Ile Ser Ala Leu Ile Val Glu Glu Gly Gly Lys
85 90 95

Ile Gln Gln Leu Ala Glu Val Glu Val Ala Phe Thr Ala Asp Tyr Ile
100 105 110

Asp Tyr Met Ala Glu Trp Ala Arg Arg Tyr Glu Gly Glu Ile Ile Gln
115 120 125

Ser Asp Arg Pro Gly Glu Asn Ile Leu Leu Phe Lys Arg Ala Leu Gly
130 135 140

Val Thr Thr Gly Ile Leu Pro Trp Asn Phe Pro Phe Phe Leu Ile Ala
145 150 155 160

Arg Lys Met Ala Pro Ala Leu Leu Thr Gly Asn Thr Ile Val Ile Lys
165 170 175

Pro Ser Glu Phe Thr Pro Asn Asn Ala Ile Ala Phe Ala Lys Ile Val
180 185 190

Asp Glu Ile Gly Leu Pro Arg Gly Val Phe Asn Leu Val Leu Gly Arg
195 200 205

Gly Glu Thr Val Gly Gln Glu Leu Ala Gly Asn Pro Lys Val Ala Met
210 215 220

Val Ser Met Thr Gly Ser Val Ser Ala Gly Glu Lys Ile Met Ala Thr
225 230 235 240

Ala Ala Lys Asn Ile Thr Lys Val Cys Leu Glu Leu Gly Gly Lys Ala
245 250 255

Pro Ala Ile Val Met Asp Asp Ala Asp Leu Glu Leu Ala Val Lys Ala
260 265 270

Ile Val Asp Ser Arg Val Ile Asn Ser Gly Gln Val Cys Asn Cys Ala
275 280 285

Glu Arg Val Tyr Val Gln Lys Gly Ile Tyr Asp Gln Phe Val Asn Arg
290 295 300

Leu Gly Glu Ala Met Gln Ala Val Gln Phe Gly Asn Pro Ala Glu Arg
305 310 315 320

Asn Asp Ile Ala Met Gly Pro Leu Ile Asn Ala Ala Ala Leu Glu Arg

325 330 335

Val Glu Gln Lys Val Ala Arg Ala Val Glu Glu Gly Ala Arg Val Ala
340 345 350

Phe Gly Gly Lys Ala Val Glu Gly Lys Gly Tyr Tyr Tyr Pro Pro Thr
355 360 365

Leu Leu Leu Asp Val Arg Gln Glu Met Ser Ile Met His Glu Glu Thr
370 375 380

Phe Gly Pro Val Leu Pro Val Val Ala Phe Asp Thr Leu Glu Asp Ala
385 390 395 400

Ile Ser Met Ala Asn Asp Ser Asp Tyr Gly Leu Thr Ser Ser Ile Tyr
405 410 415

Thr Gln Asn Leu Asn Val Ala Met Lys Ala Ile Lys Gly Leu Lys Phe
420 425 430

Gly Glu Thr Tyr Ile Asn Arg Glu Asn Phe Glu Ala Met Gln Gly Phe
435 440 445

His Ala Gly Trp Arg Lys Ser Gly Ile Gly Gly Ala Asp Gly Lys His
450 455 460

Gly Leu His Glu Tyr Leu Gln Thr Gln Val Val Tyr Leu Gln Ser
465 470 475

<210> 19
<211> 1488
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1488)

<400> 19
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Met Asn Phe His His Leu Ala Tyr Trp Gln Asp Lys Ala Leu Ser Leu
1 5 10 15

gcc att gaa aac cgc tta ttt att aac ggt gaa tat act gct gcg gcg 96
Ala Ile Glu Asn Arg Leu Phe Ile Asn Gly Glu Tyr Thr Ala Ala Ala
20 25 30

gaa aat gaa acc ttt gaa acc gtt gat ccg gtc acc cag gca ccg ctg 144
Glu Asn Glu Thr Phe Glu Thr Val Asp Pro Val Thr Gln Ala Pro Leu
35 40 45

gcg aaa att gcc cgc ggc aag agc gtc gat atc gac cgt gcg atg agc 192
Ala Lys Ile Ala Arg Gly Lys Ser Val Asp Ile Asp Arg Ala Met Ser
50 55 60

gca gca cgc ggc gta ttt gaa cgc ggc gac tgg tca ctc tct tct ccg 240
Ala Ala Arg Gly Val Phe Glu Arg Gly Asp Trp Ser Leu Ser Ser Pro

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65                  70                  75                  80

gct aaa cgt aaa gcg gta ctg aat aaa ctc gcc gat tta atg gaa gcc        288
Ala Lys Arg Lys Ala Val Leu Asn Lys Leu Ala Asp Leu Met Glu Ala
                85                  90                  95

cac gcc gaa gag ctg gca ctg ctg gaa act ctc gac acc ggc aaa ccg        336
His Ala Glu Glu Leu Ala Leu Leu Glu Thr Leu Asp Thr Gly Lys Pro
            100                 105                 110

att cgt cac agt ctg cgt gat gat att ccc ggc gcg gcg cgc gcc att        384
Ile Arg His Ser Leu Arg Asp Asp Ile Pro Gly Ala Ala Arg Ala Ile
        115                 120                 125

cgc tgg tac gcc gaa gcg atc gac aaa gtg tat ggc gaa gtg gcg acc        432
Arg Trp Tyr Ala Glu Ala Ile Asp Lys Val Tyr Gly Glu Val Ala Thr
    130                 135                 140

acc agt agc cat gag ctg gcg atg atc gtg cgt gaa ccg gtc ggc gtg        480
Thr Ser Ser His Glu Leu Ala Met Ile Val Arg Glu Pro Val Gly Val
145                 150                 155                 160

att gcc gcc atc gtg ccg tgg aac ttc ccg ctg ttg ctg act tgc tgg        528
Ile Ala Ala Ile Val Pro Trp Asn Phe Pro Leu Leu Leu Thr Cys Trp
                165                 170                 175

aaa ctc ggc ccg gcg ctg gcg gcg gga aac agc gtg att cta aaa ccg        576
Lys Leu Gly Pro Ala Leu Ala Ala Gly Asn Ser Val Ile Leu Lys Pro
            180                 185                 190

tct gaa aaa tca ccg ctc agt gcg att cgt ctc gcg ggg ctg gcg aaa        624
Ser Glu Lys Ser Pro Leu Ser Ala Ile Arg Leu Ala Gly Leu Ala Lys
        195                 200                 205

gaa gca ggc ttg ccg gat ggt gtg ttg aac gtg gtg acg ggt ttt ggt        672
Glu Ala Gly Leu Pro Asp Gly Val Leu Asn Val Val Thr Gly Phe Gly
    210                 215                 220

cat gaa gcc ggg cag gcg ctg tcg cgt cat aac gat atc gac gcc att        720
His Glu Ala Gly Gln Ala Leu Ser Arg His Asn Asp Ile Asp Ala Ile
225                 230                 235                 240

gcc ttt acc ggt tca acc cgt acc ggg aaa cag ctg ctg aaa gat gcg        768
Ala Phe Thr Gly Ser Thr Arg Thr Gly Lys Gln Leu Leu Lys Asp Ala
                245                 250                 255

ggc gac agc aac atg aaa cgc gtc tgg ctg gaa gcg ggc ggc aaa agc        816
Gly Asp Ser Asn Met Lys Arg Val Trp Leu Glu Ala Gly Gly Lys Ser
            260                 265                 270

gcc aac atc gtt ttc gct gac tgc ccg gat ttg caa cag gcg gca agc        864
Ala Asn Ile Val Phe Ala Asp Cys Pro Asp Leu Gln Gln Ala Ala Ser
        275                 280                 285

gcc acc gca gca ggc att ttc tac aac cag gga cag gtg tgc atc gcc        912
Ala Thr Ala Ala Gly Ile Phe Tyr Asn Gln Gly Gln Val Cys Ile Ala
    290                 295                 300

gga acg cgc ctg ttg ctg gaa gag agc atc gcc gat gaa ttc tta gcc        960
Gly Thr Arg Leu Leu Leu Glu Glu Ser Ile Ala Asp Glu Phe Leu Ala
305                 310                 315                 320

ctg tta aaa cag cag gcg caa aac tgg cag ccg ggc cat cca ctt gat       1008
Leu Leu Lys Gln Gln Ala Gln Asn Trp Gln Pro Gly His Pro Leu Asp
                325                 330                 335

ccc gca acc acc atg ggc acc tta atc gac tgc gcc cac gcc gac tcg       1056
Pro Ala Thr Thr Met Gly Thr Leu Ile Asp Cys Ala His Ala Asp Ser
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            340                 345                 350

gtc cat agc ttt att cgg gaa ggc gaa agc aaa ggg caa ctg ttg ttg       1104
Val His Ser Phe Ile Arg Glu Gly Glu Ser Lys Gly Gln Leu Leu Leu
        355                 360                 365

gat ggc cgt aac gcc ggg ctg gct gcc gcc atc ggc ccg acc atc ttt       1152
Asp Gly Arg Asn Ala Gly Leu Ala Ala Ala Ile Gly Pro Thr Ile Phe
    370                 375                 380

gtg gat gtg gac ccg aat gcg tcc tta agt cgc gaa gag att ttc ggt       1200
Val Asp Val Asp Pro Asn Ala Ser Leu Ser Arg Glu Glu Ile Phe Gly
385                 390                 395                 400

ccg gtg ctg gtg gtc acg cgt ttc aca tca gaa gaa cag gcg cta cag       1248
Pro Val Leu Val Val Thr Arg Phe Thr Ser Glu Glu Gln Ala Leu Gln
                405                 410                 415

ctt gcc aac gac agc cag tac ggc ctt ggc gcg gcg gta tgg acg cgc       1296
Leu Ala Asn Asp Ser Gln Tyr Gly Leu Gly Ala Ala Val Trp Thr Arg
            420                 425                 430

gac ctc tcc cgc gcg cac cgc atg agc cga cgc ctg aaa gcc ggt tcc       1344
Asp Leu Ser Arg Ala His Arg Met Ser Arg Arg Leu Lys Ala Gly Ser
        435                 440                 445

gtc ttc gtc aat aac tac aac gac ggc gat atg acc gtg ccg ttt ggc       1392
Val Phe Val Asn Asn Tyr Asn Asp Gly Asp Met Thr Val Pro Phe Gly
    450                 455                 460

ggc tat aag cag agc ggc aac ggt cgc gac aaa tcc ctg cat gcc ctt       1440
Gly Tyr Lys Gln Ser Gly Asn Gly Arg Asp Lys Ser Leu His Ala Leu
465                 470                 475                 480

gaa aaa ttc act gaa ctg aaa acc atc tgg ata agc ctg gag gcc tga       1488
Glu Lys Phe Thr Glu Leu Lys Thr Ile Trp Ile Ser Leu Glu Ala
                485                 490                 495


<210>  20
<211>  495
<212>  PRT
<213>  Escherichia coli

<400>  20

Met Asn Phe His His Leu Ala Tyr Trp Gln Asp Lys Ala Leu Ser Leu
1               5                   10                  15


Ala Ile Glu Asn Arg Leu Phe Ile Asn Gly Glu Tyr Thr Ala Ala Ala
            20                  25                  30


Glu Asn Glu Thr Phe Glu Thr Val Asp Pro Val Thr Gln Ala Pro Leu
        35                  40                  45


Ala Lys Ile Ala Arg Gly Lys Ser Val Asp Ile Asp Arg Ala Met Ser
    50                  55                  60


Ala Ala Arg Gly Val Phe Glu Arg Gly Asp Trp Ser Leu Ser Ser Pro
65                  70                  75                  80


Ala Lys Arg Lys Ala Val Leu Asn Lys Leu Ala Asp Leu Met Glu Ala
                85                  90                  95
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His Ala Glu Glu Leu Ala Leu Leu Glu Thr Leu Asp Thr Gly Lys Pro
            100                 105                 110

Ile Arg His Ser Leu Arg Asp Asp Ile Pro Gly Ala Ala Arg Ala Ile
        115                 120                 125

Arg Trp Tyr Ala Glu Ala Ile Asp Lys Val Tyr Gly Glu Val Ala Thr
    130                 135                 140

Thr Ser Ser His Glu Leu Ala Met Ile Val Arg Glu Pro Val Gly Val
145                 150                 155                 160

Ile Ala Ala Ile Val Pro Trp Asn Phe Pro Leu Leu Leu Thr Cys Trp
                165                 170                 175

Lys Leu Gly Pro Ala Leu Ala Ala Gly Asn Ser Val Ile Leu Lys Pro
            180                 185                 190

Ser Glu Lys Ser Pro Leu Ser Ala Ile Arg Leu Ala Gly Leu Ala Lys
        195                 200                 205

Glu Ala Gly Leu Pro Asp Gly Val Leu Asn Val Val Thr Gly Phe Gly
    210                 215                 220

His Glu Ala Gly Gln Ala Leu Ser Arg His Asn Asp Ile Asp Ala Ile
225                 230                 235                 240

Ala Phe Thr Gly Ser Thr Arg Thr Gly Lys Gln Leu Leu Lys Asp Ala
                245                 250                 255

Gly Asp Ser Asn Met Lys Arg Val Trp Leu Glu Ala Gly Gly Lys Ser
            260                 265                 270

Ala Asn Ile Val Phe Ala Asp Cys Pro Asp Leu Gln Gln Ala Ala Ser
        275                 280                 285

Ala Thr Ala Ala Gly Ile Phe Tyr Asn Gln Gly Gln Val Cys Ile Ala
    290                 295                 300

Gly Thr Arg Leu Leu Leu Glu Glu Ser Ile Ala Asp Glu Phe Leu Ala
305                 310                 315                 320

Leu Leu Lys Gln Gln Ala Gln Asn Trp Gln Pro Gly His Pro Leu Asp
                325                 330                 335

Pro Ala Thr Thr Met Gly Thr Leu Ile Asp Cys Ala His Ala Asp Ser
            340                 345                 350

Val His Ser Phe Ile Arg Glu Gly Glu Ser Lys Gly Gln Leu Leu Leu
        355                 360                 365
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Asp Gly Arg Asn Ala Gly Leu Ala Ala Ala Ile Gly Pro Thr Ile Phe
370 375 380

Val Asp Val Asp Pro Asn Ala Ser Leu Ser Arg Glu Glu Ile Phe Gly
385 390 395 400

Pro Val Leu Val Val Thr Arg Phe Thr Ser Glu Glu Gln Ala Leu Gln
405 410 415

Leu Ala Asn Asp Ser Gln Tyr Gly Leu Gly Ala Ala Val Trp Thr Arg
420 425 430

Asp Leu Ser Arg Ala His Arg Met Ser Arg Arg Leu Lys Ala Gly Ser
435 440 445

Val Phe Val Asn Asn Tyr Asn Asp Gly Asp Met Thr Val Pro Phe Gly
450 455 460

Gly Tyr Lys Gln Ser Gly Asn Gly Arg Asp Lys Ser Leu His Ala Leu
465 470 475 480

Glu Lys Phe Thr Glu Leu Lys Thr Ile Trp Ile Ser Leu Glu Ala
485 490 495

<210> 21
<211> 1395
<212> DNA
<213> Escherichia coli

<400> 21
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cttgccgctc tggcgggatt actctttggc ctggatatcg gtgtaattgc tggcgcactg 120

ccgtttattg cagatgaatt ccagattact tcgcacacgc aagaatgggt cgtaagctcc 180

atgatgttcg gtgcggcagt cggtgcggtg ggcagcggct ggctctcctt taaactcggg 240

cgcaaaaaga gcctgatgat cggcgcaatt ttgtttgttg ccggttcgct gttctctgcg 300

gctgcgccaa acgttgaagt actgattctt tcccgcgttc tactggggct ggcggtgggt 360

gtggcctctt ataccgcacc gctgtacctc tctgaaattg cgccggaaaa aattcgtggc 420

agtatgatct cgatgtatca gttgatgatc actatcggga tcctcggtgc ttatctttct 480

gataccgcct tcagctacac cggtgcatgg cgctggatgc tgggtgtgat tatcatcccg 540

gcaattttgc tgctgattgg tgtcttcttc ctgccagaca gcccacgttg gtttgccgcc 600

aaacgccgtt ttgttgatgc cgaacgcgtg ctgctacgcc tgcgtgacac cagcgcggaa 660

gcgaaacgcg aactggatga aatccgtgaa agtttgcagg ttaaacagag tggctgggcg 720

ctgtttaaag agaacagcaa cttccgccgc gcggtgttcc ttggcgtact gttgcaggta 780

atgcagcaat tcaccgggat gaacgtcatc atgtattacg cgccgaaaat cttcgaactg 840

gcgggttata ccaacactac cgagcaaatg tgggggaccg tgattgtcgg cctgaccaac 900

gtacttgcca cctttatcgc aatcggcctt gttgaccgct ggggacgtaa accaacgcta 960

acgctgggct tcctggtgat ggctgctggc atgggcgtac tcggtacaat gatgcatatc 1020

ggtattcact ctccgtcggc gcagtatttc gccatcgcca tgctgctgat gtttattgtc 1080

ggttttgcca tgagtgccgg tccgctgatt tgggtactgt gctccgaaat tcagccgctg 1140

aaaggccgcg attttggcat cacctgctcc actgccacca actggattgc caacatgatc 1200

gttggcgcaa cgttcctgac catgctcaac acgctgggta acgccaacac cttctgggtg 1260

tatgcggctc tgaacgtact gtttatcctg ctgacattgt ggctggtacc ggaaaccaaa 1320

cacgtttcgc tggaacatat tgaacgtaat ctgatgaaag gtcgtaaact gcgcgaaata 1380

ggcgctcacg attaa 1395

<210> 22
<211> 464
<212> PRT
<213> Escherichia coli

<400> 22

Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn Lys Ala Met Thr Phe
1 5 10 15

Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp
20 25 30

Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln
35 40 45

Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
50 55 60

Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
65 70 75 80

Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
85 90 95

Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
100 105 110

Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
115 120 125

Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
130 135 140

Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
145 150 155 160

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Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val
                165                 170                 175

Ile Ile Ile Pro Ala Ile Leu Leu Leu Ile Gly Val Phe Phe Leu Pro
            180                 185                 190

Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
        195                 200                 205

Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
    210                 215                 220

Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
225                 230                 235                 240

Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
                245                 250                 255

Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
            260                 265                 270

Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu
        275                 280                 285

Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
    290                 295                 300

Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu
305                 310                 315                 320

Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
                325                 330                 335

Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
            340                 345                 350

Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
        355                 360                 365

Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp
    370                 375                 380

Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile
385                 390                 395                 400

Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn
                405                 410                 415

Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr
            420                 425                 430
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Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu
435 440 445

Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp
450 455 460

<210> 23
<211> 1248
<212> DNA
<213> Escherichia coli

<400> 23
atggcactga atattccatt cagaaatgcg tactatcgtt ttgcatccag ttactcattt 60

ctcttttta tttcctggtc gctgtggtgg tcgttatacg ctatttggct gaaaggacat 120

ctaggattaa cagggacgga attaggtaca ctttattcgg tcaaccagtt taccagcatt 180

ctatttatga tgttctacgg catcgttcag gataaactcg gtctgaagaa accgctcatc 240

tggtgtatga gtttcattct ggtcttgacc ggaccgttta tgatttacgt ttatgaaccg 300

ttactgcaaa gcaatttttc tgtaggtcta attctggggg cgctcttttt tggcctgggg 360

tatctggcgg gatgcggttt gcttgacagc ttcaccgaaa aaatggcgcg aaattttcat 420

ttcgaatatg gaacagcgcg cgcctgggga tcttttggct atgctattgg cgcgttcttt 480

gccggtatat tttttagtat cagtccccat atcaacttct ggttggtctc gctatttggc 540

gctgtattta tgatgatcaa catgcgtttt aaagataagg atcaccagtg catagcggcg 600

gatgcgggag gggtaaaaaa agaggatttt atcgcagttt tcaaggatcg aaacttctgg 660

gttttcgtca tatttattgt ggggacgtgg tctttctata acatttttga tcaacaactc 720

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gccattgagg ttccactttg tgtcatatcc gtcttcaaat acagcgtggc aaactttgat 1020

aagcgcctgt cgtcgacgat ctttctgatt ggttttcaaa ttgccagttc gcttgggatt 1080

gtgctgcttt caacgccgac tgggatactc tttgaccacg caggctacca gacagttttc 1140

ttcgcaattt cgggtattgt ctgcctgatg ttgctatttg gcattttctt cctgagtaaa 1200

aaacgcgagc aaatagttat ggaaacgcct gtaccttcag caatatag 1248

<210> 24
<211> 415
<212> PRT
<213> Escherichia coli

<400> 24

Met Ala Leu Asn Ile Pro Phe Arg Asn Ala Tyr Tyr Arg Phe Ala Ser
1 5 10 15

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Ser Tyr Ser Phe Leu Phe Phe Ile Ser Trp Ser Leu Trp Trp Ser Leu
            20                  25                  30

Tyr Ala Ile Trp Leu Lys Gly His Leu Gly Leu Thr Gly Thr Glu Leu
        35                  40                  45

Gly Thr Leu Tyr Ser Val Asn Gln Phe Thr Ser Ile Leu Phe Met Met
    50                  55                  60

Phe Tyr Gly Ile Val Gln Asp Lys Leu Gly Leu Lys Lys Pro Leu Ile
65                  70                  75                  80

Trp Cys Met Ser Phe Ile Leu Val Leu Thr Gly Pro Phe Met Ile Tyr
                85                  90                  95

Val Tyr Glu Pro Leu Leu Gln Ser Asn Phe Ser Val Gly Leu Ile Leu
            100                 105                 110

Gly Ala Leu Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Leu
        115                 120                 125

Asp Ser Phe Thr Glu Lys Met Ala Arg Asn Phe His Phe Glu Tyr Gly
    130                 135                 140

Thr Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Gly Ala Phe Phe
145                 150                 155                 160

Ala Gly Ile Phe Phe Ser Ile Ser Pro His Ile Asn Phe Trp Leu Val
                165                 170                 175

Ser Leu Phe Gly Ala Val Phe Met Met Ile Asn Met Arg Phe Lys Asp
            180                 185                 190

Lys Asp His Gln Cys Ile Ala Ala Asp Ala Gly Gly Val Lys Lys Glu
        195                 200                 205

Asp Phe Ile Ala Val Phe Lys Asp Arg Asn Phe Trp Val Phe Val Ile
    210                 215                 220

Phe Ile Val Gly Thr Trp Ser Phe Tyr Asn Ile Phe Asp Gln Gln Leu
225                 230                 235                 240

Phe Pro Val Phe Tyr Ala Gly Leu Phe Glu Ser His Asp Val Gly Thr
                245                 250                 255

Arg Leu Tyr Gly Tyr Leu Asn Ser Phe Gln Val Val Leu Glu Ala Leu
            260                 265                 270

Cys Met Ala Ile Ile Pro Phe Phe Val Asn Arg Val Gly Pro Lys Asn
        275                 280                 285
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Ala Leu Leu Ile Gly Val Val Ile Met Ala Leu Arg Ile Leu Ser Cys
290 295 300

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
305 310 315 320

Ala Ile Glu Val Pro Leu Cys Val Ile Ser Val Phe Lys Tyr Ser Val
325 330 335

Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile Phe Leu Ile Gly Phe
340 345 350

Gln Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
355 360 365

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
370 375 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
385 390 395 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
405 410 415

<210> 25
<211> 1248
<212> DNA
<213> Escherichia coli

<400> 25
atggcactga atattccatt cagaaatgcg tactatcgtt ttgcatccag ttactcattt 60

ctcttttta tttcctggtc gctgtggtgg tcgttatacg ctatttggct gaaaggacat 120

ctagggttga cagggacgga attaggtaca ctttattcgg tcaaccagtt taccagcatt 180

ctatttatga tgttctacgg catcgttcag gataaactcg gtctgaagaa accgctcatc 240

tggtgtatga gtttcatcct ggtcttgacc ggaccgttta tgatttacgt ttatgaaccg 300

ttactgcaaa gcaatttttc tgtaggtcta attctggggg cgctattttt tggcttgggg 360

tatctggcgg gatgcggttt gcttgatagc ttcaccgaaa aaatggcgcg aaatttcat 420

ttcgaatatg gaacagcgcg cgcctgggga tcttttggct atgctattgg cgcgttcttt 480

gccggcatat tttttagtat cagtccccat atcaacttct ggttggtctc gctatttggc 540

gctgtattta tgatgatcaa catgcgtttt aaagataagg atcaccagtg cgtagcggca 600

gatgcgggag gggtaaaaaa agaggatttt atcgcagttt tcaaggatcg aaacttctgg 660

gttttcgtca tatttattgt ggggacgtgg tctttctata acatttttga tcaacaactt 720

tttcctgtct tttattcagg tttattcgaa tcacacgatg taggaacgcg cctgtatggt 780

tatctcaact cattccaggt ggtactcgaa gcgctgtgca tggcgattat tcctttcttt 840

gtgaatcggg tagggccaaa aaatgcatta cttatcggag ttgtgattat ggcgttgcgt 900

atcctttcct gcgcgctgtt cgttaacccc tggattattt cattagtgaa gttgttacat 960

gccattgagg ttccactttg tgtcatatcc gtcttcaaat acagcgtggc aaactttgat 1020

aagcgcctgt cgtcgacgat ctttctgatt ggttttcaaa ttgccagttc gcttgggatt 1080

gtgctgcttt caacgccgac tgggatactc tttgaccacg caggctacca gacagttttc 1140

ttcgcaattt cgggtattgt ctgcctgatg ttgctatttg gcattttctt cttgagtaaa 1200

aaacgcgagc aaatagttat ggaaacgcct gtaccttcag caatatag 1248

<210> 26
<211> 415
<212> PRT
<213> Escherichia coli

<400> 26

Met Ala Leu Asn Ile Pro Phe Arg Asn Ala Tyr Tyr Arg Phe Ala Ser
1 5 10 15

Ser Tyr Ser Phe Leu Phe Phe Ile Ser Trp Ser Leu Trp Trp Ser Leu
20 25 30

Tyr Ala Ile Trp Leu Lys Gly His Leu Gly Leu Thr Gly Thr Glu Leu
35 40 45

Gly Thr Leu Tyr Ser Val Asn Gln Phe Thr Ser Ile Leu Phe Met Met
50 55 60

Phe Tyr Gly Ile Val Gln Asp Lys Leu Gly Leu Lys Lys Pro Leu Ile
65 70 75 80

Trp Cys Met Ser Phe Ile Leu Val Leu Thr Gly Pro Phe Met Ile Tyr
85 90 95

Val Tyr Glu Pro Leu Leu Gln Ser Asn Phe Ser Val Gly Leu Ile Leu
100 105 110

Gly Ala Leu Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Leu
115 120 125

Asp Ser Phe Thr Glu Lys Met Ala Arg Asn Phe His Phe Glu Tyr Gly
130 135 140

Thr Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Gly Ala Phe Phe
145 150 155 160

Ala Gly Ile Phe Phe Ser Ile Ser Pro His Ile Asn Phe Trp Leu Val
165 170 175

Ser Leu Phe Gly Ala Val Phe Met Met Ile Asn Met Arg Phe Lys Asp
180 185 190

```
Lys Asp His Gln Cys Val Ala Ala Asp Ala Gly Gly Val Lys Lys Glu
        195                 200                 205

Asp Phe Ile Ala Val Phe Lys Asp Arg Asn Phe Trp Val Phe Val Ile
    210                 215                 220

Phe Ile Val Gly Thr Trp Ser Phe Tyr Asn Ile Phe Asp Gln Gln Leu
225                 230                 235                 240

Phe Pro Val Phe Tyr Ser Gly Leu Phe Glu Ser His Asp Val Gly Thr
                245                 250                 255

Arg Leu Tyr Gly Tyr Leu Asn Ser Phe Gln Val Val Leu Glu Ala Leu
            260                 265                 270

Cys Met Ala Ile Ile Pro Phe Phe Val Asn Arg Val Gly Pro Lys Asn
        275                 280                 285

Ala Leu Leu Ile Gly Val Val Ile Met Ala Leu Arg Ile Leu Ser Cys
    290                 295                 300

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
305                 310                 315                 320

Ala Ile Glu Val Pro Leu Cys Val Ile Ser Val Phe Lys Tyr Ser Val
                325                 330                 335

Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile Phe Leu Ile Gly Phe
            340                 345                 350

Gln Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
        355                 360                 365

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
    370                 375                 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
385                 390                 395                 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
                405                 410                 415
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<210> 27
<211> 1434
<212> DNA
<213> Escherichia coli

<400> 27
atgacgcaat ctcgattgca tgcggcgcaa aacgcactag caaaacttca cgagcgccga 60

ggtaacactt tctatcccca ttttcacctc gcgcctcctg ccgggtggat gaacgatcca 120

aacggcctga tctggtttaa cgatcgttat cacgcgtttt atcaacatca cccgatgagc 180

gaacactggg ggccaatgca ctggggacat gccaccagcg acgatatgat ccactggcag 240

catgagccta ttgcgctagc gccaggagac gagaatgaca aagacgggtg tttttcaggt 300

agtgctgtcg atgacaatgg tgtcctctca cttatctaca ccggacacgt ctggctcgat 360

ggtgcaggta atgacgatgc aattcgcgaa gtacaatgtc tggctaccag tcgggatggt 420

attcatttcg agaaacaggg tgtgatcctc actccaccag aaggcatcat gcacttccgc 480

gatcctaaag tgtggcgtga agccgacaca tggtggatgg tagtcggggc gaaagaccca 540

ggcaacacgg ggcagatcct gctttatcgc ggcagttcat tgcgtgaatg gactttcgat 600

cgcgtactgg cccacgctga tgcgggtgaa agctatatgt gggaatgtcc ggacttttc 660

agccttggcg atcagcatta tctgatgttt tccccgcagg gaatgaatgc cgagggatac 720

agttatcgaa atcgctttca aagtggcgta atacccggaa tgtggtcgcc aggacgactt 780

tttgcacaat ccgggcattt tactgaactt gataacgggc atgactttta tgcaccacaa 840

agctttgtag cgaaggatgg tcggcgtatt gttatcggct ggatggatat gtgggaatcg 900

ccaatgccct caaaacgtga aggctgggca ggctgcatga cgctggcgcg cgagctatca 960

gagagcaatg gcaaactcct acaacgcccg gtacacgaag ctgagtcgtt acgccagcag 1020

catcaatcta tctctccccg cacaatcagc aataaatatg ttttgcagga aaacgcgcaa 1080

gcagttgaga ttcagttgca gtgggcgctg aagaacagtg atgccgaaca ttacggatta 1140

cagctcggcg ctggaatgcg gctgtatatt gataaccaat ctgagcgact tgttttgtgg 1200

cggtattacc cacacgagaa tttagatggc taccgtagta ttcccctccc gcagggtgac 1260

atgctcgccc taaggatatt tatcgataca tcatccgtgg aagtatttat taacgacggg 1320

gaggcggtga tgagtagccg aatatatccg cagccagaag aacgggaact gtcgctctat 1380

gcctcccacg gagtggctgt gctgcaacat ggagcactct ggcaactggg ttaa 1434

<210> 28
<211> 477
<212> PRT
<213> Escherichia coli

<400> 28

Met Thr Gln Ser Arg Leu His Ala Ala Gln Asn Ala Leu Ala Lys Leu
1 5 10 15

His Glu Arg Arg Gly Asn Thr Phe Tyr Pro His Phe His Leu Ala Pro
20 25 30

Pro Ala Gly Trp Met Asn Asp Pro Asn Gly Leu Ile Trp Phe Asn Asp
35 40 45

Arg Tyr His Ala Phe Tyr Gln His His Pro Met Ser Glu His Trp Gly
50 55 60

Pro Met His Trp Gly His Ala Thr Ser Asp Asp Met Ile His Trp Gln
65 70 75 80

```
His Glu Pro Ile Ala Leu Ala Pro Gly Asp Glu Asn Asp Lys Asp Gly
                85                  90                  95

Cys Phe Ser Gly Ser Ala Val Asp Asp Asn Gly Val Leu Ser Leu Ile
            100                 105                 110

Tyr Thr Gly His Val Trp Leu Asp Gly Ala Gly Asn Asp Asp Ala Ile
        115                 120                 125

Arg Glu Val Gln Cys Leu Ala Thr Ser Arg Asp Gly Ile His Phe Glu
    130                 135                 140

Lys Gln Gly Val Ile Leu Thr Pro Pro Glu Gly Ile Met His Phe Arg
145                 150                 155                 160

Asp Pro Lys Val Trp Arg Glu Ala Asp Thr Trp Trp Met Val Val Gly
                165                 170                 175

Ala Lys Asp Pro Gly Asn Thr Gly Gln Ile Leu Leu Tyr Arg Gly Ser
            180                 185                 190

Ser Leu Arg Glu Trp Thr Phe Asp Arg Val Leu Ala His Ala Asp Ala
        195                 200                 205

Gly Glu Ser Tyr Met Trp Glu Cys Pro Asp Phe Phe Ser Leu Gly Asp
    210                 215                 220

Gln His Tyr Leu Met Phe Ser Pro Gln Gly Met Asn Ala Glu Gly Tyr
225                 230                 235                 240

Ser Tyr Arg Asn Arg Phe Gln Ser Gly Val Ile Pro Gly Met Trp Ser
                245                 250                 255

Pro Gly Arg Leu Phe Ala Gln Ser Gly His Phe Thr Glu Leu Asp Asn
            260                 265                 270

Gly His Asp Phe Tyr Ala Pro Gln Ser Phe Val Ala Lys Asp Gly Arg
        275                 280                 285

Arg Ile Val Ile Gly Trp Met Asp Met Trp Glu Ser Pro Met Pro Ser
    290                 295                 300

Lys Arg Glu Gly Trp Ala Gly Cys Met Thr Leu Ala Arg Glu Leu Ser
305                 310                 315                 320

Glu Ser Asn Gly Lys Leu Leu Gln Arg Pro Val His Glu Ala Glu Ser
                325                 330                 335

Leu Arg Gln Gln His Gln Ser Ile Ser Pro Arg Thr Ile Ser Asn Lys
            340                 345                 350
```

Tyr Val Leu Gln Glu Asn Ala Gln Ala Val Glu Ile Gln Leu Gln Trp
355 360 365

Ala Leu Lys Asn Ser Asp Ala Glu His Tyr Gly Leu Gln Leu Gly Ala
370 375 380

Gly Met Arg Leu Tyr Ile Asp Asn Gln Ser Glu Arg Leu Val Leu Trp
385 390 395 400

Arg Tyr Tyr Pro His Glu Asn Leu Asp Gly Tyr Arg Ser Ile Pro Leu
405 410 415

Pro Gln Gly Asp Met Leu Ala Leu Arg Ile Phe Ile Asp Thr Ser Ser
420 425 430

Val Glu Val Phe Ile Asn Asp Gly Glu Ala Val Met Ser Ser Arg Ile
435 440 445

Tyr Pro Gln Pro Glu Glu Arg Glu Leu Ser Leu Tyr Ala Ser His Gly
450 455 460

Val Ala Val Leu Gln His Gly Ala Leu Trp Gln Leu Gly
465 470 475

<210> 29
<211> 1434
<212> DNA
<213> Escherichia coli

<400> 29
atgacgcaat ctcgattgca tgcggcgcaa aacgccctag caaaacttca tgagcaccgg 60

ggtaacactt tctatcccca ttttcacctc gcgcctcctg ccgggtggat gaacgatcca 120

aacggcctga tctggtttaa cgatcgttat cacgcgtttt atcaacatca tccgatgagc 180

gaacactggg ggccaatgca ctggggacat gccaccagcg acgatatgat ccactggcag 240

catgagccta ttgcgctagc gccaggagac gataatgaca aagacgggtg tttttcaggt 300

agtgctgtcg atgacaatgg tgtcctctca cttatctaca ccggacacgt ctggctcgat 360

ggtgcaggta atgacgatgc aattcgcgaa gtacaatgtc tggctaccag tcgggatggt 420

attcatttcg agaaacaggg tgtgatcctc actccaccag aaggaatcat gcacttccgc 480

gatcctaaag tgtggcgtga agccgacaca tggtggatgg tagtcggggc gaaagatcca 540

ggcaacacgg ggcagatcct gctttatcgc ggcagttcgt tgcgtgaatg gaccttcgat 600

cgcgtactgg cccacgctga tgcgggtgaa agctatatgt gggaatgtcc ggacttttc 660

agccttggcg atcagcatta tctgatgttt tccccgcagg gaatgaatgc cgagggatac 720

agttaccgaa atcgctttca aagtggcgta atacccggaa tgtggtcgcc aggacgactt 780

tttgcacaat ccgggcattt tactgaactt gataacgggc atgactttta tgcaccacaa 840

agctttttag cgaaggatgg tcggcgtatt gttatcggct ggatggatat gtgggaatcg 900

ccaatgccct caaaacgtga aggatgggca ggctgcatga cgctggcgcg cgagctatca 960

gagagcaatg gcaaacttct acaacgcccg gtacacgaag ctgagtcgtt acgccagcag 1020

catcaatctg tctctccccg cacaatcagc aataaatatg ttttgcagga aaacgcgcaa 1080

gcagttgaga ttcagttgca gtgggcgctg aagaacagtg atgccgaaca ttacggatta 1140

cagctcggca ctggaatgcg gctgtatatt gataaccaat ctgagcgact tgttttgtgg 1200

cggtattacc cacacgagaa tttagacggc taccgtagta ttcccctccc gcagcgtgac 1260

acgctcgccc taaggatatt tatcgataca tcatccgtgg aagtatttat taacgacggg 1320

gaagcggtga tgagtagtcg aatctatccg cagccagaag aacgggaact gtcgctttat 1380

gcctcccacg gagtggctgt gctgcaacat ggagcactct ggctactggg ttaa 1434

<210> 30
<211> 477
<212> PRT
<213> Escherichia coli

<400> 30

Met Thr Gln Ser Arg Leu His Ala Ala Gln Asn Ala Leu Ala Lys Leu
1 5 10 15

His Glu His Arg Gly Asn Thr Phe Tyr Pro His Phe His Leu Ala Pro
20 25 30

Pro Ala Gly Trp Met Asn Asp Pro Asn Gly Leu Ile Trp Phe Asn Asp
35 40 45

Arg Tyr His Ala Phe Tyr Gln His His Pro Met Ser Glu His Trp Gly
50 55 60

Pro Met His Trp Gly His Ala Thr Ser Asp Asp Met Ile His Trp Gln
65 70 75 80

His Glu Pro Ile Ala Leu Ala Pro Gly Asp Asp Asn Asp Lys Asp Gly
85 90 95

Cys Phe Ser Gly Ser Ala Val Asp Asp Asn Gly Val Leu Ser Leu Ile
100 105 110

Tyr Thr Gly His Val Trp Leu Asp Gly Ala Gly Asn Asp Asp Ala Ile
115 120 125

Arg Glu Val Gln Cys Leu Ala Thr Ser Arg Asp Gly Ile His Phe Glu
130 135 140

Lys Gln Gly Val Ile Leu Thr Pro Pro Glu Gly Ile Met His Phe Arg
145 150 155 160

```
Asp Pro Lys Val Trp Arg Glu Ala Asp Thr Trp Trp Met Val Val Gly
                165                 170                 175

Ala Lys Asp Pro Gly Asn Thr Gly Gln Ile Leu Leu Tyr Arg Gly Ser
            180                 185                 190

Ser Leu Arg Glu Trp Thr Phe Asp Arg Val Leu Ala His Ala Asp Ala
        195                 200                 205

Gly Glu Ser Tyr Met Trp Glu Cys Pro Asp Phe Phe Ser Leu Gly Asp
    210                 215                 220

Gln His Tyr Leu Met Phe Ser Pro Gln Gly Met Asn Ala Glu Gly Tyr
225                 230                 235                 240

Ser Tyr Arg Asn Arg Phe Gln Ser Gly Val Ile Pro Gly Met Trp Ser
                245                 250                 255

Pro Gly Arg Leu Phe Ala Gln Ser Gly His Phe Thr Glu Leu Asp Asn
            260                 265                 270

Gly His Asp Phe Tyr Ala Pro Gln Ser Phe Leu Ala Lys Asp Gly Arg
        275                 280                 285

Arg Ile Val Ile Gly Trp Met Asp Met Trp Glu Ser Pro Met Pro Ser
    290                 295                 300

Lys Arg Glu Gly Trp Ala Gly Cys Met Thr Leu Ala Arg Glu Leu Ser
305                 310                 315                 320

Glu Ser Asn Gly Lys Leu Leu Gln Arg Pro Val His Glu Ala Glu Ser
                325                 330                 335

Leu Arg Gln Gln His Gln Ser Val Ser Pro Arg Thr Ile Ser Asn Lys
            340                 345                 350

Tyr Val Leu Gln Glu Asn Ala Gln Ala Val Glu Ile Gln Leu Gln Trp
        355                 360                 365

Ala Leu Lys Asn Ser Asp Ala Glu His Tyr Gly Leu Gln Leu Gly Thr
    370                 375                 380

Gly Met Arg Leu Tyr Ile Asp Asn Gln Ser Glu Arg Leu Val Leu Trp
385                 390                 395                 400

Arg Tyr Tyr Pro His Glu Asn Leu Asp Gly Tyr Arg Ser Ile Pro Leu
                405                 410                 415

Pro Gln Arg Asp Thr Leu Ala Leu Arg Ile Phe Ile Asp Thr Ser Ser
            420                 425                 430
```

Val Glu Val Phe Ile Asn Asp Gly Glu Ala Val Met Ser Ser Arg Ile
435 440 445

Tyr Pro Gln Pro Glu Glu Arg Glu Leu Ser Leu Tyr Ala Ser His Gly
450 455 460

Val Ala Val Leu Gln His Gly Ala Leu Trp Leu Leu Gly
465 470 475

<210> 31
<211> 1599
<212> DNA
<213> Bifidobacterium lactis

<400> 31
atggcaaccc ttcccaccaa tattcccgcc aacggcattc tgacccccga cccggcgctc 60

gaccctgtgc tcacgccgat ctcggaccat gccgagcagc tgtcactcgc cgaagcaggc 120

gtgtcggcac tggaaaccac ccgcaacgac cgctggtacc cgaagttcca cattgcctcc 180

aatggcgggt ggatcaacga cccgaacggc ctgtgccgct acaacggacg ctggcacgtg 240

ttctaccagc tgcatcccca cggcacacag tggggcccga tgcattgggg ccacgtctcc 300

tccgacaaca tggtcgactg gcaccgcgaa cccatcgcct tcgcgccaag cctcgaacag 360

gaacgccacg gtgtgttctc cggttccgcc gtgattggcg acgacggcaa gccgtggatt 420

ttctacaccg gccaccgctg ggccaacggc aaggacaaca ccggaggcga ctggcaggtg 480

cagatgctcg ccaagccgaa cgacgacgaa ctgaagacct tcacgaagga gggcatgatc 540

atcgactgcc ccaccgacga ggtggaccac cacttccgcg acccgaaggt gtggaagacc 600

ggtgacacct ggtatatgac cttcggtgtc tcgtcgaagg agcatcgtgg ccagatgtgg 660

ctgtacacgt cgagcgacat ggtgcactgg agcttcgatc gggtgctgtt cgagcatccg 720

gatccgaacg tgttcatgct tgaatgcccc gatttcttcc cgatccgcga tgcgcggggc 780

aacgagaaat gggtcatcgg cttctccgcg atgggtgcca agccaaatgg cttcatgaac 840

cgcaacgtga acaatgccgg ctacatggtg ggcacatgga agccaggcga gagcttcaag 900

ccggagaccg agttccgcct gtgggacgaa ggccataact tctatgcacc acagtcgttc 960

aacaccgaag ggcgccagat catgtacggc tggatgagcc cgttcgtcgc ccccatcccg 1020

atggaggagg acggctggtg cggcaacctc accctccccc gcgagatcac gctgggcgat 1080

gacggtgacc tggtcaccgc ccccaccatc gaaatggagg ggctgcgcga gaataccata 1140

ggcttcgact cgctcgacct tggtacgaac cagacctcca cgatcctcga cgatgacggc 1200

ggcgccctgg aaatcgagat gagactcgat ctgaacaaaa ccaccgccga acgcgccgga 1260

ctgcatgtgc atgccacaag cgacggccac tacacggcaa tcgtattcga cgcgcagatc 1320

ggcggcgtcg tcatcgaccg gcagaacgtg gcgaacggag acaaaggcta ccgggtggcc 1380

aagctcagcg acaccgagct cgcagccgat acgcttgact tgcgcgtgtt catcgaccgc 1440

ggatgcgtcg aggtctacgt cgacggcggc aagcatgcga tgagctcgta ctcgttccct 1500

ggcgatggcg cacgcgccgt cgaactcgtg agcgaatccg gcaccacgca catcgacacc 1560

ctcaccatgc actcgctcaa gtccatcgga ctcgagtga 1599

<210> 32
<211> 532
<212> PRT
<213> Bifidobacterium lactis

<400> 32

Met Ala Thr Leu Pro Thr Asn Ile Pro Ala Asn Gly Ile Leu Thr Pro
1 5 10 15

Asp Pro Ala Leu Asp Pro Val Leu Thr Pro Ile Ser Asp His Ala Glu
20 25 30

Gln Leu Ser Leu Ala Glu Ala Gly Val Ser Ala Leu Glu Thr Thr Arg
35 40 45

Asn Asp Arg Trp Tyr Pro Lys Phe His Ile Ala Ser Asn Gly Gly Trp
50 55 60

Ile Asn Asp Pro Asn Gly Leu Cys Arg Tyr Asn Gly Arg Trp His Val
65 70 75 80

Phe Tyr Gln Leu His Pro His Gly Thr Gln Trp Gly Pro Met His Trp
85 90 95

Gly His Val Ser Ser Asp Asn Met Val Asp Trp His Arg Glu Pro Ile
100 105 110

Ala Phe Ala Pro Ser Leu Glu Gln Glu Arg His Gly Val Phe Ser Gly
115 120 125

Ser Ala Val Ile Gly Asp Asp Gly Lys Pro Trp Ile Phe Tyr Thr Gly
130 135 140

His Arg Trp Ala Asn Gly Lys Asp Asn Thr Gly Gly Asp Trp Gln Val
145 150 155 160

Gln Met Leu Ala Lys Pro Asn Asp Asp Glu Leu Lys Thr Phe Thr Lys
165 170 175

Glu Gly Met Ile Ile Asp Cys Pro Thr Asp Glu Val Asp His His Phe
180 185 190

Arg Asp Pro Lys Val Trp Lys Thr Gly Asp Thr Trp Tyr Met Thr Phe
195 200 205

Gly Val Ser Ser Lys Glu His Arg Gly Gln Met Trp Leu Tyr Thr Ser
210 215 220

```
Ser Asp Met Val His Trp Ser Phe Asp Arg Val Leu Phe Glu His Pro
225                 230                 235                 240

Asp Pro Asn Val Phe Met Leu Glu Cys Pro Asp Phe Phe Pro Ile Arg
                245                 250                 255

Asp Ala Arg Gly Asn Glu Lys Trp Val Ile Gly Phe Ser Ala Met Gly
            260                 265                 270

Ala Lys Pro Asn Gly Phe Met Asn Arg Asn Val Asn Asn Ala Gly Tyr
        275                 280                 285

Met Val Gly Thr Trp Lys Pro Gly Glu Ser Phe Lys Pro Glu Thr Glu
    290                 295                 300

Phe Arg Leu Trp Asp Glu Gly His Asn Phe Tyr Ala Pro Gln Ser Phe
305                 310                 315                 320

Asn Thr Glu Gly Arg Gln Ile Met Tyr Gly Trp Met Ser Pro Phe Val
                325                 330                 335

Ala Pro Ile Pro Met Glu Glu Asp Gly Trp Cys Gly Asn Leu Thr Leu
            340                 345                 350

Pro Arg Glu Ile Thr Leu Gly Asp Asp Gly Asp Leu Val Thr Ala Pro
        355                 360                 365

Thr Ile Glu Met Glu Gly Leu Arg Glu Asn Thr Ile Gly Phe Asp Ser
    370                 375                 380

Leu Asp Leu Gly Thr Asn Gln Thr Ser Thr Ile Leu Asp Asp Asp Gly
385                 390                 395                 400

Gly Ala Leu Glu Ile Glu Met Arg Leu Asp Leu Asn Lys Thr Thr Ala
                405                 410                 415

Glu Arg Ala Gly Leu His Val His Ala Thr Ser Asp Gly His Tyr Thr
            420                 425                 430

Ala Ile Val Phe Asp Ala Gln Ile Gly Gly Val Val Ile Asp Arg Gln
        435                 440                 445

Asn Val Ala Asn Gly Asp Lys Gly Tyr Arg Val Ala Lys Leu Ser Asp
    450                 455                 460

Thr Glu Leu Ala Ala Asp Thr Leu Asp Leu Arg Val Phe Ile Asp Arg
465                 470                 475                 480

Gly Cys Val Glu Val Tyr Val Asp Gly Gly Lys His Ala Met Ser Ser
                485                 490                 495
```

Tyr Ser Phe Pro Gly Asp Gly Ala Arg Ala Val Glu Leu Val Ser Glu
500 505 510

Ser Gly Thr Thr His Ile Asp Thr Leu Thr Met His Ser Leu Lys Ser
515 520 525

Ile Gly Leu Glu
530

<210> 33
<211> 1599
<212> DNA
<213> Saccharomyces cerevisiae

<400> 33
atgcttttgc aagctttcct ttcctttttg gctggttttg cagccaaaat atctgcatca 60

atgacaaacg aaactagcga tagacctttg gtccacttca cacccaacaa gggctggatg 120

aatgacccaa atgggttgtg gtacgatgaa aaagatgcca aatggcatct gtactttcaa 180

tacaacccaa atgacaccgt atggggtacg ccattgtttt ggggccatgc tacttccgat 240

gatttgacta attgggaaga tcaacccatt gctatcgctc ccaagcgtaa cgattcaggt 300

gctttctctg gctccatggt ggttgattac aacaacacga gtgggttttt caatgatact 360

attgatccaa gacaaagatg cgttgcgatt tggacttata acactcctga aagtgaagag 420

caatacatta gctattctct tgatggtggt tacactttta ctgaatacca aaagaaccct 480

gttttagctg ccaactccac tcaattcaga gatccaaagg tgttctggta tgaaccttct 540

caaaaatgga ttatgacggc tgccaaatca caagactaca aaattgaaat ttactcctct 600

gatgacttga agtcctggaa gctagaatct gcatttgcca atgaaggttt cttaggctac 660

caatacgaat gtccaggttt gattgaagtc ccaactgagc aagatccttc caaatcttat 720

tgggtcatgt ttatttctat caacccaggt gcacctgctg gcggttcctt caaccaatat 780

tttgttggat ccttcaatgg tactcatttt gaagcgtttg acaatcaatc tagagtggta 840

gattttggta aggactacta tgccttgcaa actttcttca acactgaccc aacctacggt 900

tcagcattag gtattgcctg ggcttcaaac tgggagtaca gtgcctttgt cccaactaac 960

ccatggagat catccatgtc tttggtccgc aagttttctt tgaacactga atatcaagct 1020

aatccagaga ctgaattgat caatttgaaa gccgaaccaa tattgaacat tagtaatgct 1080

ggtccctggt ctcgttttgc tactaacaca actctaacta aggccaattc ttacaatgtc 1140

gatttgagca actcgactgg taccctagag tttgagttgg tttacgctgt taacaccaca 1200

caaaccatat ccaaatccgt ctttgccgac ttatcacttt ggttcaaggg tttagaagat 1260

cctgaagaat atttgagaat gggttttgaa gtcagtgctt cttccttctt tttggaccgt 1320

ggtaactcta aggtcaagtt tgtcaaggag aacccatatt tcacaaacag aatgtctgtc 1380

aacaaccaac cattcaagtc tgagaacgac ctaagttact ataaagtgta cggcctactg 1440

gatcaaaaca tcttggaatt gtacttcaac gatggagatg tggtttctac aaatacctac 1500

ttcatgacca ccggtaacgc tctaggatct gtgaacatga ccactggtgt cgataatttg 1560

ttctacattg acaagttcca agtaagggaa gtaaaatag 1599

<210> 34
<211> 532
<212> PRT
<213> Saccharomyces cerevisiae

<400> 34

Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
1 5 10 15

Ile Ser Ala Ser Met Thr Asn Glu Thr Ser Asp Arg Pro Leu Val His
20 25 30

Phe Thr Pro Asn Lys Gly Trp Met Asn Asp Pro Asn Gly Leu Trp Tyr
35 40 45

Asp Glu Lys Asp Ala Lys Trp His Leu Tyr Phe Gln Tyr Asn Pro Asn
50 55 60

Asp Thr Val Trp Gly Thr Pro Leu Phe Trp Gly His Ala Thr Ser Asp
65 70 75 80

Asp Leu Thr Asn Trp Glu Asp Gln Pro Ile Ala Ile Ala Pro Lys Arg
85 90 95

Asn Asp Ser Gly Ala Phe Ser Gly Ser Met Val Val Asp Tyr Asn Asn
100 105 110

Thr Ser Gly Phe Phe Asn Asp Thr Ile Asp Pro Arg Gln Arg Cys Val
115 120 125

Ala Ile Trp Thr Tyr Asn Thr Pro Glu Ser Glu Glu Gln Tyr Ile Ser
130 135 140

Tyr Ser Leu Asp Gly Gly Tyr Thr Phe Thr Glu Tyr Gln Lys Asn Pro
145 150 155 160

Val Leu Ala Ala Asn Ser Thr Gln Phe Arg Asp Pro Lys Val Phe Trp
165 170 175

Tyr Glu Pro Ser Gln Lys Trp Ile Met Thr Ala Ala Lys Ser Gln Asp
180 185 190

Tyr Lys Ile Glu Ile Tyr Ser Ser Asp Asp Leu Lys Ser Trp Lys Leu
195 200 205

Glu Ser Ala Phe Ala Asn Glu Gly Phe Leu Gly Tyr Gln Tyr Glu Cys
210 215 220

```
Pro Gly Leu Ile Glu Val Pro Thr Glu Gln Asp Pro Ser Lys Ser Tyr
225                 230                 235                 240

Trp Val Met Phe Ile Ser Ile Asn Pro Gly Ala Pro Ala Gly Gly Ser
                245                 250                 255

Phe Asn Gln Tyr Phe Val Gly Ser Phe Asn Gly Thr His Phe Glu Ala
            260                 265                 270

Phe Asp Asn Gln Ser Arg Val Val Asp Phe Gly Lys Asp Tyr Tyr Ala
        275                 280                 285

Leu Gln Thr Phe Phe Asn Thr Asp Pro Thr Tyr Gly Ser Ala Leu Gly
    290                 295                 300

Ile Ala Trp Ala Ser Asn Trp Glu Tyr Ser Ala Phe Val Pro Thr Asn
305                 310                 315                 320

Pro Trp Arg Ser Ser Met Ser Leu Val Arg Lys Phe Ser Leu Asn Thr
                325                 330                 335

Glu Tyr Gln Ala Asn Pro Glu Thr Glu Leu Ile Asn Leu Lys Ala Glu
            340                 345                 350

Pro Ile Leu Asn Ile Ser Asn Ala Gly Pro Trp Ser Arg Phe Ala Thr
        355                 360                 365

Asn Thr Thr Leu Thr Lys Ala Asn Ser Tyr Asn Val Asp Leu Ser Asn
    370                 375                 380

Ser Thr Gly Thr Leu Glu Phe Glu Leu Val Tyr Ala Val Asn Thr Thr
385                 390                 395                 400

Gln Thr Ile Ser Lys Ser Val Phe Ala Asp Leu Ser Leu Trp Phe Lys
                405                 410                 415

Gly Leu Glu Asp Pro Glu Glu Tyr Leu Arg Met Gly Phe Glu Val Ser
            420                 425                 430

Ala Ser Ser Phe Phe Leu Asp Arg Gly Asn Ser Lys Val Lys Phe Val
        435                 440                 445

Lys Glu Asn Pro Tyr Phe Thr Asn Arg Met Ser Val Asn Asn Gln Pro
    450                 455                 460

Phe Lys Ser Glu Asn Asp Leu Ser Tyr Tyr Lys Val Tyr Gly Leu Leu
465                 470                 475                 480

Asp Gln Asn Ile Leu Glu Leu Tyr Phe Asn Asp Gly Asp Val Val Ser
                485                 490                 495
```

Thr Asn Thr Tyr Phe Met Thr Thr Gly Asn Ala Leu Gly Ser Val Asn
500 505 510

Met Thr Thr Gly Val Asp Asn Leu Phe Tyr Ile Asp Lys Phe Gln Val
515 520 525

Arg Glu Val Lys
530

<210> 35
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum

<400> 35
gtgtgtgggg ctatgcacac agaactttcc agtttgcgcc ctgcgtacca tgtgactcct 60

ccgcagggca ggctcaatga tcccaacgga atgtacgtcg atggcgatac cctccacgtc 120

tactaccagc acgatccagg tttccccttc gcaccaaagc gcaccggctg ggctcacacc 180

accacgccgt tgaccggacc gcagcgattg cagtggacgc acctgcccga cgctctttac 240

ccggatgcat cctatgacct ggatggatgc tattccggtg gagccgtatt tactgacggc 300

acacttaaac ttttctacac cggcaaccta aaaattgacg gcaagcgccg cgccacccaa 360

aacctcgtcg aagtcgagga cccaactggg ctgatgggcg gcattcatcg ccgttcgcct 420

aaaaatccgc ttatcgacgg acccgccagc ggtttcacac cccattaccg cgatcccatg 480

atcagccctg atggtgatgg ttggaaaatg gttcttgggg cccaacgcga aaacctcacc 540

ggtgcagcgg ttctataccg ctcgacagat cttgaaaact gggaattctc cggtgaaatc 600

acctttgacc tcagtgatgc acaacctggt tctgctcctg atctcgttcc cggtggctac 660

atgtgggaat gccccaacct ttttacgctt cgcgatgaag aaactggcga agatctcgac 720

gtgctgattt tctgtccaca aggattggac cgaatccacg atgaggttac tcactacgca 780

agctctgacc agtgcggata tgtcgtcggc aagcttgaag gaacgacctt ccgcgtcttg 840

cgaggattca gcgagctgga tttcggccat gaattctacg caccgcaggt tgcagtaaac 900

ggttctgatg cctggctcgt gggctggatg gggctgcccg cgcaggatga tcacccaaca 960

gttgcacggg aaggatgggt gcactgcctg actgtgcccc gcaagcttca tttgcgcaac 1020

cacgcgatct atcaagagct tcttctccca gaggggggagt caggggtaat cagatctgta 1080

ttaggttctg aacctgtccg agtagacatc cgaggcaata tttccctcga gtgggatggt 1140

gtccgtttgt ctgtggatcg tggtggtgat cgtcgcgtag ctgaggtaaa acctggcgaa 1200

ttagtgatcg cggacgataa tacagccatt gagataactg caggtgatgg acaggtttca 1260

ttcgctttcc gggctttcaa aggtgacact attgagagat aa 1302

<210> 36
<211> 433
<212> PRT
<213> Corynebacterium glutamicum

<400> 36

```
Met Cys Gly Ala Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr
1               5                  10                  15

His Val Thr Pro Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr
            20                  25                  30

Val Asp Gly Asp Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe
        35                  40                  45

Pro Phe Ala Pro Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu
    50                  55                  60

Thr Gly Pro Gln Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr
65                  70                  75                  80

Pro Asp Ala Ser Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val
                85                  90                  95

Phe Thr Asp Gly Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile
            100                 105                 110

Asp Gly Lys Arg Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro
        115                 120                 125

Thr Gly Leu Met Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu
    130                 135                 140

Ile Asp Gly Pro Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met
145                 150                 155                 160

Ile Ser Pro Asp Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg
                165                 170                 175

Glu Asn Leu Thr Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu
            180                 185                 190

Asn Trp Glu Phe Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln
        195                 200                 205

Pro Gly Ser Ala Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys
    210                 215                 220

Pro Asn Leu Phe Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp
225                 230                 235                 240

Val Leu Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val
                245                 250                 255

Thr His Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu
            260                 265                 270
```

Glu Gly Thr Thr Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe
275 280 285

Gly His Glu Phe Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala
290 295 300

Trp Leu Val Gly Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr
305 310 315 320

Val Ala Arg Glu Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu
325 330 335

His Leu Arg Asn His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly
340 345 350

Glu Ser Gly Val Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val
355 360 365

Asp Ile Arg Gly Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser
370 375 380

Val Asp Arg Gly Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu
385 390 395 400

Leu Val Ile Ala Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp
405 410 415

Gly Gln Val Ser Phe Ala Phe Arg Ala Phe Lys Gly Asp Thr Ile Glu
420 425 430

Arg

<210> 37
<211> 1473
<212> DNA
<213> Leuconostoc mesenteroides

<400> 37
atggaaattc aaaacaaagc aatgttgatc acttatgctg attcgttggg caaaaactta 60

aaagatgttc atcaagtctt gaaagaagat attggagatg cgattggtgg ggttcatttg 120

ttgcctttct tcccttcaac aggtgatcgc ggttttgcgc cagccgatta tactcgtgtt 180

gatgccgcat ttggtgattg ggcagatgtc gaagcattgg gtgaagaata ctatttgatg 240

tttgacttca tgattaacca tatttctcgt gaatcagtga tgtatcaaga ttttaagaag 300

aatcatgacg attcaaagta taaagatttc tttattcgtt gggaaaagtt ctgggcaaag 360

gccggcgaaa accgtccaac acaagccgat gttgacttaa tttacaagcg taaagataag 420

gcaccaacgc aagaaatcac ttttgatgat ggcacaacag aaaacttgtg gaatactttt 480

ggtgaagaac aaattgacat tgatgttaat tcagccattg ccaaggaatt tattaagaca 540

acccttgaag acatggtaaa acatggtgct aacttgattc gtttggatgc ctttgcgtat 600

gcagttaaaa aagttgacac aaatgacttc ttcgttgagc cagaaatctg ggacactttg 660

aatgaagtac gtgaaatttt gacaccatta aaggctgaaa ttttaccaga aattcatgaa 720

cattactcaa tccctaaaaa gatcaatgat catggttact tcacctatga ctttgcatta 780

ccaatgacaa cgctttacac attgtattca ggtaagacaa atcaattggc aaagtggttg 840

aagatgtcac caatgaagca attcacaaca ttggacacgc atgatggtat tggtgtcgtt 900

gatgcccgtg atattctaac tgatgatgaa attgactacg cttctgaaca actttacaag 960

gttggcgcga atgtcaaaaa gacatattca tctgcttcat acaacaacct tgatatttac 1020

caaattaact caacttatta ttcagcattg ggaaatgatg atgcagcata cttgttgagt 1080

cgtgtcttcc aagtctttgc gcctggaatt ccacaaattt attacgttgg tttgttggca 1140

ggtgaaaacg atatcgcgct tttggagtca actaaagaag gtcgtaatat taaccgtcat 1200

tactatacgc gtgaagaagt taagtcagaa gttaagcgac cagttgttgc taacttattg 1260

aagctattgt catggcgtaa tgaaagccct gcatttgatt tggctggctc aatcacagtt 1320

gacacgccaa ctgatacaac aattgtggtg acacgtcaag atgaaaatgg tcaaaacaaa 1380

gctgtattaa cagccgatgc ggccaacaaa acttttgaaa tcgttgagaa tggtcaaact 1440

gttatgagca gtgataattt gactcagaac taa 1473

<210> 38
<211> 490
<212> PRT
<213> Leuconostoc mesenteroides

<400> 38

Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
1 5 10 15

Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp Ile Gly
20 25 30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45

Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe
50 55 60

Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met
65 70 75 80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Val Met Tyr Gln
85 90 95

Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe Ile
100 105 110

```
Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln
        115                 120                 125

Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Thr Gln
    130                 135                 140

Glu Ile Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe
145                 150                 155                 160

Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Ala Ile Ala Lys Glu
                165                 170                 175

Phe Ile Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu
            180                 185                 190

Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn
        195                 200                 205

Asp Phe Phe Val Glu Pro Glu Ile Trp Asp Thr Leu Asn Glu Val Arg
    210                 215                 220

Glu Ile Leu Thr Pro Leu Lys Ala Glu Ile Leu Pro Glu Ile His Glu
225                 230                 235                 240

His Tyr Ser Ile Pro Lys Lys Ile Asn Asp His Gly Tyr Phe Thr Tyr
                245                 250                 255

Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys
            260                 265                 270

Thr Asn Gln Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe
        275                 280                 285

Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
    290                 295                 300

Ile Leu Thr Asp Asp Glu Ile Asp Tyr Ala Ser Glu Gln Leu Tyr Lys
305                 310                 315                 320

Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn
                325                 330                 335

Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
            340                 345                 350

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
        355                 360                 365

Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
    370                 375                 380
```

Ile Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His
385 390 395 400

Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val
405 410 415

Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe
420 425 430

Asp Leu Ala Gly Ser Ile Thr Val Asp Thr Pro Thr Asp Thr Thr Ile
435 440 445

Val Val Thr Arg Gln Asp Glu Asn Gly Gln Asn Lys Ala Val Leu Thr
450 455 460

Ala Asp Ala Ala Asn Lys Thr Phe Glu Ile Val Glu Asn Gly Gln Thr
465 470 475 480

Val Met Ser Ser Asp Asn Leu Thr Gln Asn
485 490

<210> 39
<211> 1515
<212> DNA
<213> Bifidobacterium adolescentis

<400> 39
atgaaaaaca aggtgcagct catcacttac gccgaccgcc ttggcgacgg caccatcaag 60

tcgatgaccg acattctgcg cacccgcttc gacggcgtgt acgacggcgt tcacatcctg 120

ccgttcttca ccccgttcga cggcgccgac gcaggcttcg acccgatcga ccacaccaag 180

gtcgacgaac gtctcggcag ctgggacgac gtcgccgaac tctccaagac ccacaacatc 240

atggtcgacg ccatcgtcaa ccacatgagt tgggaatcca agcagttcca ggacgtgctg 300

gccaagggcg aggagtccga atactatccg atgttcctca ccatgagctc cgtgttcccg 360

aacggcgcca ccgaagagga cctggccggc atctaccgtc cgcgtccggg cctgccgttc 420

acccactaca agttcgccgg caagacccgc ctcgtgtggg tcagcttcac cccgcagcag 480

gtggacatcg acaccgattc cgacaagggt tgggaatacc tcatgtcgat tttcgaccag 540

atggccgcct ctcacgtcag ctacatccgc ctcgacgccg tcggctatgg cgccaaggaa 600

gccggcacca gctgcttcat gaccccgaag accttcaagc tgatctcccg tctgcgtgag 660

gaaggcgtca agcgcggtct ggaaatcctc atcgaagtgc actcctacta caagaagcag 720

gtcgaaatcg catccaaggt ggaccgcgtc tacgacttcg ccctgcctcc gctgctgctg 780

cacgcgctga gcaccggcca cgtcgagccc gtcgcccact ggaccgacat acgcccgaac 840

aacgccgtca ccgtgctcga tacgcacgac ggcatcggcg tgatcgacat cggctccgac 900

cagctcgacc gctcgctcaa gggtctcgtg ccggatgagg acgtggacaa cctcgtcaac 960

accatccacg ccaacaccca cggcgaatcc caggcagcca ctggcgccgc cgcatccaat 1020

ctcgacctct accaggtcaa cagcacctac tattcggcgc tcgggtgcaa cgaccagcac 1080

tacatcgccg cccgcgcggt gcagttcttc ctgccgggcg tgccgcaagt ctactacgtc 1140

ggcgcgctcg ccggcaagaa cgacatggag ctgctgcgta agacgaataa cggccgcgac 1200

atcaatcgcc attactactc caccgcggaa atcgacgaga acctcaagcg tccggtcgtc 1260

aaggccctga acgcgctcgc caagttccgc aacgagctcg acgcgttcga cggcacgttc 1320

tcgtacacca ccgatgacga cacgtccatc agcttcacct ggcgcggcga aaccagccag 1380

gccacgctga cgttcgagcc gaagcgcggt ctcggtgtgg acaacactac gccggtcgcc 1440

atgttggaat gggaggattc cgcgggagac caccgttcgg atgatctgat cgccaatccg 1500

cctgtcgtcg cctga 1515

<210> 40
<211> 504
<212> PRT
<213> Bifidobacterium adolescentis

<400> 40

Met Lys Asn Lys Val Gln Leu Ile Thr Tyr Ala Asp Arg Leu Gly Asp
1 5 10 15

Gly Thr Ile Lys Ser Met Thr Asp Ile Leu Arg Thr Arg Phe Asp Gly
20 25 30

Val Tyr Asp Gly Val His Ile Leu Pro Phe Phe Thr Pro Phe Asp Gly
35 40 45

Ala Asp Ala Gly Phe Asp Pro Ile Asp His Thr Lys Val Asp Glu Arg
50 55 60

Leu Gly Ser Trp Asp Asp Val Ala Glu Leu Ser Lys Thr His Asn Ile
65 70 75 80

Met Val Asp Ala Ile Val Asn His Met Ser Trp Glu Ser Lys Gln Phe
85 90 95

Gln Asp Val Leu Ala Lys Gly Glu Glu Ser Glu Tyr Tyr Pro Met Phe
100 105 110

Leu Thr Met Ser Ser Val Phe Pro Asn Gly Ala Thr Glu Glu Asp Leu
115 120 125

Ala Gly Ile Tyr Arg Pro Arg Pro Gly Leu Pro Phe Thr His Tyr Lys
130 135 140

Phe Ala Gly Lys Thr Arg Leu Val Trp Val Ser Phe Thr Pro Gln Gln
145 150 155 160

```
Val Asp Ile Asp Thr Asp Ser Asp Lys Gly Trp Glu Tyr Leu Met Ser
                165                 170                 175

Ile Phe Asp Gln Met Ala Ala Ser His Val Ser Tyr Ile Arg Leu Asp
            180                 185                 190

Ala Val Gly Tyr Gly Ala Lys Glu Ala Gly Thr Ser Cys Phe Met Thr
        195                 200                 205

Pro Lys Thr Phe Lys Leu Ile Ser Arg Leu Arg Glu Glu Gly Val Lys
    210                 215                 220

Arg Gly Leu Glu Ile Leu Ile Glu Val His Ser Tyr Tyr Lys Lys Gln
225                 230                 235                 240

Val Glu Ile Ala Ser Lys Val Asp Arg Val Tyr Asp Phe Ala Leu Pro
                245                 250                 255

Pro Leu Leu Leu His Ala Leu Ser Thr Gly His Val Glu Pro Val Ala
            260                 265                 270

His Trp Thr Asp Ile Arg Pro Asn Asn Ala Val Thr Val Leu Asp Thr
        275                 280                 285

His Asp Gly Ile Gly Val Ile Asp Ile Gly Ser Asp Gln Leu Asp Arg
    290                 295                 300

Ser Leu Lys Gly Leu Val Pro Asp Glu Asp Val Asp Asn Leu Val Asn
305                 310                 315                 320

Thr Ile His Ala Asn Thr His Gly Glu Ser Gln Ala Ala Thr Gly Ala
                325                 330                 335

Ala Ala Ser Asn Leu Asp Leu Tyr Gln Val Asn Ser Thr Tyr Tyr Ser
            340                 345                 350

Ala Leu Gly Cys Asn Asp Gln His Tyr Ile Ala Ala Arg Ala Val Gln
        355                 360                 365

Phe Phe Leu Pro Gly Val Pro Gln Val Tyr Tyr Val Gly Ala Leu Ala
    370                 375                 380

Gly Lys Asn Asp Met Glu Leu Leu Arg Lys Thr Asn Asn Gly Arg Asp
385                 390                 395                 400

Ile Asn Arg His Tyr Tyr Ser Thr Ala Glu Ile Asp Glu Asn Leu Lys
                405                 410                 415

Arg Pro Val Val Lys Ala Leu Asn Ala Leu Ala Lys Phe Arg Asn Glu
            420                 425                 430
```

Leu Asp Ala Phe Asp Gly Thr Phe Ser Tyr Thr Thr Asp Asp Asp Thr
435 440 445

Ser Ile Ser Phe Thr Trp Arg Gly Glu Thr Ser Gln Ala Thr Leu Thr
450 455 460

Phe Glu Pro Lys Arg Gly Leu Gly Val Asp Asn Thr Thr Pro Val Ala
465 470 475 480

Met Leu Glu Trp Glu Asp Ser Ala Gly Asp His Arg Ser Asp Asp Leu
485 490 495

Ile Ala Asn Pro Pro Val Val Ala
500

<210> 41
<211> 927
<212> DNA
<213> Agrobacterium tumefaciens

<400> 41
atgatcctgt gttgtggtga agccctgatc gacatgctgc cccggcagac gacgctgggt 60

gaggcgggct ttgcccctta cgcaggcgga gcggtcttca acacggcaat tgcgctgggg 120

cgtcttggcg tcccttcagc ctttttttacc ggtctttccg acgacatgat gggcgatatc 180

ctgcgggaga ccctgcgggc cagcaaggtg gatttcagct attgcgccac cctgtcgcgc 240

cccaccacca ttgcgttcgt taagctggtt gatggccatg cgacctacgc tttttacgac 300

gagaacaccg ccggccggat gatcaccgag gccgaacttc cggccttggg agcggattgc 360

gaagcgctgc atttcggcgc catcagcctt attcccgaac cctgcggcag cacctatgag 420

gcgctgatga cgcgcgagca tgagacccgc gtcatctcgc tcgatccgaa cattcgtccc 480

ggcttcatcc agaacaagca gtcgcacatg gcccgcatcc gccgcatggc ggcgatgtct 540

gacatcgtca agttctcgga tgaggacctg gcgtggttcg gtctggaagg cgacgaggac 600

acgcttgccc gccactggct gcaccacggt gcaaaactcg tcgttgtcac ccgtggcgcc 660

aagggtgccg tgggttacag cgccaatctc aaggtggaag tggcctccga gcgcgtcgaa 720

gtggtcgata cggtcggcgc cggcgatacg ttcgatgccg gcattcttgc ttcgctgaaa 780

atgcagggcc tgctgaccaa agcgcaggtg gcttcgctga gcgaagagca gatcagaaaa 840

gctttggcgc ttggcgcgaa agccgctgcg gtcactgtct cgcgggctgg cgcaaatccg 900

cctttcgcgc atgaaatcgg tttgtga 927

<210> 42
<211> 308
<212> PRT
<213> Agrobacterium tumefaciens

<400> 42

Met Ile Leu Cys Cys Gly Glu Ala Leu Ile Asp Met Leu Pro Arg Gln
1 5 10 15

```
Thr Thr Leu Gly Glu Ala Gly Phe Ala Pro Tyr Ala Gly Gly Ala Val
            20                  25                  30

Phe Asn Thr Ala Ile Ala Leu Gly Arg Leu Gly Val Pro Ser Ala Phe
        35                  40                  45

Phe Thr Gly Leu Ser Asp Asp Met Met Gly Asp Ile Leu Arg Glu Thr
    50                  55                  60

Leu Arg Ala Ser Lys Val Asp Phe Ser Tyr Cys Ala Thr Leu Ser Arg
65                  70                  75                  80

Pro Thr Thr Ile Ala Phe Val Lys Leu Val Asp Gly His Ala Thr Tyr
                85                  90                  95

Ala Phe Tyr Asp Glu Asn Thr Ala Gly Arg Met Ile Thr Glu Ala Glu
            100                 105                 110

Leu Pro Ala Leu Gly Ala Asp Cys Glu Ala Leu His Phe Gly Ala Ile
        115                 120                 125

Ser Leu Ile Pro Glu Pro Cys Gly Ser Thr Tyr Glu Ala Leu Met Thr
    130                 135                 140

Arg Glu His Glu Thr Arg Val Ile Ser Leu Asp Pro Asn Ile Arg Pro
145                 150                 155                 160

Gly Phe Ile Gln Asn Lys Gln Ser His Met Ala Arg Ile Arg Arg Met
                165                 170                 175

Ala Ala Met Ser Asp Ile Val Lys Phe Ser Asp Glu Asp Leu Ala Trp
            180                 185                 190

Phe Gly Leu Glu Gly Asp Glu Asp Thr Leu Ala Arg His Trp Leu His
        195                 200                 205

His Gly Ala Lys Leu Val Val Val Thr Arg Gly Ala Lys Gly Ala Val
    210                 215                 220

Gly Tyr Ser Ala Asn Leu Lys Val Glu Val Ala Ser Glu Arg Val Glu
225                 230                 235                 240

Val Val Asp Thr Val Gly Ala Gly Asp Thr Phe Asp Ala Gly Ile Leu
                245                 250                 255

Ala Ser Leu Lys Met Gln Gly Leu Leu Thr Lys Ala Gln Val Ala Ser
            260                 265                 270

Leu Ser Glu Glu Gln Ile Arg Lys Ala Leu Ala Leu Gly Ala Lys Ala
        275                 280                 285
```

Ala Ala Val Thr Val Ser Arg Ala Gly Ala Asn Pro Pro Phe Ala His
290 295 300

Glu Ile Gly Leu
305

<210> 43
<211> 1404
<212> DNA
<213> Streptococcus mutans

<400> 43
cagctgatta tgcgtcagtt gaaaccctcg cttcttcagg aactgttgct gtaggtgata 60

gcttacttga agttaaaaaa taagaaatat tatcagaaag accgtaaggt ctttttgact 120

gcttaaaaga ttcagtaaca atagtattaa agccttttgg ctaactaata cttgaaattt 180

agcaaattat gatataatgt taagtagtcc ttaagggtag attaagggta ttcaaatcca 240

aaaattgatt tggtaagtta agtaaaatat aagaggttta ttatgtctaa attatatggc 300

agcatcgaag ctggcggaac aaaatttgtc tgtgctgtag gtgatgaaaa ttttcaaatt 360

ttagaaaaag ttcagttccc aacaacaaca ccttatgaaa caatagaaaa aacagttgct 420

ttctttaaaa aatttgaagc tgatttagcc agtgttgcca ttggttcttt tggccctatt 480

gatattgatc aaaattcaga cacttatggt tacattactt caacaccaaa gccaaactgg 540

gctaacgttg attttgtcgg cttaatttct aaagatttta aaattccatt ttactttacg 600

acagatgtta attcttctgc ttatggggaa acaattgctc gttcaaatgt taaaagtctg 660

gtttattata ctattggaac aggcattgga gcaggggcta ttcaaaatgg cgaattcatt 720

ggcggtatgg gacatacgga agctggacac gtttacatgg ctccgcatcc caatgatgtt 780

catcatggtt ttgtaggcac ctgtcctttc cataaaggct gtttagaagg acttgcagcg 840

ggtcctagct tagaggctcg tactggtatt cgtggtgagt taattgagca aaactcagaa 900

gtttgggata ttcaggcata ctacattgct caggcggcta ttcaagcgac tgtcctttat 960

cgtccgcaag tcattgtatt tggcggaggc gttatggcac aagaacatat gctcaatcgg 1020

gttcgtgaaa aatttacttc acttttgaat gactatcttc agttccaga tgttaaagat 1080

tatattgtga caccagctgt tgcagaaaat ggttcagcaa cattgggaaa tctcgcttta 1140

gctaaaaaga tagcagcgcg ttaattaaaa atgaattgga agattaaagc accttctaat 1200

attcaatatt aaactgttag aatttacgtg aacgaaattt tcattttatg aggataatga 1260

agtgaatata attactcttg atttcctctg aaactagata gtggtatatt gaaaaacaga 1320

aaggagaaca ctatggaagg acctttgttt ttacaatcac aaatgcataa aaaaatctgg 1380

ggcggcaatc ggctcagaaa agaa 1404

<210> 44
<211> 293
<212> PRT

<213> Streptococcus mutans

<400> 44

```
Met Ser Lys Leu Tyr Gly Ser Ile Glu Ala Gly Gly Thr Lys Phe Val
1               5                  10                  15

Cys Ala Val Gly Asp Glu Asn Phe Gln Ile Leu Glu Lys Val Gln Phe
            20                  25                  30

Pro Thr Thr Thr Pro Tyr Glu Thr Ile Glu Lys Thr Val Ala Phe Phe
        35                  40                  45

Lys Lys Phe Glu Ala Asp Leu Ala Ser Val Ala Ile Gly Ser Phe Gly
    50                  55                  60

Pro Ile Asp Ile Asp Gln Asn Ser Asp Thr Tyr Gly Tyr Ile Thr Ser
65                  70                  75                  80

Thr Pro Lys Pro Asn Trp Ala Asn Val Asp Phe Val Gly Leu Ile Ser
                85                  90                  95

Lys Asp Phe Lys Ile Pro Phe Tyr Phe Thr Thr Asp Val Asn Ser Ser
            100                 105                 110

Ala Tyr Gly Glu Thr Ile Ala Arg Ser Asn Val Lys Ser Leu Val Tyr
        115                 120                 125

Tyr Thr Ile Gly Thr Gly Ile Gly Ala Gly Ala Ile Gln Asn Gly Glu
    130                 135                 140

Phe Ile Gly Gly Met Gly His Thr Glu Ala Gly His Val Tyr Met Ala
145                 150                 155                 160

Pro His Pro Asn Asp Val His His Gly Phe Val Gly Thr Cys Pro Phe
                165                 170                 175

His Lys Gly Cys Leu Glu Gly Leu Ala Ala Gly Pro Ser Leu Glu Ala
            180                 185                 190

Arg Thr Gly Ile Arg Gly Glu Leu Ile Glu Gln Asn Ser Glu Val Trp
        195                 200                 205

Asp Ile Gln Ala Tyr Tyr Ile Ala Gln Ala Ala Ile Gln Ala Thr Val
    210                 215                 220

Leu Tyr Arg Pro Gln Val Ile Val Phe Gly Gly Gly Val Met Ala Gln
225                 230                 235                 240

Glu His Met Leu Asn Arg Val Arg Glu Lys Phe Thr Ser Leu Leu Asn
                245                 250                 255
```

Asp Tyr Leu Pro Val Pro Asp Val Lys Asp Tyr Ile Val Thr Pro Ala
260 265 270

Val Ala Glu Asn Gly Ser Ala Thr Leu Gly Asn Leu Ala Leu Ala Lys
275 280 285

Lys Ile Ala Ala Arg
290

<210> 45
<211> 915
<212> DNA
<213> Escherichia coli

<400> 45
atgtcagcca aagtatgggt tttaggggat gcggtcgtag atctcttgcc agaatcagac 60

gggcgcctac tgccttgtcc tggcggcgcg ccagctaacg ttgcggtggg aatcgccaga 120

ttaggcggaa caagtgggtt tataggtcgg gtgggggatg atccttttgg tgcgttaatg 180

caaagaacgc tgctaactga gggagtcgat atcacgtatc tgaagcaaga tgaatggcac 240

cggacatcca cggtgcttgt cgatctgaac gatcaagggg aacgttcatt tacgtttatg 300

gtccgcccca gtgccgatct ttttttagag acgacagact tgccctgctg gcgacatggc 360

gaatggttac atctctgttc aattgcgttg tctgccgagc cttcgcgtac cagcgcattt 420

actgcgatga cggcgatccg gcatgccgga ggttttgtca gcttcgatcc taatattcgt 480

gaagatctat ggcaagacga gcatttgctc cgcttgtgtt tgcggcaggc gctacaactg 540

gcggatgtcg tcaagctctc ggaagaagaa tggcgactta tcagtggaaa aacacagaac 600

gatcaggata tatgcgccct ggcaaaagag tatgagatcg ccatgctgtt ggtgactaaa 660

ggtgcagaag gggtggtggt ctgttatcga ggacaagttc accattttgc tggaatgtct 720

gtgaattgtg tcgatagcac gggggcggga gatgcgttcg ttgccgggtt actcacaggt 780

ctgtcctcta cgggattatc tacagatgag agagaaatgc gacgaattat cgatctcgct 840

caacgttgcg gagcgcttgc agtaacggcg aaaggggcaa tgacagcgct gccatgtcga 900

caagaactgg aatag 915

<210> 46
<211> 304
<212> PRT
<213> Escherichia coli

<400> 46

Met Ser Ala Lys Val Trp Val Leu Gly Asp Ala Val Val Asp Leu Leu
1 5 10 15

Pro Glu Ser Asp Gly Arg Leu Leu Pro Cys Pro Gly Gly Ala Pro Ala
20 25 30

Asn Val Ala Val Gly Ile Ala Arg Leu Gly Gly Thr Ser Gly Phe Ile
35 40 45

```
Gly Arg Val Gly Asp Asp Pro Phe Gly Ala Leu Met Gln Arg Thr Leu
    50                  55                  60

Leu Thr Glu Gly Val Asp Ile Thr Tyr Leu Lys Gln Asp Glu Trp His
65                  70                  75                  80

Arg Thr Ser Thr Val Leu Val Asp Leu Asn Asp Gln Gly Glu Arg Ser
                85                  90                  95

Phe Thr Phe Met Val Arg Pro Ser Ala Asp Leu Phe Leu Glu Thr Thr
            100                 105                 110

Asp Leu Pro Cys Trp Arg His Gly Glu Trp Leu His Leu Cys Ser Ile
        115                 120                 125

Ala Leu Ser Ala Glu Pro Ser Arg Thr Ser Ala Phe Thr Ala Met Thr
    130                 135                 140

Ala Ile Arg His Ala Gly Gly Phe Val Ser Phe Asp Pro Asn Ile Arg
145                 150                 155                 160

Glu Asp Leu Trp Gln Asp Glu His Leu Leu Arg Leu Cys Leu Arg Gln
                165                 170                 175

Ala Leu Gln Leu Ala Asp Val Val Lys Leu Ser Glu Glu Glu Trp Arg
            180                 185                 190

Leu Ile Ser Gly Lys Thr Gln Asn Asp Gln Asp Ile Cys Ala Leu Ala
        195                 200                 205

Lys Glu Tyr Glu Ile Ala Met Leu Leu Val Thr Lys Gly Ala Glu Gly
    210                 215                 220

Val Val Val Cys Tyr Arg Gly Gln Val His His Phe Ala Gly Met Ser
225                 230                 235                 240

Val Asn Cys Val Asp Ser Thr Gly Ala Gly Asp Ala Phe Val Ala Gly
                245                 250                 255

Leu Leu Thr Gly Leu Ser Ser Thr Gly Leu Ser Thr Asp Glu Arg Glu
            260                 265                 270

Met Arg Arg Ile Ile Asp Leu Ala Gln Arg Cys Gly Ala Leu Ala Val
        275                 280                 285

Thr Ala Lys Gly Ala Met Thr Ala Leu Pro Cys Arg Gln Glu Leu Glu
    290                 295                 300
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<210> 47
<211> 924

<212> DNA
<213> Klebsiella pneumoniae

<400> 47
atgaatggaa aaatctgggt actcggcgat gcggtcgtcg atctcctgcc cgatggagag 60

ggccgcctgc tgcaatgccc cggcggcgcg ccggccaacg tggcggtcgg cgtggcgcgg 120

ctcggcggtg acagcgggtt tatcggccgc gtcggcgacg atcccttcgg ccgttttatg 180

cgtcacaccc tggcgcagga gcaagtggat gtgaactata tgcgcctcga tgcggcgcag 240

cgcacctcca cggtggtggt cgatctcgat agccacgggg agcgcacctt tacctttatg 300

gtccgtccga gcgccgacct gttccttcag cccgaggatc tcccgccgtt tgccgccggt 360

cagtggctgc acgtctgctc catcgctctc agcgcggagc cgagccgcag cacgacattc 420

gcggcgatgg aggcgataaa gcgcgccggg ggctatgtca gcttcgaccc caatatccgc 480

agcgacctgt ggcaggatcc gcaggacctt cgcgactgtc tcgaccgggc gctggccctc 540

gccgacgcca taaaactttc ggaagaggag ctggcgttta tcagcggcag cgacgacatc 600

gtcagcggca ccgcccggct gaacgcccgc ttccagccga cgctactgct ggtgacccag 660

ggtaaagcgg gggtccaggc cgccctgcgc gggcaggtta gccacttccc tgcccgcccg 720

gtggtggccg tcgataccac cggcgccggc gatgcctttg tcgccgggct actcgccggc 780

ctcgccgccc acggtatccc ggacaacctc gcagccctgg ctcccgacct cgcgctggcg 840

caaacctgcg gcgccctggc caccaccgcc aaaggcgcca tgaccgccct gccctacagg 900

gacgatcttc agcgctcgct gtga 924

<210> 48
<211> 307
<212> PRT
<213> Klebsiella pneumoniae

<400> 48

Met Asn Gly Lys Ile Trp Val Leu Gly Asp Ala Val Val Asp Leu Leu
1 5 10 15

Pro Asp Gly Glu Gly Arg Leu Leu Gln Cys Pro Gly Gly Ala Pro Ala
20 25 30

Asn Val Ala Val Gly Val Ala Arg Leu Gly Gly Asp Ser Gly Phe Ile
35 40 45

Gly Arg Val Gly Asp Asp Pro Phe Gly Arg Phe Met Arg His Thr Leu
50 55 60

Ala Gln Glu Gln Val Asp Val Asn Tyr Met Arg Leu Asp Ala Ala Gln
65 70 75 80

Arg Thr Ser Thr Val Val Val Asp Leu Asp Ser His Gly Glu Arg Thr
85 90 95

Phe Thr Phe Met Val Arg Pro Ser Ala Asp Leu Phe Leu Gln Pro Glu
100 105 110

Asp Leu Pro Pro Phe Ala Ala Gly Gln Trp Leu His Val Cys Ser Ile
115 120 125

Ala Leu Ser Ala Glu Pro Ser Arg Ser Thr Thr Phe Ala Ala Met Glu
130 135 140

Ala Ile Lys Arg Ala Gly Gly Tyr Val Ser Phe Asp Pro Asn Ile Arg
145 150 155 160

Ser Asp Leu Trp Gln Asp Pro Gln Asp Leu Arg Asp Cys Leu Asp Arg
165 170 175

Ala Leu Ala Leu Ala Asp Ala Ile Lys Leu Ser Glu Glu Glu Leu Ala
180 185 190

Phe Ile Ser Gly Ser Asp Asp Ile Val Ser Gly Thr Ala Arg Leu Asn
195 200 205

Ala Arg Phe Gln Pro Thr Leu Leu Leu Val Thr Gln Gly Lys Ala Gly
210 215 220

Val Gln Ala Ala Leu Arg Gly Gln Val Ser His Phe Pro Ala Arg Pro
225 230 235 240

Val Val Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Val Ala Gly
245 250 255

Leu Leu Ala Gly Leu Ala Ala His Gly Ile Pro Asp Asn Leu Ala Ala
260 265 270

Leu Ala Pro Asp Leu Ala Leu Ala Gln Thr Cys Gly Ala Leu Ala Thr
275 280 285

Thr Ala Lys Gly Ala Met Thr Ala Leu Pro Tyr Arg Asp Asp Leu Gln
290 295 300

Arg Ser Leu
305

<210> 49
<211> 915
<212> DNA
<213> Escherichia coli

<400> 49
atgtcagcca aagtatgggt tttaggggat gcggtcgtag atctcttgcc agaatcagac 60

gggcgcctac tgccttgtcc tggcggcgcg ccagctaacg ttgcggtggg aatcgccaga 120

ttaggcggaa caagtgggtt tataggtcgg gtgggggatg atccttttgg tgcgttaatg 180

caaagaacgc tgctaactga gggagtcgat atcacgtatc tgaagcaaga tgaatggcac 240

cggacatcca cggtgcttgt cgatctgaac gatcaagggg aacgttcatt tacgtttatg 300

gtccgcccca gtgccgatct ttttttagag acgacagact tgccctgctg gcgacatggc 360

gaatggttac atctctgttc aattgcgttg tctgccgagc cttcgcgtac cagcgcattt 420

actgcgatga cggcgatccg gcatgccgga ggttttgtca gcttcgatcc taatattcgt 480

gaagatctat ggcaagacga gcatttgctc cgcttgtgtt tgcggcaggc gctacaactg 540

gcggatgtcg tcaagctctc ggaagaagaa tggcgactta tcagtggaaa aacacagaac 600

gatcaggata tatgcgccct ggcaaaagag tatgagatcg ccatgctgtt ggtgactaaa 660

ggtgcagaag gggtggtggt ctgttatcga ggacaagttc accattttgc tggaatgtct 720

gtgaattgtg tcgatagcac gggggcggga gatgcgttcg ttgccgggtt actcacaggt 780

ctgtcctcta cgggattatc tacagatgag agagaaatgc gacgaattat cgatctcgct 840

caacgttgcg gagcgcttgc agtaacggcg aaaggggcaa tgacagcgct gccatgtcga 900

caagaactgg aatag 915

<210> 50
<211> 304
<212> PRT
<213> Escherichia coli

<400> 50

Met Ser Ala Lys Val Trp Val Leu Gly Asp Ala Val Val Asp Leu Leu
1 5 10 15

Pro Glu Ser Asp Gly Arg Leu Leu Pro Cys Pro Gly Gly Ala Pro Ala
20 25 30

Asn Val Ala Val Gly Ile Ala Arg Leu Gly Gly Thr Ser Gly Phe Ile
35 40 45

Gly Arg Val Gly Asp Asp Pro Phe Gly Ala Leu Met Gln Arg Thr Leu
50 55 60

Leu Thr Glu Gly Val Asp Ile Thr Tyr Leu Lys Gln Asp Glu Trp His
65 70 75 80

Arg Thr Ser Thr Val Leu Val Asp Leu Asn Asp Gln Gly Glu Arg Ser
85 90 95

Phe Thr Phe Met Val Arg Pro Ser Ala Asp Leu Phe Leu Glu Thr Thr
100 105 110

Asp Leu Pro Cys Trp Arg His Gly Glu Trp Leu His Leu Cys Ser Ile
115 120 125

Ala Leu Ser Ala Glu Pro Ser Arg Thr Ser Ala Phe Thr Ala Met Thr
130 135 140

```
Ala Ile Arg His Ala Gly Gly Phe Val Ser Phe Asp Pro Asn Ile Arg
145                 150                 155                 160

Glu Asp Leu Trp Gln Asp Glu His Leu Leu Arg Leu Cys Leu Arg Gln
                165                 170                 175

Ala Leu Gln Leu Ala Asp Val Val Lys Leu Ser Glu Glu Glu Trp Arg
            180                 185                 190

Leu Ile Ser Gly Lys Thr Gln Asn Asp Gln Asp Ile Cys Ala Leu Ala
        195                 200                 205

Lys Glu Tyr Glu Ile Ala Met Leu Leu Val Thr Lys Gly Ala Glu Gly
    210                 215                 220

Val Val Val Cys Tyr Arg Gly Gln Val His His Phe Ala Gly Met Ser
225                 230                 235                 240

Val Asn Cys Val Asp Ser Thr Gly Ala Gly Asp Ala Phe Val Ala Gly
                245                 250                 255

Leu Leu Thr Gly Leu Ser Ser Thr Gly Leu Ser Thr Asp Glu Arg Glu
            260                 265                 270

Met Arg Arg Ile Ile Asp Leu Ala Gln Arg Cys Gly Ala Leu Ala Val
        275                 280                 285

Thr Ala Lys Gly Ala Met Thr Ala Leu Pro Cys Arg Gln Glu Leu Glu
    290                 295                 300
```

<210> 51
<211> 879
<212> DNA
<213> Enterococcus faecalis

<400> 51

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atgacagaaa aacttttagg aagtatcgaa gccggtggca caaaatttgt atgtggcgtt       60

gggacagatg atttgaccat cgtagaacgt gtcagttttc ccacaacaac cccagaagaa      120

acaatgaaaa aagtaataga atttttccaa caatatcctt taaaagcgat tgggattggt      180

tcatttggtc cgattgatat tcacgttgat tctcctacgt atggttatat cacttctaca      240

ccaaaattag cttggcgtaa ctttgacttg ttaggaacta tgaaacaaca ttttgatgtg      300

ccaatggctt ggacaacgga tgtgaatgct gcggcatatg gtgagtatgt tgctggaaat      360

gggcaacata catctagttg tgtatattat acaattggaa ctggtgttgg cgctggagcg      420

attcaaaacg gtgagtttat tgaaggcttt agccacccag aaatggggca tgcgttagtt      480

cgtcgtcatc ctgaagatac gtatgcagga aattgtcctt atcatggaga ttgtttagaa      540

gggattgcag caggaccagc agttgaaggt cgttctggta aaaaaggaca tttattggaa      600
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gaggatcata aaacttggga attagaagct tattatttag cgcaagcggc gtacaatacg 660

actttattat tagcgccaga agtgatcatt ttaggtggcg gcgtcatgaa acaacgtcat 720

ttgatgccga aagttcgtga aaaatttgct gaattagtca atggatatgt ggaaacaccg 780

cctttagaaa aatacttggt gacgcctctt ttagaagata atccaggaac aatcggttgc 840

tttgccttgg caaaaaaagc tttaatggct caaaaataa 879

<210> 52
<211> 292
<212> PRT
<213> Enterococcus faecalis

<400> 52

Met Thr Glu Lys Leu Leu Gly Ser Ile Glu Ala Gly Gly Thr Lys Phe
1 5 10 15

Val Cys Gly Val Gly Thr Asp Asp Leu Thr Ile Val Glu Arg Val Ser
20 25 30

Phe Pro Thr Thr Thr Pro Glu Glu Thr Met Lys Lys Val Ile Glu Phe
35 40 45

Phe Gln Gln Tyr Pro Leu Lys Ala Ile Gly Ile Gly Ser Phe Gly Pro
50 55 60

Ile Asp Ile His Val Asp Ser Pro Thr Tyr Gly Tyr Ile Thr Ser Thr
65 70 75 80

Pro Lys Leu Ala Trp Arg Asn Phe Asp Leu Leu Gly Thr Met Lys Gln
85 90 95

His Phe Asp Val Pro Met Ala Trp Thr Thr Asp Val Asn Ala Ala Ala
100 105 110

Tyr Gly Glu Tyr Val Ala Gly Asn Gly Gln His Thr Ser Ser Cys Val
115 120 125

Tyr Tyr Thr Ile Gly Thr Gly Val Gly Ala Gly Ala Ile Gln Asn Gly
130 135 140

Glu Phe Ile Glu Gly Phe Ser His Pro Glu Met Gly His Ala Leu Val
145 150 155 160

Arg Arg His Pro Glu Asp Thr Tyr Ala Gly Asn Cys Pro Tyr His Gly
165 170 175

Asp Cys Leu Glu Gly Ile Ala Ala Gly Pro Ala Val Glu Gly Arg Ser
180 185 190

Gly Lys Lys Gly His Leu Leu Glu Glu Asp His Lys Thr Trp Glu Leu
195 200 205

Glu Ala Tyr Tyr Leu Ala Gln Ala Ala Tyr Asn Thr Thr Leu Leu Leu
210 215 220

Ala Pro Glu Val Ile Ile Leu Gly Gly Gly Val Met Lys Gln Arg His
225 230 235 240

Leu Met Pro Lys Val Arg Glu Lys Phe Ala Glu Leu Val Asn Gly Tyr
245 250 255

Val Glu Thr Pro Pro Leu Glu Lys Tyr Leu Val Thr Pro Leu Leu Glu
260 265 270

Asp Asn Pro Gly Thr Ile Gly Cys Phe Ala Leu Ala Lys Lys Ala Leu
275 280 285

Met Ala Gln Lys
290

<210> 53
<211> 1458
<212> DNA
<213> Saccharomyces cerevisiae

<400> 53
atggttcatt taggtccaaa gaaaccacag gctagaaagg gttccatggc tgatgtgccc 60

aaggaattga tggatgaaat tcatcagttg gaagatatgt ttacagttga cagcgagacc 120

ttgagaaagg ttgttaagca ctttatcgac gaattgaata aaggtttgac aaagaaggga 180

ggtaacattc caatgattcc cggttgggtc atggaattcc caacaggtaa agaatctggt 240

aactatttgg ccattgattt gggtggtact aacttaagag tcgtgttggt caagttgagc 300

ggtaaccata cctttgacac cactcaatcc aagtataaac taccacatga catgagaacc 360

actaagcacc aagaggagtt atggtccttt attgccgact ctttgaagga ctttatggtc 420

gagcaagaat tgctaaacac caaggacacc ttaccattag gtttcacctt ctcgtaccca 480

gcttcccaaa acaagattaa cgaaggtatt ttgcaaagat ggaccaaggg tttcgatatt 540

ccaaatgtcg aaggccacga tgtcgtccca ttgctacaaa acgaaatttc caagagagag 600

ttgcctattg aaattgtagc attgattaat gatactgttg gtactttaat tgcctcatac 660

tacactgacc cagagactaa gatgggtgtg attttcggta ctggtgtcaa cggtgctttc 720

tatgatgttg tttccgatat cgaaaagttg gagggcaaat tagcagacga tattccaagt 780

aactctccaa tggctatcaa ttgtgaatat ggttccttcg ataatgaaca tttggtcttg 840

ccaagaacca agtacgatgt tgctgtcgac gaacaatctc caagacctgg tcaacaagct 900

tttgaaaaga tgacctccgg ttactacttg ggtgaattgt tgcgtctagt gttacttgaa 960

ttaaacgaga agggcttgat gttgaaggat caagatctaa gcaagttgaa acaaccatac 1020

atcatggata cctcctaccc agcaagaatc gaggatgatc catttgaaaa cttggaagat 1080

actgatgaca tcttccaaaa ggactttggt gtcaagacca ctctgccaga acgtaagttg 1140

attagaagac tttgtgaatt gatcggtacc agagctgcta gattagctgt ttgtggtatt 1200

gccgctattt gccaaaagag aggttacaag actggtcaca ttgccgctga cggttctgtc 1260

tataacaaat acccaggttt caaggaagcc gccgctaagg gtttgagaga tatctatgga 1320

tggactggtg acgcaagcaa agatccaatt acgattgttc cagctgagga tggttcaggt 1380

gcaggtgctg ctgttattgc tgcattgtcc gaaaaaagaa ttgccgaagg taagtctctt 1440

ggtatcattg gcgcttaa 1458

<210> 54
<211> 485
<212> PRT
<213> Saccharomyces cerevisiae

<400> 54

Met Val His Leu Gly Pro Lys Lys Pro Gln Ala Arg Lys Gly Ser Met
1 5 10 15

Ala Asp Val Pro Lys Glu Leu Met Asp Glu Ile His Gln Leu Glu Asp
20 25 30

Met Phe Thr Val Asp Ser Glu Thr Leu Arg Lys Val Val Lys His Phe
35 40 45

Ile Asp Glu Leu Asn Lys Gly Leu Thr Lys Lys Gly Gly Asn Ile Pro
50 55 60

Met Ile Pro Gly Trp Val Met Glu Phe Pro Thr Gly Lys Glu Ser Gly
65 70 75 80

Asn Tyr Leu Ala Ile Asp Leu Gly Gly Thr Asn Leu Arg Val Val Leu
85 90 95

Val Lys Leu Ser Gly Asn His Thr Phe Asp Thr Thr Gln Ser Lys Tyr
100 105 110

Lys Leu Pro His Asp Met Arg Thr Thr Lys His Gln Glu Glu Leu Trp
115 120 125

Ser Phe Ile Ala Asp Ser Leu Lys Asp Phe Met Val Glu Gln Glu Leu
130 135 140

Leu Asn Thr Lys Asp Thr Leu Pro Leu Gly Phe Thr Phe Ser Tyr Pro
145 150 155 160

Ala Ser Gln Asn Lys Ile Asn Glu Gly Ile Leu Gln Arg Trp Thr Lys
165 170 175

Gly Phe Asp Ile Pro Asn Val Glu Gly His Asp Val Val Pro Leu Leu
180 185 190

```
Gln Asn Glu Ile Ser Lys Arg Glu Leu Pro Ile Glu Ile Val Ala Leu
        195                 200                 205

Ile Asn Asp Thr Val Gly Thr Leu Ile Ala Ser Tyr Tyr Thr Asp Pro
    210                 215                 220

Glu Thr Lys Met Gly Val Ile Phe Gly Thr Gly Val Asn Gly Ala Phe
225                 230                 235                 240

Tyr Asp Val Val Ser Asp Ile Glu Lys Leu Glu Gly Lys Leu Ala Asp
                245                 250                 255

Asp Ile Pro Ser Asn Ser Pro Met Ala Ile Asn Cys Glu Tyr Gly Ser
            260                 265                 270

Phe Asp Asn Glu His Leu Val Leu Pro Arg Thr Lys Tyr Asp Val Ala
        275                 280                 285

Val Asp Glu Gln Ser Pro Arg Pro Gly Gln Gln Ala Phe Glu Lys Met
    290                 295                 300

Thr Ser Gly Tyr Tyr Leu Gly Glu Leu Leu Arg Leu Val Leu Leu Glu
305                 310                 315                 320

Leu Asn Glu Lys Gly Leu Met Leu Lys Asp Gln Asp Leu Ser Lys Leu
                325                 330                 335

Lys Gln Pro Tyr Ile Met Asp Thr Ser Tyr Pro Ala Arg Ile Glu Asp
            340                 345                 350

Asp Pro Phe Glu Asn Leu Glu Asp Thr Asp Asp Ile Phe Gln Lys Asp
        355                 360                 365

Phe Gly Val Lys Thr Thr Leu Pro Glu Arg Lys Leu Ile Arg Arg Leu
    370                 375                 380

Cys Glu Leu Ile Gly Thr Arg Ala Ala Arg Leu Ala Val Cys Gly Ile
385                 390                 395                 400

Ala Ala Ile Cys Gln Lys Arg Gly Tyr Lys Thr Gly His Ile Ala Ala
                405                 410                 415

Asp Gly Ser Val Tyr Asn Lys Tyr Pro Gly Phe Lys Glu Ala Ala Ala
            420                 425                 430

Lys Gly Leu Arg Asp Ile Tyr Gly Trp Thr Gly Asp Ala Ser Lys Asp
        435                 440                 445

Pro Ile Thr Ile Val Pro Ala Glu Asp Gly Ser Gly Ala Gly Ala Ala
    450                 455                 460
```

Val Ile Ala Ala Leu Ser Glu Lys Arg Ile Ala Glu Gly Lys Ser Leu
465 470 475 480

Gly Ile Ile Gly Ala
485

<210> 55
<211> 1461
<212> DNA
<213> Saccharomyces cerevisiae

<400> 55
atggttcatt taggtccaaa aaaaccacaa gccagaaagg gttccatggc cgatgtgcca 60

aaggaattga tgcaacaaat tgagaatttt gaaaaaattt tcactgttcc aactgaaact 120

ttacaagccg ttaccaagca cttcatttcc gaattggaaa agggtttgtc caagaagggt 180

ggtaacattc caatgattcc aggttgggtt atggatttcc caactggtaa ggaatccggt 240

gatttcttgg ccattgattt gggtggtacc aacttgagag ttgtcttagt caagttgggc 300

ggtgaccgta cctttgacac cactcaatct aagtacagat taccagatgc tatgagaact 360

actcaaaatc cagacgaatt gtgggaattt attgccgact ctttgaaagc ttttattgat 420

gagcaattcc cacaaggtat ctctgagcca attccattgg gtttcacctt ttctttccca 480

gcttctcaaa acaaaatcaa tgaaggtatc ttgcaaagat ggactaaagg ttttgatatt 540

ccaaacattg aaaaccacga tgttgttcca atgttgcaaa agcaaatcac taagaggaat 600

atcccaattg aagttgttgc tttgataaac gacactaccg gtactttggt tgcttcttac 660

tacactgacc cagaaactaa gatgggtgtt atcttcggta ctggtgtcaa tggtgcttac 720

tacgatgttt gttccgatat cgaaaagcta caaggaaaac tatctgatga cattccacca 780

tctgctccaa tggccatcaa ctgtgaatac ggttccttcg ataatgaaca tgtcgttttg 840

ccaagaacta aatacgatat caccattgat gaagaatctc caagaccagg ccaacaaacc 900

tttgaaaaaa tgtcttctgg ttactactta ggtgaaattt tgcgtttggc cttgatggac 960

atgtacaaac aaggtttcat cttcaagaac caagacttgt ctaagttcga caagcctttc 1020

gtcatggaca cttcttaccc agccagaatc gaggaagatc cattcgagaa cctagaagat 1080

accgatgact tgttccaaaa tgagttcggt atcaacacta ctgttcaaga acgtaaattg 1140

atcagacgtt tatctgaatt gattggtgct agagctgcta gattgtccgt ttgtggtatt 1200

gctgctatct gtcaaaagag aggttacaag accggtcaca tcgctgcaga cggttccgtt 1260

tacaacagat acccaggttt caaagaaaag gctgccaatg ctttgaagga catttacggc 1320

tggactcaaa cctcactaga cgactaccca atcaagattg ttcctgctga agatggttcc 1380

ggtgctggtg ccgctgttat tgctgctttg gcccaaaaaa gaattgctga aggtaagtcc 1440

gttggtatca tcggtgctta a 1461

<210> 56

<211> 486
<212> PRT
<213> Saccharomyces cerevisiae

<400> 56

Met Val His Leu Gly Pro Lys Lys Pro Gln Ala Arg Lys Gly Ser Met
1 5 10 15

Ala Asp Val Pro Lys Glu Leu Met Gln Gln Ile Glu Asn Phe Glu Lys
20 25 30

Ile Phe Thr Val Pro Thr Glu Thr Leu Gln Ala Val Thr Lys His Phe
35 40 45

Ile Ser Glu Leu Glu Lys Gly Leu Ser Lys Lys Gly Gly Asn Ile Pro
50 55 60

Met Ile Pro Gly Trp Val Met Asp Phe Pro Thr Gly Lys Glu Ser Gly
65 70 75 80

Asp Phe Leu Ala Ile Asp Leu Gly Gly Thr Asn Leu Arg Val Val Leu
85 90 95

Val Lys Leu Gly Gly Asp Arg Thr Phe Asp Thr Thr Gln Ser Lys Tyr
100 105 110

Arg Leu Pro Asp Ala Met Arg Thr Thr Gln Asn Pro Asp Glu Leu Trp
115 120 125

Glu Phe Ile Ala Asp Ser Leu Lys Ala Phe Ile Asp Glu Gln Phe Pro
130 135 140

Gln Gly Ile Ser Glu Pro Ile Pro Leu Gly Phe Thr Phe Ser Phe Pro
145 150 155 160

Ala Ser Gln Asn Lys Ile Asn Glu Gly Ile Leu Gln Arg Trp Thr Lys
165 170 175

Gly Phe Asp Ile Pro Asn Ile Glu Asn His Asp Val Val Pro Met Leu
180 185 190

Gln Lys Gln Ile Thr Lys Arg Asn Ile Pro Ile Glu Val Val Ala Leu
195 200 205

Ile Asn Asp Thr Thr Gly Thr Leu Val Ala Ser Tyr Tyr Thr Asp Pro
210 215 220

Glu Thr Lys Met Gly Val Ile Phe Gly Thr Gly Val Asn Gly Ala Tyr
225 230 235 240

Tyr Asp Val Cys Ser Asp Ile Glu Lys Leu Gln Gly Lys Leu Ser Asp
245 250 255

```
Asp Ile Pro Pro Ser Ala Pro Met Ala Ile Asn Cys Glu Tyr Gly Ser
            260                 265                 270

Phe Asp Asn Glu His Val Val Leu Pro Arg Thr Lys Tyr Asp Ile Thr
        275                 280                 285

Ile Asp Glu Glu Ser Pro Arg Pro Gly Gln Gln Thr Phe Glu Lys Met
    290                 295                 300

Ser Ser Gly Tyr Tyr Leu Gly Glu Ile Leu Arg Leu Ala Leu Met Asp
305                 310                 315                 320

Met Tyr Lys Gln Gly Phe Ile Phe Lys Asn Gln Asp Leu Ser Lys Phe
                325                 330                 335

Asp Lys Pro Phe Val Met Asp Thr Ser Tyr Pro Ala Arg Ile Glu Glu
            340                 345                 350

Asp Pro Phe Glu Asn Leu Glu Asp Thr Asp Asp Leu Phe Gln Asn Glu
        355                 360                 365

Phe Gly Ile Asn Thr Thr Val Gln Glu Arg Lys Leu Ile Arg Arg Leu
    370                 375                 380

Ser Glu Leu Ile Gly Ala Arg Ala Ala Arg Leu Ser Val Cys Gly Ile
385                 390                 395                 400

Ala Ala Ile Cys Gln Lys Arg Gly Tyr Lys Thr Gly His Ile Ala Ala
                405                 410                 415

Asp Gly Ser Val Tyr Asn Arg Tyr Pro Gly Phe Lys Glu Lys Ala Ala
            420                 425                 430

Asn Ala Leu Lys Asp Ile Tyr Gly Trp Thr Gln Thr Ser Leu Asp Asp
        435                 440                 445

Tyr Pro Ile Lys Ile Val Pro Ala Glu Asp Gly Ser Gly Ala Gly Ala
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Ala Val Ile Ala Ala Leu Ala Gln Lys Arg Ile Ala Glu Gly Lys Ser
465                 470                 475                 480

Val Gly Ile Ile Gly Ala
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<212> DNA
<213> Klebsiella pneumoniae

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gacaaaggcc tgcgggcaat taaagatggc gcagtggaca aaaccctgca ttatctgcgg 180

gaggccggga tcgaggtggc gatctttgac ggcgtcgagc cgaacccgaa agacaccaac 240

gtgcgcgacg gcctcgccgt gtttcgccgc gaacagtgcg acatcatcgt caccgtgggc 300

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accaaagtga agtttgtgat cgtcagctgg cgcaacctgc cgtcggtctc tatcaacgat 540

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gctctgaaag acggcaatgc gttctcgaac ccgcgtaaag gcaacgagca ggagattgcc 1140

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<212> PRT
<213> Klebsiella pneumoniae

<400> 58

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Gly Pro Asn Ala Ile Ser Val Val Gly Glu Arg Cys Gln Leu Leu Gly
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Gly Lys Lys Ala Leu Leu Val Thr Asp Lys Gly Leu Arg Ala Ile Lys
35 40 45

Asp Gly Ala Val Asp Lys Thr Leu His Tyr Leu Arg Glu Ala Gly Ile
50 55 60

Glu Val Ala Ile Phe Asp Gly Val Glu Pro Asn Pro Lys Asp Thr Asn
65 70 75 80

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Val Arg Asp Gly Leu Ala Val Phe Arg Arg Glu Gln Cys Asp Ile Ile
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Val Thr Val Gly Gly Gly Ser Pro His Asp Cys Gly Lys Gly Ile Gly
            100                 105                 110

Ile Ala Ala Thr His Glu Gly Asp Leu Tyr Gln Tyr Ala Gly Ile Glu
        115                 120                 125

Thr Leu Thr Asn Pro Leu Pro Pro Ile Val Ala Val Asn Thr Thr Ala
    130                 135                 140

Gly Thr Ala Ser Glu Val Thr Arg His Cys Val Leu Thr Asn Thr Glu
145                 150                 155                 160

Thr Lys Val Lys Phe Val Ile Val Ser Trp Arg Asn Leu Pro Ser Val
                165                 170                 175

Ser Ile Asn Asp Pro Leu Leu Met Ile Gly Lys Pro Ala Ala Leu Thr
            180                 185                 190

Ala Ala Thr Gly Met Asp Ala Leu Thr His Ala Val Glu Ala Tyr Ile
        195                 200                 205

Ser Lys Asp Ala Asn Pro Val Thr Asp Ala Ala Ala Met Gln Ala Ile
    210                 215                 220

Arg Leu Ile Ala Arg Asn Leu Arg Gln Ala Val Ala Leu Gly Ser Asn
225                 230                 235                 240

Leu Gln Ala Arg Glu Asn Met Ala Tyr Ala Ser Leu Leu Ala Gly Met
                245                 250                 255

Ala Phe Asn Asn Ala Asn Leu Gly Tyr Val His Ala Met Ala His Gln
            260                 265                 270

Leu Gly Gly Leu Tyr Asp Met Pro His Gly Val Ala Asn Ala Val Leu
        275                 280                 285

Leu Pro His Val Ala Arg Tyr Asn Leu Ile Ala Asn Pro Glu Lys Phe
    290                 295                 300

Ala Asp Ile Ala Glu Leu Met Gly Glu Asn Ile Thr Gly Leu Ser Thr
305                 310                 315                 320

Leu Asp Ala Ala Glu Lys Ala Ile Ala Ala Ile Thr Arg Leu Ser Met
                325                 330                 335

Asp Ile Gly Ile Pro Gln His Leu Arg Asp Leu Gly Val Lys Glu Ala
            340                 345                 350
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Asp Phe Pro Tyr Met Ala Glu Met Ala Leu Lys Asp Gly Asn Ala Phe
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Ser Asn Pro Arg Lys Gly Asn Glu Gln Glu Ile Ala Ala Ile Phe Arg
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Gln Ala Phe
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gcg ctg gcg tcc gac tac ccg cag gcg agg gcg ttt gtt gcc agc ggg          96
Ala Leu Ala Ser Asp Tyr Pro Gln Ala Arg Ala Phe Val Ala Ser Gly
            20                  25                  30

atc gtc gcg acg acg ggc atg aaa ggg acg cgg gac aat atc gcc ggg         144
Ile Val Ala Thr Thr Gly Met Lys Gly Thr Arg Asp Asn Ile Ala Gly
        35                  40                  45

acc ctc gcc gcg ctg gag cag gcc ctg gcg aaa aca ccg tgg tcg atg         192
Thr Leu Ala Ala Leu Glu Gln Ala Leu Ala Lys Thr Pro Trp Ser Met
    50                  55                  60

agc gat gtc tct cgc atc tat ctt aac gaa gcc gcg ccg gtg att ggc         240
Ser Asp Val Ser Arg Ile Tyr Leu Asn Glu Ala Ala Pro Val Ile Gly
65                  70                  75                  80

gat gtg gcg atg gag acc atc acc gag acc att atc acc gaa tcg acc         288
Asp Val Ala Met Glu Thr Ile Thr Glu Thr Ile Ile Thr Glu Ser Thr
                85                  90                  95

atg atc ggt cat aac ccg cag acg ccg ggc ggg gtg ggc gtt ggc gtg         336
Met Ile Gly His Asn Pro Gln Thr Pro Gly Gly Val Gly Val Gly Val
            100                 105                 110

ggg acg act atc gcc ctc ggg cgg ctg gcg acg ctg ccg gcg gcg cag         384
Gly Thr Thr Ile Ala Leu Gly Arg Leu Ala Thr Leu Pro Ala Ala Gln
        115                 120                 125

tat gcc gag ggg tgg atc gta ctg att gac gac gcc gtc gat ttc ctt         432
Tyr Ala Glu Gly Trp Ile Val Leu Ile Asp Asp Ala Val Asp Phe Leu
    130                 135                 140

gac gcc gtg tgg tgg ctc aat gag gcg ctc gac cgg ggg atc aac gtg         480
Asp Ala Val Trp Trp Leu Asn Glu Ala Leu Asp Arg Gly Ile Asn Val
145                 150                 155                 160

gtg gcg gcg atc ctc aaa aag gac gac ggc gtg ctg gtg aac aac cgc         528
Val Ala Ala Ile Leu Lys Lys Asp Asp Gly Val Leu Val Asn Asn Arg
                165                 170                 175

ctg cgt aaa acc ctg ccg gtg gtg gat gaa gtg acg ctg ctg gag cag         576
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Leu Arg Lys Thr Leu Pro Val Val Asp Glu Val Thr Leu Leu Glu Gln
            180                 185                 190

gtc ccc gag ggg gta atg gcg gcg gtg gaa gtg gcc gcg ccg ggc cag        624
Val Pro Glu Gly Val Met Ala Ala Val Glu Val Ala Ala Pro Gly Gln
        195                 200                 205

gtg gtg cgg atc ctg tcg aat ccc tac ggg atc gcc acc ttc ttc ggg        672
Val Val Arg Ile Leu Ser Asn Pro Tyr Gly Ile Ala Thr Phe Phe Gly
    210                 215                 220

cta agc ccg gaa gag acc cag gcc atc gtc ccc atc gcc cgc gcc ctg        720
Leu Ser Pro Glu Glu Thr Gln Ala Ile Val Pro Ile Ala Arg Ala Leu
225                 230                 235                 240

att ggc aac cgt tcc gcg gtg gtg ctc aag acc ccg cag ggg gat gtg        768
Ile Gly Asn Arg Ser Ala Val Val Leu Lys Thr Pro Gln Gly Asp Val
                245                 250                 255

cag tcg cgg gtg atc ccg gcg ggc aac ctc tac att agc ggc gaa aag        816
Gln Ser Arg Val Ile Pro Ala Gly Asn Leu Tyr Ile Ser Gly Glu Lys
            260                 265                 270

cgc cgc gga gag gcc gat gtc gcc gag ggc gcg gaa gcc atc atg cag        864
Arg Arg Gly Glu Ala Asp Val Ala Glu Gly Ala Glu Ala Ile Met Gln
        275                 280                 285

gcg atg agc gcc tgc gct ccg gta cgc gac atc cgc ggc gaa ccg ggc        912
Ala Met Ser Ala Cys Ala Pro Val Arg Asp Ile Arg Gly Glu Pro Gly
    290                 295                 300

acc cac gcc ggc ggc atg ctt gag cgg gtg cgc aag gta atg gcg tcc        960
Thr His Ala Gly Gly Met Leu Glu Arg Val Arg Lys Val Met Ala Ser
305                 310                 315                 320

ctg acc ggc cat gag atg agc gcg ata tac atc cag gat ctg ctg gcg       1008
Leu Thr Gly His Glu Met Ser Ala Ile Tyr Ile Gln Asp Leu Leu Ala
                325                 330                 335

gtg gat acg ttt att ccg cgc aag gtg cag ggc ggg atg gcc ggc gag       1056
Val Asp Thr Phe Ile Pro Arg Lys Val Gln Gly Gly Met Ala Gly Glu
            340                 345                 350

tgc gcc atg gag aat gcc gtc ggg atg gcg gcg atg gtg aaa gcg gat       1104
Cys Ala Met Glu Asn Ala Val Gly Met Ala Ala Met Val Lys Ala Asp
        355                 360                 365

cgt ctg caa atg cag gtt atc gcc cgc gaa ctg agc gcc cga ctg cag       1152
Arg Leu Gln Met Gln Val Ile Ala Arg Glu Leu Ser Ala Arg Leu Gln
    370                 375                 380

acc gag gtg gtg gtg ggc ggc gtg gag gcc aac atg gcc atc gcc ggg       1200
Thr Glu Val Val Val Gly Gly Val Glu Ala Asn Met Ala Ile Ala Gly
385                 390                 395                 400

gcg tta acc act ccc ggc tgt gcg gcg ccg ctg gcg atc ctc gac ctc       1248
Ala Leu Thr Thr Pro Gly Cys Ala Ala Pro Leu Ala Ile Leu Asp Leu
                405                 410                 415

ggc gcc ggc tcg acg gat gcg gcg atc gtc aac gcg gag ggg cag ata       1296
Gly Ala Gly Ser Thr Asp Ala Ala Ile Val Asn Ala Glu Gly Gln Ile
            420                 425                 430

acg gcg gtc cat ctc gcc ggg gcg ggg aat atg gtc agc ctg ttg att       1344
Thr Ala Val His Leu Ala Gly Ala Gly Asn Met Val Ser Leu Leu Ile
        435                 440                 445

aaa acc gag ctg ggc ctc gag gat ctt tcg ctg gcg gaa gcg ata aaa       1392
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Lys Thr Glu Leu Gly Leu Glu Asp Leu Ser Leu Ala Glu Ala Ile Lys
    450                 455                 460

aaa tac ccg ctg gcc aaa gtg gaa agc ctg ttc agt att cgt cac gag       1440
Lys Tyr Pro Leu Ala Lys Val Glu Ser Leu Phe Ser Ile Arg His Glu
465                 470                 475                 480

aat ggc gcg gtg gag ttc ttt cgg gaa gcc ctc agc ccg gcg gtg ttc       1488
Asn Gly Ala Val Glu Phe Phe Arg Glu Ala Leu Ser Pro Ala Val Phe
                485                 490                 495

gcc aaa gtg gtg tac atc aag gag ggc gaa ctg gtg ccg atc gat aac       1536
Ala Lys Val Val Tyr Ile Lys Glu Gly Glu Leu Val Pro Ile Asp Asn
            500                 505                 510

gcc agc ccg ctg gaa aaa att cgt ctc gtg cgc cgg cag gcg aaa gag       1584
Ala Ser Pro Leu Glu Lys Ile Arg Leu Val Arg Arg Gln Ala Lys Glu
        515                 520                 525

aaa gtg ttt gtc acc aac tgc ctg cgc gcg ctg cgc cag gtc tca ccc       1632
Lys Val Phe Val Thr Asn Cys Leu Arg Ala Leu Arg Gln Val Ser Pro
    530                 535                 540

ggc ggt tcc att cgc gat atc gcc ttt gtg gtg ctg gtg ggc ggc tca       1680
Gly Gly Ser Ile Arg Asp Ile Ala Phe Val Val Leu Val Gly Gly Ser
545                 550                 555                 560

tcg ctg gac ttt gag atc ccg cag ctt atc acg gaa gcc ttg tcg cac       1728
Ser Leu Asp Phe Glu Ile Pro Gln Leu Ile Thr Glu Ala Leu Ser His
                565                 570                 575

tat ggc gtg gtc gcc ggg cag ggc aat att cgg gga aca gaa ggg ccg       1776
Tyr Gly Val Val Ala Gly Gln Gly Asn Ile Arg Gly Thr Glu Gly Pro
            580                 585                 590

cgc aat gcg gtc gcc acc ggg ctg cta ctg gcc ggt cag gcg aat taa       1824
Arg Asn Ala Val Ala Thr Gly Leu Leu Leu Ala Gly Gln Ala Asn
        595                 600                 605


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<213>  Klebsiella pneumoniae

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            20                  25                  30


Ile Val Ala Thr Thr Gly Met Lys Gly Thr Arg Asp Asn Ile Ala Gly
        35                  40                  45


Thr Leu Ala Ala Leu Glu Gln Ala Leu Ala Lys Thr Pro Trp Ser Met
    50                  55                  60


Ser Asp Val Ser Arg Ile Tyr Leu Asn Glu Ala Ala Pro Val Ile Gly
65                  70                  75                  80


Asp Val Ala Met Glu Thr Ile Thr Glu Thr Ile Ile Thr Glu Ser Thr
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85 90 95

Met Ile Gly His Asn Pro Gln Thr Pro Gly Gly Val Gly Val Gly Val
100 105 110

Gly Thr Thr Ile Ala Leu Gly Arg Leu Ala Thr Leu Pro Ala Ala Gln
115 120 125

Tyr Ala Glu Gly Trp Ile Val Leu Ile Asp Asp Ala Val Asp Phe Leu
130 135 140

Asp Ala Val Trp Trp Leu Asn Glu Ala Leu Asp Arg Gly Ile Asn Val
145 150 155 160

Val Ala Ala Ile Leu Lys Lys Asp Asp Gly Val Leu Val Asn Asn Arg
165 170 175

Leu Arg Lys Thr Leu Pro Val Val Asp Glu Val Thr Leu Leu Glu Gln
180 185 190

Val Pro Glu Gly Val Met Ala Ala Val Glu Val Ala Ala Pro Gly Gln
195 200 205

Val Val Arg Ile Leu Ser Asn Pro Tyr Gly Ile Ala Thr Phe Phe Gly
210 215 220

Leu Ser Pro Glu Glu Thr Gln Ala Ile Val Pro Ile Ala Arg Ala Leu
225 230 235 240

Ile Gly Asn Arg Ser Ala Val Val Leu Lys Thr Pro Gln Gly Asp Val
245 250 255

Gln Ser Arg Val Ile Pro Ala Gly Asn Leu Tyr Ile Ser Gly Glu Lys
260 265 270

Arg Arg Gly Glu Ala Asp Val Ala Glu Gly Ala Glu Ala Ile Met Gln
275 280 285

Ala Met Ser Ala Cys Ala Pro Val Arg Asp Ile Arg Gly Glu Pro Gly
290 295 300

Thr His Ala Gly Gly Met Leu Glu Arg Val Arg Lys Val Met Ala Ser
305 310 315 320

Leu Thr Gly His Glu Met Ser Ala Ile Tyr Ile Gln Asp Leu Leu Ala
325 330 335

Val Asp Thr Phe Ile Pro Arg Lys Val Gln Gly Gly Met Ala Gly Glu
340 345 350

Cys Ala Met Glu Asn Ala Val Gly Met Ala Ala Met Val Lys Ala Asp

355 360 365

Arg Leu Gln Met Gln Val Ile Ala Arg Glu Leu Ser Ala Arg Leu Gln
370 375 380

Thr Glu Val Val Val Gly Gly Val Glu Ala Asn Met Ala Ile Ala Gly
385 390 395 400

Ala Leu Thr Thr Pro Gly Cys Ala Ala Pro Leu Ala Ile Leu Asp Leu
405 410 415

Gly Ala Gly Ser Thr Asp Ala Ala Ile Val Asn Ala Glu Gly Gln Ile
420 425 430

Thr Ala Val His Leu Ala Gly Ala Gly Asn Met Val Ser Leu Leu Ile
435 440 445

Lys Thr Glu Leu Gly Leu Glu Asp Leu Ser Leu Ala Glu Ala Ile Lys
450 455 460

Lys Tyr Pro Leu Ala Lys Val Glu Ser Leu Phe Ser Ile Arg His Glu
465 470 475 480

Asn Gly Ala Val Glu Phe Phe Arg Glu Ala Leu Ser Pro Ala Val Phe
485 490 495

Ala Lys Val Val Tyr Ile Lys Glu Gly Glu Leu Val Pro Ile Asp Asn
500 505 510

Ala Ser Pro Leu Glu Lys Ile Arg Leu Val Arg Arg Gln Ala Lys Glu
515 520 525

Lys Val Phe Val Thr Asn Cys Leu Arg Ala Leu Arg Gln Val Ser Pro
530 535 540

Gly Gly Ser Ile Arg Asp Ile Ala Phe Val Val Leu Val Gly Gly Ser
545 550 555 560

Ser Leu Asp Phe Glu Ile Pro Gln Leu Ile Thr Glu Ala Leu Ser His
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Tyr Gly Val Val Ala Gly Gln Gly Asn Ile Arg Gly Thr Glu Gly Pro
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Arg Asn Ala Val Ala Thr Gly Leu Leu Leu Ala Gly Gln Ala Asn
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acgattgaaa accctacaag gaaagaacgg acggtatcgt tcacttataa ccaatacgct 13200

cagatgatga acatcagtag ggaaaatgct tatggtgtat tagctaaagc aaccagagag 13260

ctgatgacga gaactgtgga aatcaggaat cctttggtta aaggctttga gattttccag 13320

tggacaaact atgccaagtt ctcaagcgaa aaattagaat tagtttttag tgaagagata 13380

ttgccttatc ttttccagtt aaaaaaattc ataaaatata atctggaaca tgttaagtct 13440

tttgaaaaca aatactctat gaggatttat gagtggttat taaaagaact aacacaaaag 13500

aaaactcaca aggcaaatat agagattagc cttgatgaat ttaagttcat gttaatgctt 13560

gaaaataact accatgagtt taaaaggctt aaccaatggg ttttgaaacc aataagtaaa 13620

gatttaaaca cttacagcaa tatgaaattg gtggttgata agcgaggccg cccgactgat 13680

acgttgattt tccaagttga actagataga caaatggatc tcgtaaccga acttgagaac 13740

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ccatgaacag atcgacaatg taacagatga acagcatgta acacctaata gaacaggtga 14220

aaccagtaaa acaaagcaac tagaacatga aattgaacac ctgagacaac ttgttacagc 14280

tcaacagtca cacatagaca gcctgaaaca ggcgatgctg cttatcgaat caaagctgcc 14340

gacaacacgg gagccagtga cgcctcccgt ggggaaaaaa tcatggcaat tctggaagaa 14400

atagcgcttt cagccggcaa accggctgaa gccggatctg cga 14443

<210> 67
<211> 1260
<212> DNA
<213> Citrobacter sp

<400> 67
atgaagataa atatgccgtt cagtaatgac aaatatcggt actcgtccgg gtatctgctt 60

tttttctttg ccgcctggtc gttgtggtgg tctttttatg cgatatggct aaaaaataaa 120

cttggcctgt ccggaacgga gctgggaatg ctgtatgccg taaaccagtt ctttagcatg 180

ctgtttatgc tggtctacgg ttttctgcag gataagctcg gcacccgtaa acaccttatc 240

tggctgatgg ggatagtcat cacgctcagc ggcccgttcc tgatttatgt ttacgaaccg 300

ctgctgacct ccaacttcaa acttggtatg gcgctgggag ccattttctt tggccttggc 360

tacctcgcgg gttgtggtct ggtagaaagc ttcgtcgaaa aagtgagccg caaattcaac 420

tttgaattcg gcaccgcccg cttgtgggga tcgcttggct acgccgcagg gacatttgtt 480

ggcggtatct tcttcagcat caacccacac attaacttct ggtgcgtatc ggtaatgggg 540

gtgttattcc tgttgattaa cgtgttgttc aaaaccaact cacccgcccc atcttctgta 600

aaaacgcgtt ctcctgaacc tgacgcgctg acccgaaagg attttctcac tatctttaaa 660

gatacgcagt tctggttttt cgttatcttt gtcgtcggta cctggtcgtt ctatagcatc 720

tacgatcagc agatgttccc ggtgttttac gccagcttat ttgacgatcc cgaactggca 780

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gtagcgaatt ttgataaacg cctgtcatca acgatatatc tcattggctt caatatcgcc 1080

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ttctcgttga gcaaaaagca tcatcagcag aagatgggaa atgaactggt gacagagtag 1260

<210> 68
<211> 419
<212> PRT
<213> Citrobacter sp

<400> 68

Met Lys Ile Asn Met Pro Phe Ser Asn Asp Lys Tyr Arg Tyr Ser Ser
1 5 10 15

Gly Tyr Leu Leu Phe Phe Phe Ala Ala Trp Ser Leu Trp Trp Ser Phe
20 25 30

Tyr Ala Ile Trp Leu Lys Asn Lys Leu Gly Leu Ser Gly Thr Glu Leu
35 40 45

Gly Met Leu Tyr Ala Val Asn Gln Phe Phe Ser Met Leu Phe Met Leu
50 55 60

Val Tyr Gly Phe Leu Gln Asp Lys Leu Gly Thr Arg Lys His Leu Ile
65 70 75 80

Trp Leu Met Gly Ile Val Ile Thr Leu Ser Gly Pro Phe Leu Ile Tyr
85 90 95

Val Tyr Glu Pro Leu Leu Thr Ser Asn Phe Lys Leu Gly Met Ala Leu
100 105 110

Gly Ala Ile Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Val
115 120 125

Glu Ser Phe Val Glu Lys Val Ser Arg Lys Phe Asn Phe Glu Phe Gly
130 135 140

Thr Ala Arg Leu Trp Gly Ser Leu Gly Tyr Ala Ala Gly Thr Phe Val
145 150 155 160

Gly Gly Ile Phe Phe Ser Ile Asn Pro His Ile Asn Phe Trp Cys Val
165 170 175

Ser Val Met Gly Val Leu Phe Leu Leu Ile Asn Val Leu Phe Lys Thr
180 185 190

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Asn Ser Pro Ala Pro Ser Ser Val Lys Thr Arg Ser Pro Glu Pro Asp
        195                 200                 205

Ala Leu Thr Arg Lys Asp Phe Leu Thr Ile Phe Lys Asp Thr Gln Phe
    210                 215                 220

Trp Phe Phe Val Ile Phe Val Val Gly Thr Trp Ser Phe Tyr Ser Ile
225                 230                 235                 240

Tyr Asp Gln Gln Met Phe Pro Val Phe Tyr Ala Ser Leu Phe Asp Asp
                245                 250                 255

Pro Glu Leu Ala Pro Arg Val Tyr Gly Tyr Leu Asn Ser Val Gln Val
            260                 265                 270

Phe Met Glu Ala Val Gly Met Ala Leu Val Pro Phe Leu Ile Asn Arg
        275                 280                 285

Ile Gly Pro Lys Ser Ala Leu Leu Leu Gly Gly Thr Ile Met Ala Cys
    290                 295                 300

Arg Ile Leu Gly Ser Ala Leu Phe Thr Asp Ile Tyr Ile Ile Ser Leu
305                 310                 315                 320

Ile Lys Met Leu His Ala Leu Glu Val Pro Leu Phe Val Ile Ser Val
                325                 330                 335

Phe Lys Phe Ser Val Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile
            340                 345                 350

Tyr Leu Ile Gly Phe Asn Ile Ala Ser Ser Ile Gly Ile Ile Val Leu
        355                 360                 365

Ser Leu Pro Val Gly Lys Leu Phe Asp Lys Val Gly Tyr Gln Glu Ile
    370                 375                 380

Phe Leu Ile Met Ala Ser Ile Val Ile Ile Thr Leu Ile Phe Gly Tyr
385                 390                 395                 400

Phe Ser Leu Ser Lys Lys His His Gln Gln Lys Met Gly Asn Glu Leu
                405                 410                 415

Val Thr Glu
```

<210> 69
<211> 1314
<212> DNA
<213> Enterococcus faecium

<400> 69

atgaaagggg atacaaatat atcgttggag gataaaaata tgtcaaaagt taacgtattt 60

aaaaatcaat cttatttaca aagttcagct acattattac tatttttgc ttcttggggt 120

gtttggtggt catttttca actttggcta acatctgaat caaatggttt agggttatct 180

ggcagtgctg taggaacagt attctcggca aattcgttag ttaccttaat tttgatgttt 240

atttatggaa cattacaaga taaattgtat attaaacgaa atttattaat ttttgcttct 300

gtattagcga cacttgttgg accatttttt atatggatat atgggccatt gctagataac 360

aattttaatt taggcattat tatgggagcg ctatttttgt cagctggata tttagcttct 420

gtaggagttt ttgaagctgt gtcagaaagg tttagtcgtt tatttggctt tgaatatgga 480

caagcaaggg cgtggggatc atttggttat gccttggtag cgcttttggc aggatttta 540

tttgtaaaaa atcctcattt aaacttttgg gcgggatctt tctttggttc tttactattg 600

ttaaatttat tattttggaa ccctaaagtt gaacgggaag caaatcaaaa ttttaatcaa 660

gaacaagctg aatcaaatag tattccttct ttaaaagaaa tgtttgatct aatgaaactg 720

cctcaattat ggacgataat catctttatt gtttttacat ggacatttta tacggtattc 780

gatcaacaaa tgtttccggg attttatact ggtttgtttt caacatcagc taatggtgaa 840

aaaatatatg ggacattgaa tgctattcaa gtattttgtg aagcgttaat gatgggaatt 900

gttccaatca ttatgagaaa attaggggtt cgaaatactt tgttattagg tgtaaccatt 960

atgtgtgtac gaattggatt gtgcgggttt gcctcgacac cattatctgt ttcatgcata 1020

aaaatgttgc atgctttaga agtaccatta tttacattac caatgtttcg ctattttaca 1080

cttcattttg atacaaagct atcagcaacc ctctatatga taggatttca gatagctgct 1140

caaattgggc aagtgatttt atcaacacca ttgggaatat taagagacaa cgttggctat 1200

caaccaacat ttaaaattat ttctcttatt gtattactag caggcatata tgcattcttt 1260

attcttaaac aagatgatag agatgttcaa ggggatccat ttattcgagg ataa 1314

<210> 70
<211> 437
<212> PRT
<213> Enterococcus faecium

<400> 70

Met Lys Gly Asp Thr Asn Ile Ser Leu Glu Asp Lys Asn Met Ser Lys
1 5 10 15

Val Asn Val Phe Lys Asn Gln Ser Tyr Leu Gln Ser Ser Ala Thr Leu
20 25 30

Leu Leu Phe Phe Ala Ser Trp Gly Val Trp Trp Ser Phe Phe Gln Leu
35 40 45

Trp Leu Thr Ser Glu Ser Asn Gly Leu Gly Leu Ser Gly Ser Ala Val
50 55 60

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Gly Thr Val Phe Ser Ala Asn Ser Leu Val Thr Leu Ile Leu Met Phe
65                  70                  75                  80

Ile Tyr Gly Thr Leu Gln Asp Lys Leu Tyr Ile Lys Arg Asn Leu Leu
                85                  90                  95

Ile Phe Ala Ser Val Leu Ala Thr Leu Val Gly Pro Phe Phe Ile Trp
            100                 105                 110

Ile Tyr Gly Pro Leu Leu Asp Asn Asn Phe Asn Leu Gly Ile Ile Met
        115                 120                 125

Gly Ala Leu Phe Leu Ser Ala Gly Tyr Leu Ala Ser Val Gly Val Phe
    130                 135                 140

Glu Ala Val Ser Glu Arg Phe Ser Arg Leu Phe Gly Phe Glu Tyr Gly
145                 150                 155                 160

Gln Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Leu Val Ala Leu Leu
                165                 170                 175

Ala Gly Phe Leu Phe Val Lys Asn Pro His Leu Asn Phe Trp Ala Gly
            180                 185                 190

Ser Phe Phe Gly Ser Leu Leu Leu Leu Asn Leu Leu Phe Trp Asn Pro
        195                 200                 205

Lys Val Glu Arg Glu Ala Asn Gln Asn Phe Asn Gln Glu Gln Ala Glu
    210                 215                 220

Ser Asn Ser Ile Pro Ser Leu Lys Glu Met Phe Asp Leu Met Lys Leu
225                 230                 235                 240

Pro Gln Leu Trp Thr Ile Ile Ile Phe Ile Val Phe Thr Trp Thr Phe
                245                 250                 255

Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Gly Phe Tyr Thr Gly Leu
            260                 265                 270

Phe Ser Thr Ser Ala Asn Gly Glu Lys Ile Tyr Gly Thr Leu Asn Ala
        275                 280                 285

Ile Gln Val Phe Cys Glu Ala Leu Met Met Gly Ile Val Pro Ile Ile
    290                 295                 300

Met Arg Lys Leu Gly Val Arg Asn Thr Leu Leu Leu Gly Val Thr Ile
305                 310                 315                 320

Met Cys Val Arg Ile Gly Leu Cys Gly Phe Ala Ser Thr Pro Leu Ser
                325                 330                 335
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Val Ser Cys Ile Lys Met Leu His Ala Leu Glu Val Pro Leu Phe Thr
340 345 350

Leu Pro Met Phe Arg Tyr Phe Thr Leu His Phe Asp Thr Lys Leu Ser
355 360 365

Ala Thr Leu Tyr Met Ile Gly Phe Gln Ile Ala Ala Gln Ile Gly Gln
370 375 380

Val Ile Leu Ser Thr Pro Leu Gly Ile Leu Arg Asp Asn Val Gly Tyr
385 390 395 400

Gln Pro Thr Phe Lys Ile Ile Ser Leu Ile Val Leu Leu Ala Gly Ile
405 410 415

Tyr Ala Phe Phe Ile Leu Lys Gln Asp Asp Arg Asp Val Gln Gly Asp
420 425 430

Pro Phe Ile Arg Gly
435

<210> 71
<211> 1299
<212> DNA
<213> Corynebacterium glucuronolyticum

<400> 71
atgtcaaaat tcatgcagca gctgaaaaac actgcgtatc agcagtcatc agcgcaactc 60

ctgctcttct tcatgtcctg gggcatctgg tggtccttct tccagctttg gctctccagc 120

gaaacccgcg gtctcggctt caacggcagt gagatcggca ccatctactc ggtgaactcc 180

gccgtcacgc tcgtcctcat gctcgtctac ggaactgccc aagataagct tcgtactcgc 240

cgtaatttgg tgatcggtat tgcagttcta atgagcttga ccggcccgtt cttcatgtgg 300

gtctactggc cactgctgca gagcgagtcg ctctatgtcc tcggtgttgg acttggcgca 360

atcttcatcg gtacggcttt tgtggggtca tgcccgctgt tcgaggcgct tgccgagcgc 420

atgtcccgaa aacacaactt cgaatatggc caggcccgcg cgtggggttc ctttggctac 480

gccatcgtcg cactcctcgc cggcttcaac ttcaccatca acccggcgat taacttctgg 540

atggcctcgg ccttcggcgt tctgttgctt ctcatcctcg ttttctggaa ggaaccggta 600

gcgcctcgta acgaaattgc agaggaggaa gtggaaaaca ccacacctag cgtcaaggaa 660

atggtgtctg ttctcaaagt gcccgccctc tgggtcgtca ttgtcctcgt gttcttcacg 720

tggacgttct acacggtctt cgaccagcag atgttcccgc agttctacac ctcacttttt 780

agtgactccg ccaccggcga gcgaacctat ggcgtgctca actccgtcca agtgttcgtc 840

gaggcgttga tgatgggaat cgtgcccatc tacatgcgga aggtcggcgt gaagaacacc 900

ctcatgacgg gcttcgccgt catggcactg cgcatcctag gttgcgcggt cttcgcggac 960

ccagtcacca tctcctttgt caagatgttc cacgctctcg aggtaccact gtgcatcctc 1020

cccatcttcc gctacttcac cctgcacttc cccacgaaga tctcggccac cttgtacatg 1080

gtcggcttcc agattgcctc gcaggtgggt aacgtcgtca tgtccccgat cctcggttcg 1140

ctgcgtgacc gcctcggttt ccagccgacc ttctatgtca tctcgggaat cgtccttgtc 1200

tccgctatct tcgcctggtt ggctctcaag ggcgataagg aacaagtgga gggcgatccc 1260

ttctaccgcg attcggaact taaggagata caccaatga 1299

<210> 72
<211> 432
<212> PRT
<213> Corynebacterium glucuronolyticum

<400> 72

Met Ser Lys Phe Met Gln Gln Leu Lys Asn Thr Ala Tyr Gln Gln Ser
1 5 10 15

Ser Ala Gln Leu Leu Leu Phe Phe Met Ser Trp Gly Ile Trp Trp Ser
20 25 30

Phe Phe Gln Leu Trp Leu Ser Ser Glu Thr Arg Gly Leu Gly Phe Asn
35 40 45

Gly Ser Glu Ile Gly Thr Ile Tyr Ser Val Asn Ser Ala Val Thr Leu
50 55 60

Val Leu Met Leu Val Tyr Gly Thr Ala Gln Asp Lys Leu Arg Thr Arg
65 70 75 80

Arg Asn Leu Val Ile Gly Ile Ala Val Leu Met Ser Leu Thr Gly Pro
85 90 95

Phe Phe Met Trp Val Tyr Trp Pro Leu Leu Gln Ser Glu Ser Leu Tyr
100 105 110

Val Leu Gly Val Gly Leu Gly Ala Ile Phe Ile Gly Thr Ala Phe Val
115 120 125

Gly Ser Cys Pro Leu Phe Glu Ala Leu Ala Glu Arg Met Ser Arg Lys
130 135 140

His Asn Phe Glu Tyr Gly Gln Ala Arg Ala Trp Gly Ser Phe Gly Tyr
145 150 155 160

Ala Ile Val Ala Leu Leu Ala Gly Phe Asn Phe Thr Ile Asn Pro Ala
165 170 175

Ile Asn Phe Trp Met Ala Ser Ala Phe Gly Val Leu Leu Leu Leu Ile
180 185 190

Leu Val Phe Trp Lys Glu Pro Val Ala Pro Arg Asn Glu Ile Ala Glu
195 200 205

Glu Glu Val Glu Asn Thr Thr Pro Ser Val Lys Glu Met Val Ser Val
210 215 220

Leu Lys Val Pro Ala Leu Trp Val Val Ile Val Leu Val Phe Phe Thr
225 230 235 240

Trp Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Gln Phe Tyr
245 250 255

Thr Ser Leu Phe Ser Asp Ser Ala Thr Gly Glu Arg Thr Tyr Gly Val
260 265 270

Leu Asn Ser Val Gln Val Phe Val Glu Ala Leu Met Met Gly Ile Val
275 280 285

Pro Ile Tyr Met Arg Lys Val Gly Val Lys Asn Thr Leu Met Thr Gly
290 295 300

Phe Ala Val Met Ala Leu Arg Ile Leu Gly Cys Ala Val Phe Ala Asp
305 310 315 320

Pro Val Thr Ile Ser Phe Val Lys Met Phe His Ala Leu Glu Val Pro
325 330 335

Leu Cys Ile Leu Pro Ile Phe Arg Tyr Phe Thr Leu His Phe Pro Thr
340 345 350

Lys Ile Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser Gln
355 360 365

Val Gly Asn Val Val Met Ser Pro Ile Leu Gly Ser Leu Arg Asp Arg
370 375 380

Leu Gly Phe Gln Pro Thr Phe Tyr Val Ile Ser Gly Ile Val Leu Val
385 390 395 400

Ser Ala Ile Phe Ala Trp Leu Ala Leu Lys Gly Asp Lys Glu Gln Val
405 410 415

Glu Gly Asp Pro Phe Tyr Arg Asp Ser Glu Leu Lys Glu Ile His Gln
420 425 430

<210> 73
<211> 1326
<212> DNA
<213> Bifidobacterium animalis

<400> 73
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ttcctgttct tctgctcctg gggcatctgg tggtcgttct tccagcgctg gctcaactcg 120

atgggactca acggcgcgga agtgggcacg atctattcga tcaactcgct ggccacgctc 180

atcctcatgt tcgggtacgg cctcatccag gacaatctcg gactcaagcg ccgtcttgtg 240

ctcgtcatct cggcgatcgc cgcactcgtc ggacccttcg tgcagttcgt gtacgcgccg 300

ctgatgagga cgaacatgat ggccgccgca ctcgtgggct ccgtcgttct ctccgcgggc 360

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ttcgagtacg gccaatcccg cgcatggggt tccttcggct atgccattgt ggcgcttgtc 480

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gtgggcatgc tcatcgtgta cctcacctgg tatccggccg agcagcgcga agcgctcaag 600

gaagccgccg atccgaatgc cgcgccaact aacccgacca tcaaagacat gctcggcgtg 660

ctcaagatgc ccacgctgtg ggtgctcatc gtgttcatgc tgctcaccaa cacgttctac 720

accgtattcg accagcagat gttccccacc tactacgcct cgctcttccc gaatgaggcc 780

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atgggcgtcg tgccgatcat catgcgcaag gtaggtgtgc gcaacgcgtt gctgctcgga 900

tccacggtga tgttccttcg catcgggctg tgcggcatct tccacgatcc ggtgtccatc 960

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tcgaagaagc tgccgtcgct cgccaccgac gaggcgatcc tctccgcgga ttccgaggat 1320

atgtaa 1326

<210> 74
<211> 441
<212> PRT
<213> Bifidobacterium animalis

<400> 74

Met Ala Thr Thr Thr Lys Val Trp Arg Asn Pro Ser Tyr Leu Gln Ser
1 5 10 15

Ser Thr Gly Ile Phe Leu Phe Phe Cys Ser Trp Gly Ile Trp Trp Ser
20 25 30

Phe Phe Gln Arg Trp Leu Asn Ser Met Gly Leu Asn Gly Ala Glu Val
35 40 45

Gly Thr Ile Tyr Ser Ile Asn Ser Leu Ala Thr Leu Ile Leu Met Phe
50 55 60

Gly Tyr Gly Leu Ile Gln Asp Asn Leu Gly Leu Lys Arg Arg Leu Val
65 70 75 80

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Leu Val Ile Ser Ala Ile Ala Ala Leu Val Gly Pro Phe Val Gln Phe
                85                  90                  95

Val Tyr Ala Pro Leu Met Arg Thr Asn Met Met Ala Ala Ala Leu Val
            100                 105                 110

Gly Ser Val Val Leu Ser Ala Gly Phe Met Ala Gly Cys Ser Leu Ile
        115                 120                 125

Glu Ala Val Thr Glu Arg Tyr Ser Arg Arg Phe Asn Phe Glu Tyr Gly
    130                 135                 140

Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Val Ala Leu Val
145                 150                 155                 160

Ala Gly Phe Val Phe Asn Ile Asn Pro Met Ile Asn Phe Trp Leu Gly
                165                 170                 175

Ser Ala Phe Gly Val Gly Met Leu Ile Val Tyr Leu Thr Trp Tyr Pro
            180                 185                 190

Ala Glu Gln Arg Glu Ala Leu Lys Glu Ala Ala Asp Pro Asn Ala Ala
        195                 200                 205

Pro Thr Asn Pro Thr Ile Lys Asp Met Leu Gly Val Leu Lys Met Pro
    210                 215                 220

Thr Leu Trp Val Leu Ile Val Phe Met Leu Leu Thr Asn Thr Phe Tyr
225                 230                 235                 240

Thr Val Phe Asp Gln Gln Met Phe Pro Thr Tyr Tyr Ala Ser Leu Phe
                245                 250                 255

Pro Asn Glu Ala Thr Gly Asn Ala Val Tyr Gly Thr Leu Asn Ser Val
            260                 265                 270

Gln Val Phe Cys Glu Ser Ala Met Met Gly Val Val Pro Ile Ile Met
        275                 280                 285

Arg Lys Val Gly Val Arg Asn Ala Leu Leu Leu Gly Ser Thr Val Met
    290                 295                 300

Phe Leu Arg Ile Gly Leu Cys Gly Ile Phe His Asp Pro Val Ser Ile
305                 310                 315                 320

Ser Ile Val Lys Met Phe His Ala Ile Glu Val Pro Leu Phe Cys Leu
                325                 330                 335

Pro Ala Phe Arg Tyr Phe Thr Leu His Phe Asn Pro Lys Leu Ser Ala
            340                 345                 350
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Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser Gln Ile Gly Gln Val
355 360 365

Val Phe Ser Thr Pro Leu Gly Met Leu His Asp Arg Met Gly Asp Arg
370 375 380

Thr Thr Phe Leu Thr Ile Ser Ala Ile Val Leu Ala Ala Thr Val Tyr
385 390 395 400

Gly Phe Phe Val Ile Lys Arg Asp Asp Glu Gln Val Asp Gly Asp Pro
405 410 415

Phe Ile Arg Asp Ser Lys Lys Leu Pro Ser Leu Ala Thr Asp Glu Ala
420 425 430

Ile Leu Ser Ala Asp Ser Glu Asp Met
435 440

<210> 75
<211> 1398
<212> DNA
<213> Bifidobacterium gallicum

<400> 75
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aagttcggct tcgaatacgg ccagtcccgc gcatggggct ccttcggcta cgccattgtg 480

gccctgatcg ccggcattgt cttcaacatc aacccgatga tcaacttctg gctcggctcc 540

gcattcggcg tgggcatgct catcgtgtac ctcacgtggt acccggccga gcagcgccag 600

gccctcaagg aagcggccga cccgaacgcc gagaagtcca acccgtcctt caaggacatg 660

gtcaacgtgc tcaagatgcc gacgctgtgg gtgctcatca tcttcatgct gctgaccaac 720

acgttctaca cggtcttcga ccagcagatg ttcccgacct actacgcctc gctgttcccg 780

agcattgaaa cgggcaacac ggtctacggc gtgctcaact ccatccaggt cttctgcgaa 840

tccgcgatga tgggcgtcgt cccgatcatc atgcgcaaga tcggcgtgcg caacgcgctg 900

ctgctgggcg ccaccgtcat gttcctgcgc atcggcctgt gcggcatctt ccacgacccg 960

gtagccatct ccatcgtcaa gatgttccac gccatcgaag ttccactgtt ctgcctgccg 1020

gcgttccgct acttcacgct gcacttcaac ccgaagctct cggccacgct gtacatggtg 1080

ggcttccaga tcgcctcaca gatcggccag gttatcttct ccaccccgct gggcatgctg 1140

cacgaccgct tcggcgaccg caccaccttc ctgtccatca gcggcatcgt gctgctggca 1200

acgatctacg gcttcttcgt catcaagcgc gacgacgagc acgtggacgg cgatccgttc 1260

ctgcgtgacc gcgaccgcaa ggaaatggaa ctcatcgaag agaacctgca gccagacgcc 1320

gagctggaaa cgagccccgt aggcgtcgca gcacaggtgc gcgacaaccg cgcggtccag 1380

ccggaatacg caagctga 1398

<210> 76
<211> 465
<212> PRT
<213> Bifidobacterium gallicum

<400> 76

Met Val Asn Lys Pro Lys Thr Ala Lys Ile Trp Ser Asn Pro Ser Tyr
1 5 10 15

Leu Gln Ser Ser Phe Gly Ile Phe Leu Phe Phe Cys Ser Trp Gly Ile
20 25 30

Trp Trp Ser Phe Phe Gln Arg Trp Leu Asn Thr Ile Gly Leu Asn Gly
35 40 45

Ala Glu Val Gly Thr Val Tyr Ser Ile Asn Ser Leu Ala Thr Leu Ile
50 55 60

Leu Met Phe Gly Tyr Gly Ile Ile Gln Asp Asn Leu Gly Ile Lys Arg
65 70 75 80

Arg Leu Val Val Val Ile Ala Thr Ile Ala Ala Leu Ile Gly Pro Phe
85 90 95

Val Gln Phe Val Tyr Ala Pro Leu Met Gln Thr Asn Ile Met Ala Ala
100 105 110

Ala Leu Ile Gly Ser Val Val Leu Ser Ala Gly Phe Met Ser Gly Cys
115 120 125

Ser Leu Ile Glu Ala Leu Thr Glu Arg Tyr Ser Arg Lys Phe Gly Phe
130 135 140

Glu Tyr Gly Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Val
145 150 155 160

Ala Leu Ile Ala Gly Ile Val Phe Asn Ile Asn Pro Met Ile Asn Phe
165 170 175

Trp Leu Gly Ser Ala Phe Gly Val Gly Met Leu Ile Val Tyr Leu Thr
180 185 190

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Trp Tyr Pro Ala Glu Gln Arg Gln Ala Leu Lys Glu Ala Ala Asp Pro
        195                 200                 205

Asn Ala Glu Lys Ser Asn Pro Ser Phe Lys Asp Met Val Asn Val Leu
    210                 215                 220

Lys Met Pro Thr Leu Trp Val Leu Ile Ile Phe Met Leu Leu Thr Asn
225                 230                 235                 240

Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Thr Tyr Tyr Ala
                245                 250                 255

Ser Leu Phe Pro Ser Ile Glu Thr Gly Asn Thr Val Tyr Gly Val Leu
            260                 265                 270

Asn Ser Ile Gln Val Phe Cys Glu Ser Ala Met Met Gly Val Val Pro
        275                 280                 285

Ile Ile Met Arg Lys Ile Gly Val Arg Asn Ala Leu Leu Leu Gly Ala
    290                 295                 300

Thr Val Met Phe Leu Arg Ile Gly Leu Cys Gly Ile Phe His Asp Pro
305                 310                 315                 320

Val Ala Ile Ser Ile Val Lys Met Phe His Ala Ile Glu Val Pro Leu
                325                 330                 335

Phe Cys Leu Pro Ala Phe Arg Tyr Phe Thr Leu His Phe Asn Pro Lys
            340                 345                 350

Leu Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser Gln Ile
        355                 360                 365

Gly Gln Val Ile Phe Ser Thr Pro Leu Gly Met Leu His Asp Arg Phe
    370                 375                 380

Gly Asp Arg Thr Thr Phe Leu Ser Ile Ser Gly Ile Val Leu Leu Ala
385                 390                 395                 400

Thr Ile Tyr Gly Phe Phe Val Ile Lys Arg Asp Asp Glu His Val Asp
                405                 410                 415

Gly Asp Pro Phe Leu Arg Asp Arg Asp Arg Lys Glu Met Glu Leu Ile
            420                 425                 430

Glu Glu Asn Leu Gln Pro Asp Ala Glu Leu Glu Thr Ser Pro Val Gly
        435                 440                 445

Val Ala Ala Gln Val Arg Asp Asn Arg Ala Val Gln Pro Glu Tyr Ala
    450                 455                 460
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Ser
465

<210> 77
<211> 1338
<212> DNA
<213> Bifidobacterium longum

<400> 77
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atcttcatgt tcttctgctc ctggggcatc tggtggtcct tcttccagcg ctggctcatc 120

tcaggcgttg gattgaccaa tgctgaagtc ggcaccatct actccatcaa ctcgctggcc 180

accctggtca tcatgtttgt gtacggcgtg attcaggatc agctcggcat caagcgcaag 240

ctcgtcatcg tagtctcggt aatcgccgcc tgcgttggcc cattcgtcca attcgtttac 300

gccccgatga tcctcgccgg tggcaccacc cgctggatcg gcgcactcat cggctccatc 360

gttctgtctg ccggcttcat gtccggctgc tccctgttcg aggccgtcac cgaacgctac 420

tcccgtaaat tcggtttcga atatggccag tcccgtgctt ggggctcctt cggttacgcc 480

atcgtggcgc tgtgcgccgg cttcctgttc aacatcaacc cgctgatcaa cttctgggtc 540

ggctccgcat tcggccctgg catgctcctc gtgtacgcct tctgggtccc ggccgagcag 600

aaggaagagc tcaagaagga aaccgacccg aacgcagccc ccaccaaccc gtccctcaag 660

gaaatggtcg ccgttctcaa gatgccgacc ctgtgggtgc tcatcgtctt catgctgctg 720

accaacacct tctacaccgt gttcgatcag cagatgttcc cgacctacta cgccaacctc 780

ttccccactg aagaaatcgg caacgccacc tacggcaccc tgaacggttt ccaggtcttc 840

cttgagtccg caatgatggg cgtggtcccg atcatcatga agaagatcgg cgtgcgcaac 900

gctctgctgc tcggcgctac cgtgatgttc ctgcgcatcg gcttgtgcgg cgtgttccac 960

gacccggtca ccatctccat cgtcaagctg ttccactcca tcgaagtgcc gctgttctgc 1020

ctgccggcat tccgctactt cactctgcac ttcgacacca agctctctgc cacgctgtac 1080

atggtgggct tccagatcgc ttcccaagtg ggtcaggtca tcttctcgac ccctctgggt 1140

gccttccacg acaagatggc tcagattctg ccgaacaacg acatgggatc ccgcgtgacc 1200

ttctgggtca tctctgccat cgtgctgtgc gcactgattt acggcttctt cgtcatcaag 1260

catgatgatc aggaagtcgg cggcgacccg ttctacaccg acaagcagct tcgccagatg 1320

gaagccgcca aggcctga 1338

<210> 78
<211> 445
<212> PRT
<213> Bifidobacterium longum

<400> 78

Met Ala Ser Ala Thr Lys Ser Ala Trp Lys Asn Pro Ser Tyr Leu Gln
1 5 10 15

```
Ser Ser Phe Gly Ile Phe Met Phe Phe Cys Ser Trp Gly Ile Trp Trp
            20                  25                  30

Ser Phe Phe Gln Arg Trp Leu Ile Ser Gly Val Gly Leu Thr Asn Ala
        35                  40                  45

Glu Val Gly Thr Ile Tyr Ser Ile Asn Ser Leu Ala Thr Leu Val Ile
    50                  55                  60

Met Phe Val Tyr Gly Val Ile Gln Asp Gln Leu Gly Ile Lys Arg Lys
65                  70                  75                  80

Leu Val Ile Val Val Ser Val Ile Ala Ala Cys Val Gly Pro Phe Val
                85                  90                  95

Gln Phe Val Tyr Ala Pro Met Ile Leu Ala Gly Gly Thr Thr Arg Trp
            100                 105                 110

Ile Gly Ala Leu Ile Gly Ser Ile Val Leu Ser Ala Gly Phe Met Ser
        115                 120                 125

Gly Cys Ser Leu Phe Glu Ala Val Thr Glu Arg Tyr Ser Arg Lys Phe
    130                 135                 140

Gly Phe Glu Tyr Gly Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr Ala
145                 150                 155                 160

Ile Val Ala Leu Cys Ala Gly Phe Leu Phe Asn Ile Asn Pro Leu Ile
                165                 170                 175

Asn Phe Trp Val Gly Ser Ala Phe Gly Pro Gly Met Leu Leu Val Tyr
            180                 185                 190

Ala Phe Trp Val Pro Ala Glu Gln Lys Glu Glu Leu Lys Lys Glu Thr
        195                 200                 205

Asp Pro Asn Ala Ala Pro Thr Asn Pro Ser Leu Lys Glu Met Val Ala
    210                 215                 220

Val Leu Lys Met Pro Thr Leu Trp Val Leu Ile Val Phe Met Leu Leu
225                 230                 235                 240

Thr Asn Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Thr Tyr
                245                 250                 255

Tyr Ala Asn Leu Phe Pro Thr Glu Glu Ile Gly Asn Ala Thr Tyr Gly
            260                 265                 270

Thr Leu Asn Gly Phe Gln Val Phe Leu Glu Ser Ala Met Met Gly Val
        275                 280                 285
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Val Pro Ile Ile Met Lys Lys Ile Gly Val Arg Asn Ala Leu Leu Leu
290 295 300

Gly Ala Thr Val Met Phe Leu Arg Ile Gly Leu Cys Gly Val Phe His
305 310 315 320

Asp Pro Val Thr Ile Ser Ile Val Lys Leu Phe His Ser Ile Glu Val
325 330 335

Pro Leu Phe Cys Leu Pro Ala Phe Arg Tyr Phe Thr Leu His Phe Asp
340 345 350

Thr Lys Leu Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser
355 360 365

Gln Val Gly Gln Val Ile Phe Ser Thr Pro Leu Gly Ala Phe His Asp
370 375 380

Lys Met Ala Gln Ile Leu Pro Asn Asn Asp Met Gly Ser Arg Val Thr
385 390 395 400

Phe Trp Val Ile Ser Ala Ile Val Leu Cys Ala Leu Ile Tyr Gly Phe
405 410 415

Phe Val Ile Lys His Asp Asp Gln Glu Val Gly Gly Asp Pro Phe Tyr
420 425 430

Thr Asp Lys Gln Leu Arg Gln Met Glu Ala Ala Lys Ala
435 440 445

<210> 79
<211> 1422
<212> DNA
<213> Bifidobacterium adolescentis

<400> 79
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cggcagcgcg aagagaaaaa gagaatcaaa atggcaagca aaacacgttc tgtatggaag 120

aatccttcct atctgcagag ctccttcggc attttcatgt tcttctgttc ctggggcatc 180

tggtggtcct tcttctcccg ctggctcact gacccgaccc acggtctggg catgagctcc 240

gcggaacagg gccagatcta ctccatcaac tccttggcca ccctggtcat catgttcgtt 300

tacggcacca ttcaggacca gctgggcatt aagcgtaagc tcgtgatctt catctctgcg 360

gtcgctgcat gcgttggccc gttcgtgcag ttcgtgtacc agccgatgct gaccgccggc 420

ggcaccaccc gattcatcgg cgtgcttctc ggctccatcg tgctgtccgc aggcttcatg 480

gccggctgct ccctgttcga agccatcacc gaacgttact cccgtaagtt cggcttcgaa 540

tacggccagt cccgcgcttg gggctccttc ggctacgctg tcgtggcact gtgcgcaggc 600

ttcctgttca acatcaaccc gctgctgaac ttctgggttg gttccatctg cggcctcagc 660

atgctgtgcg tctatgcttt ctgggttccg gccgagcaga aggaagaact caagaaggaa 720

gctgatccga acgcaactcc gaccaacccg tccttcaagg aaatggtctc cgtcctgaag 780

atgccgaccc tgtgggtgct catcgtcttc atgctgttca ccaacacctt ctacaccgtg 840

ttcgatcagc agatgttccc gaactactac gcctccctct tcccgaccac cgaaatcggc 900

aacgccacct acggcaccct gaactccttc caggtgttcc ttgagtccgc catgatgggc 960

gtcgtcccga tcatcatgaa gaagatcggc gtgcgtaact ccctgctgct cggcgccacc 1020

gtgatgttcg cccgtatcgg tctgtgcggc gtgttccatg acccggtctc cgtctccatc 1080

gtcaagctgt tccactccat cgaggtaccg ctgttctgcc tgccggcgtt ccgctacttc 1140

accctgcact tcgacacgaa gctgtctgcc accctgtaca tggttggttt ccagatcgct 1200

tcccaggtcg gccaggtgat tttctccacc ccgatgggtg ctctgcatga tgccatgggc 1260

gaccgtccga ccttcttcac catctctgcc atcgtgtttg cggctctggt ctacggcttc 1320

ttcgtcatca agaaggatga tcaggaagtc ggcggcgatc cgttctacac tgacaagcag 1380

ctcaaggcca tgaaggccgc tgatgcggaa gtgaaggcct ga 1422

<210> 80
<211> 473
<212> PRT
<213> Bifidobacterium adolescentis

<400> 80

Met Lys Ser Glu Gln Ala Gln Ala Lys Thr Thr Ser Glu Ala Ile Ala
1 5 10 15

Ala Ala Arg Gln Arg Gln Arg Glu Glu Lys Lys Arg Ile Lys Met Ala
20 25 30

Ser Lys Thr Arg Ser Val Trp Lys Asn Pro Ser Tyr Leu Gln Ser Ser
35 40 45

Phe Gly Ile Phe Met Phe Phe Cys Ser Trp Gly Ile Trp Trp Ser Phe
50 55 60

Phe Ser Arg Trp Leu Thr Asp Pro Thr His Gly Leu Gly Met Ser Ser
65 70 75 80

Ala Glu Gln Gly Gln Ile Tyr Ser Ile Asn Ser Leu Ala Thr Leu Val
85 90 95

Ile Met Phe Val Tyr Gly Thr Ile Gln Asp Gln Leu Gly Ile Lys Arg
100 105 110

Lys Leu Val Ile Phe Ile Ser Ala Val Ala Ala Cys Val Gly Pro Phe
115 120 125

Val Gln Phe Val Tyr Gln Pro Met Leu Thr Ala Gly Gly Thr Thr Arg
130 135 140

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Phe Ile Gly Val Leu Leu Gly Ser Ile Val Leu Ser Ala Gly Phe Met
145                 150                 155                 160

Ala Gly Cys Ser Leu Phe Glu Ala Ile Thr Glu Arg Tyr Ser Arg Lys
                165                 170                 175

Phe Gly Phe Glu Tyr Gly Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr
            180                 185                 190

Ala Val Val Ala Leu Cys Ala Gly Phe Leu Phe Asn Ile Asn Pro Leu
        195                 200                 205

Leu Asn Phe Trp Val Gly Ser Ile Cys Gly Leu Ser Met Leu Cys Val
    210                 215                 220

Tyr Ala Phe Trp Val Pro Ala Glu Gln Lys Glu Glu Leu Lys Lys Glu
225                 230                 235                 240

Ala Asp Pro Asn Ala Thr Pro Thr Asn Pro Ser Phe Lys Glu Met Val
                245                 250                 255

Ser Val Leu Lys Met Pro Thr Leu Trp Val Leu Ile Val Phe Met Leu
            260                 265                 270

Phe Thr Asn Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Asn
        275                 280                 285

Tyr Tyr Ala Ser Leu Phe Pro Thr Thr Glu Ile Gly Asn Ala Thr Tyr
    290                 295                 300

Gly Thr Leu Asn Ser Phe Gln Val Phe Leu Glu Ser Ala Met Met Gly
305                 310                 315                 320

Val Val Pro Ile Ile Met Lys Lys Ile Gly Val Arg Asn Ser Leu Leu
                325                 330                 335

Leu Gly Ala Thr Val Met Phe Ala Arg Ile Gly Leu Cys Gly Val Phe
            340                 345                 350

His Asp Pro Val Ser Val Ser Ile Val Lys Leu Phe His Ser Ile Glu
        355                 360                 365

Val Pro Leu Phe Cys Leu Pro Ala Phe Arg Tyr Phe Thr Leu His Phe
    370                 375                 380

Asp Thr Lys Leu Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala
385                 390                 395                 400

Ser Gln Val Gly Gln Val Ile Phe Ser Thr Pro Met Gly Ala Leu His
                405                 410                 415
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Asp Ala Met Gly Asp Arg Pro Thr Phe Phe Thr Ile Ser Ala Ile Val
420 425 430

Phe Ala Ala Leu Val Tyr Gly Phe Phe Val Ile Lys Lys Asp Asp Gln
435 440 445

Glu Val Gly Gly Asp Pro Phe Tyr Thr Asp Lys Gln Leu Lys Ala Met
450 455 460

Lys Ala Ala Asp Ala Glu Val Lys Ala
465 470

<210> 81
<211> 1503
<212> DNA
<213> Bifidobacterium longum

<400> 81
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acgtcgcata ataattacta cataacaact tctacaaagg cacggccgcc cgagcagaag 120

cgttacataa ccaataacca accaagtagt aatcaaagga tgattatggc aagtgcaacc 180

aagtctgcat ggaagaatcc ttcctatctg cagagctctt tcggcatctt catgttcttc 240

tgctcctggg gcatctggtg gtccttcttc cagcgctggc tcatctcagg cgttggattg 300

accaatgctg aagtcggcac catctactcc atcaactcgc tggccaccct ggtcatcatg 360

tttgtgtacg gcgtgattca ggatcagctc ggcatcaagc gcaagctcgt catcgtagtc 420

tcggtaatcg ccgcctgcgt tggcccattc gtccaattcg tttacgcccc gatgatcctc 480

gccggtggca ccacccgctg gatcggcgca ctcatcggct ccatcgttct gtctgccggc 540

ttcatgtccg gctgctccct gttcgaggcc gtcaccgaac gctactcccg taaattcggt 600

ttcgaatatg gccagtcccg tgcttggggc tccttcggtt acgccatcgt ggcgctgtgc 660

gccggcttcc tgttcaacat caacccgctg atcaacttct gggtcggctc cgcattcggc 720

cctggcatgc tcctcgtgta cgccttctgg gtcccggccg agcagaagga agagctcaag 780

aaggaaaccg acccgaacgc agcccccacc aacccgtccc tcaaggaaat ggtcgccgtt 840

ctcaagatgc cgaccctgtg ggtgctcatc gtcttcatgc tgctgaccaa caccttctac 900

accgtgttcg atcagcagat gttcccgacc tactacgcca acctcttccc cactgaagaa 960

atcggcaacg ccacctacgg caccctgaac ggtttccagg tcttccttga gtccgcaatg 1020

atgggcgtgg tcccgatcat catgaagaag atcggcgtgc gcaacgctct gctgctcggc 1080

gctaccgtga tgttcctgcg catcggcttg tgcggcgtgt tccacgaccc ggtcaccatc 1140

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tacttcactc tgcacttcga caccaagctc tctgccacgc tgtacatggt gggcttccag 1260

atcgcttccc aagtgggtca ggtcatcttc tcgacccctc tgggtgcctt ccacgacaag 1320

atggctcaga ttctgccgaa caacgacatg ggatcccgcg tgaccttctg ggtcatctct 1380

gccatcgtgc tgtgcgcact gatttacggc ttcttcgtca tcaagcatga tgatcaggaa 1440

gtcggcggcg acccgttcta caccgacaag cagcttcgcc agatggaagc cgccaaggcc 1500

tga 1503

<210> 82
<211> 500
<212> PRT
<213> Bifidobacterium longum

<400> 82

Met Arg Val Glu Gln Val Arg His Ala Asp Leu Arg Gln Ser Ile Asp
1 5 10 15

Val Asn Arg Leu Thr Ser His Asn Asn Tyr Tyr Ile Thr Thr Ser Thr
20 25 30

Lys Ala Arg Pro Pro Glu Gln Lys Arg Tyr Ile Thr Asn Asn Gln Pro
35 40 45

Ser Ser Asn Gln Arg Met Ile Met Ala Ser Ala Thr Lys Ser Ala Trp
50 55 60

Lys Asn Pro Ser Tyr Leu Gln Ser Ser Phe Gly Ile Phe Met Phe Phe
65 70 75 80

Cys Ser Trp Gly Ile Trp Trp Ser Phe Phe Gln Arg Trp Leu Ile Ser
85 90 95

Gly Val Gly Leu Thr Asn Ala Glu Val Gly Thr Ile Tyr Ser Ile Asn
100 105 110

Ser Leu Ala Thr Leu Val Ile Met Phe Val Tyr Gly Val Ile Gln Asp
115 120 125

Gln Leu Gly Ile Lys Arg Lys Leu Val Ile Val Val Ser Val Ile Ala
130 135 140

Ala Cys Val Gly Pro Phe Val Gln Phe Val Tyr Ala Pro Met Ile Leu
145 150 155 160

Ala Gly Gly Thr Thr Arg Trp Ile Gly Ala Leu Ile Gly Ser Ile Val
165 170 175

Leu Ser Ala Gly Phe Met Ser Gly Cys Ser Leu Phe Glu Ala Val Thr
180 185 190

Glu Arg Tyr Ser Arg Lys Phe Gly Phe Glu Tyr Gly Gln Ser Arg Ala
195 200 205

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Trp Gly Ser Phe Gly Tyr Ala Ile Val Ala Leu Cys Ala Gly Phe Leu
    210                 215                 220

Phe Asn Ile Asn Pro Leu Ile Asn Phe Trp Val Gly Ser Ala Phe Gly
225                 230                 235                 240

Pro Gly Met Leu Leu Val Tyr Ala Phe Trp Val Pro Ala Glu Gln Lys
                245                 250                 255

Glu Glu Leu Lys Lys Glu Thr Asp Pro Asn Ala Ala Pro Thr Asn Pro
            260                 265                 270

Ser Leu Lys Glu Met Val Ala Val Leu Lys Met Pro Thr Leu Trp Val
        275                 280                 285

Leu Ile Val Phe Met Leu Leu Thr Asn Thr Phe Tyr Thr Val Phe Asp
    290                 295                 300

Gln Gln Met Phe Pro Thr Tyr Tyr Ala Asn Leu Phe Pro Thr Glu Glu
305                 310                 315                 320

Ile Gly Asn Ala Thr Tyr Gly Thr Leu Asn Gly Phe Gln Val Phe Leu
                325                 330                 335

Glu Ser Ala Met Met Gly Val Val Pro Ile Ile Met Lys Lys Ile Gly
            340                 345                 350

Val Arg Asn Ala Leu Leu Leu Gly Ala Thr Val Met Phe Leu Arg Ile
        355                 360                 365

Gly Leu Cys Gly Val Phe His Asp Pro Val Thr Ile Ser Ile Val Lys
    370                 375                 380

Leu Phe His Ser Ile Glu Val Pro Leu Phe Cys Leu Pro Ala Phe Arg
385                 390                 395                 400

Tyr Phe Thr Leu His Phe Asp Thr Lys Leu Ser Ala Thr Leu Tyr Met
                405                 410                 415

Val Gly Phe Gln Ile Ala Ser Gln Val Gly Gln Val Ile Phe Ser Thr
            420                 425                 430

Pro Leu Gly Ala Phe His Asp Lys Met Ala Gln Ile Leu Pro Asn Asn
        435                 440                 445

Asp Met Gly Ser Arg Val Thr Phe Trp Val Ile Ser Ala Ile Val Leu
    450                 455                 460

Cys Ala Leu Ile Tyr Gly Phe Phe Val Ile Lys His Asp Asp Gln Glu
465                 470                 475                 480
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Val Gly Gly Asp Pro Phe Tyr Thr Asp Lys Gln Leu Arg Gln Met Glu
485 490 495

Ala Ala Lys Ala
500

<210> 83
<211> 1266
<212> DNA
<213> Mitsuokella multacida

<400> 83
atgggaaatc tcttgaaggc attttcgaat ccgttctaca ggacgagctc gcttgagatc 60

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aagcagggct tcacgggcgc gcaggtcggc acgatttact ccttcggcag cgcggtcgcg 180

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ctgaagttct tcgccgtctg ccagatcctc gtcggcccgt tcttcacctg ggtctacgtg 300

ccgatgctcg ccgcgaactt ctacgtcggc gctgtcgtcg gtgccgtcta cctcgcggtg 360

gcgttcctcg cggcctgccc tgtctttgag gcggtcacag agcgcctgag ccgccgctac 420

tcctttgagt acggccaggc cagagcctgg ggctcgttcg gctatgccgt ggcagcgctc 480

tgcgcaggct tcctcttcac gatgaacccg aacctgatct tctggacggg ctccgctgtg 540

gcggcggtgc agcttatcgt cttggtctcg atgacgccgg agaacgacgc ttcgcttacg 600

gcgcagtacg aggtcaaggc agagagcatc aaggagagca agacgccgtc gttcggcgag 660

atcgtcggcg tgttcaagct catcgaggtc tggaagatga tcgtcttcgt catcatgagc 720

tggacgttct acaccgtctt tgaccagcag atgttcccgg agttcttcac gcgcttcttc 780

gcgacgccag aagcaggcca gcaggcttac ggcgtgctca actccatcga agtcttcctc 840

gaattcctca tgatgggcct cgtgccgatc ctcatgcgcc gtatcggcgt tcgcaaggcc 900

atcctgctcg gctgcgccat catgatcgtc cgcatcggcg gctgcggcct cgtcacgaat 960

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gtcggtttcc agatcgctgc acaggtcggc cagattatct tctcgacgcc gctcggcgcc 1140

ctgcatgaca gcatcggcta ccagagcact ttcctcgtca tctccggcat cgtctgtgtg 1200

gccagcctct acgctttcgt catcctcaag aaagacgacc agcaggtcga cggccagccg 1260

ctttga 1266

<210> 84
<211> 421
<212> PRT
<213> Mitsuokella multacida

<400> 84

Met Gly Asn Leu Leu Lys Ala Phe Ser Asn Pro Phe Tyr Arg Thr Ser
1 5 10 15

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Ser Leu Glu Ile Leu Leu Phe Phe Ala Gly Trp Gly Ile Trp Trp Ser
            20                  25                  30

Phe Phe Gln Ile Trp Leu Thr Thr Lys Gln Gly Phe Thr Gly Ala Gln
        35                  40                  45

Val Gly Thr Ile Tyr Ser Phe Gly Ser Ala Val Ala Leu Val Leu Met
    50                  55                  60

Phe Val Tyr Gly Ser Leu Gln Asp Lys Leu Gly Met Lys Lys Thr Met
65                  70                  75                  80

Leu Lys Phe Phe Ala Val Cys Gln Ile Leu Val Gly Pro Phe Phe Thr
                85                  90                  95

Trp Val Tyr Val Pro Met Leu Ala Ala Asn Phe Tyr Val Gly Ala Val
            100                 105                 110

Val Gly Ala Val Tyr Leu Ala Val Ala Phe Leu Ala Ala Cys Pro Val
        115                 120                 125

Phe Glu Ala Val Thr Glu Arg Leu Ser Arg Arg Tyr Ser Phe Glu Tyr
    130                 135                 140

Gly Gln Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Val Ala Ala Leu
145                 150                 155                 160

Cys Ala Gly Phe Leu Phe Thr Met Asn Pro Asn Leu Ile Phe Trp Thr
                165                 170                 175

Gly Ser Ala Val Ala Ala Val Gln Leu Ile Val Leu Val Ser Met Thr
            180                 185                 190

Pro Glu Asn Asp Ala Ser Leu Thr Ala Gln Tyr Glu Val Lys Ala Glu
        195                 200                 205

Ser Ile Lys Glu Ser Lys Thr Pro Ser Phe Gly Glu Ile Val Gly Val
    210                 215                 220

Phe Lys Leu Ile Glu Val Trp Lys Met Ile Val Phe Val Ile Met Ser
225                 230                 235                 240

Trp Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Glu Phe Phe
                245                 250                 255

Thr Arg Phe Phe Ala Thr Pro Glu Ala Gly Gln Gln Ala Tyr Gly Val
            260                 265                 270

Leu Asn Ser Ile Glu Val Phe Leu Glu Phe Leu Met Met Gly Leu Val
        275                 280                 285
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Pro Ile Leu Met Arg Arg Ile Gly Val Arg Lys Ala Ile Leu Leu Gly
290 295 300

Cys Ala Ile Met Ile Val Arg Ile Gly Gly Cys Gly Leu Val Thr Asn
305 310 315 320

Pro Leu Gly Val Ala Val Ile Lys Leu Leu His Ala Pro Glu Thr Ala
325 330 335

Leu Phe Ile Leu Ala Val Phe Arg Tyr Phe Thr Leu His Phe Asp Thr
340 345 350

Arg Ile Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ala Gln
355 360 365

Val Gly Gln Ile Ile Phe Ser Thr Pro Leu Gly Ala Leu His Asp Ser
370 375 380

Ile Gly Tyr Gln Ser Thr Phe Leu Val Ile Ser Gly Ile Val Cys Val
385 390 395 400

Ala Ser Leu Tyr Ala Phe Val Ile Leu Lys Lys Asp Asp Gln Gln Val
405 410 415

Asp Gly Gln Pro Leu
420

<210> 85
<211> 1275
<212> DNA
<213> Lactobacillus antri

<400> 85
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aatgacctcg gcttctctgg ggccaaggtc gggatgatct atactttcga ttcggcaatt 180

acgctggtct taatgttcat ctacgggtca gtgcaagaca agctcggcat taaacgccgg 240

ctgctgattg gggttaccat cctggaaatg ctccttgggc ccttctttac ctggatttac 300

gcgccactgc tgcactctaa ctttatcctc ggcgccttct taggttccct ctacctctcc 360

tttgcctttc tggcggcgtc cccgaccttc gaggccctcg cagaacggat gagccggcgg 420

tacagctttg aatacggtcg ggcccgggcc tgggggtcat ttggttacgc cgtttcggca 480

ttgtgtgccg gctacctctt caccatcagt ccctacatcg tcttttggct cagcagcggg 540

attagcttgc taaccttcct cctgctctgc tttggccgga ctaagagccc cacacaggtt 600

gcccgttacg agaataaggc cgaggaagaa cacgacgcgg ataagccgag tttcaaagag 660

atcatcagtg ttttcaagct caagcagttg tgggaattgg ttttcttcat tattttcagc 720

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ccggtcggga tctcgattgt gaagctcttt cacgccccgg aaacggccat ctttgccctg 1020

gcgatgttcc gctatttgac cctccacttt gacacccggc tatcggcgac gatgtacatg 1080

gtggttgggc agattgccgg tcaaatcggc cagatcatcc tgtcgacgcc cctgggaatg 1140

ctccacgacc ggatcggcta ccgggcgacc ttcctggtta tttcgctgat tgtgatttgc 1200

gctgcggtat acgcattcgt cattttgcgc aaggataacc aggaggttga cggtcaacca 1260

ctagaaaaca actaa 1275

<210> 86
<211> 424
<212> PRT
<213> Lactobacillus antri

<400> 86

Met Lys Asn Ser Lys Leu Ser Ala Phe Lys Asn Ser Phe Tyr Leu Glu
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Ser Ser Leu Ser Leu Leu Leu Phe Phe Ala Ala Trp Gly Ile Trp Trp
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Ser Phe Phe Gln Ile Trp Leu Thr Asn Asp Leu Gly Phe Ser Gly Ala
35 40 45

Lys Val Gly Met Ile Tyr Thr Phe Asp Ser Ala Ile Thr Leu Val Leu
50 55 60

Met Phe Ile Tyr Gly Ser Val Gln Asp Lys Leu Gly Ile Lys Arg Arg
65 70 75 80

Leu Leu Ile Gly Val Thr Ile Leu Glu Met Leu Leu Gly Pro Phe Phe
85 90 95

Thr Trp Ile Tyr Ala Pro Leu Leu His Ser Asn Phe Ile Leu Gly Ala
100 105 110

Phe Leu Gly Ser Leu Tyr Leu Ser Phe Ala Phe Leu Ala Ala Ser Pro
115 120 125

Thr Phe Glu Ala Leu Ala Glu Arg Met Ser Arg Arg Tyr Ser Phe Glu
130 135 140

Tyr Gly Arg Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Val Ser Ala
145 150 155 160

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Leu Cys Ala Gly Tyr Leu Phe Thr Ile Ser Pro Tyr Ile Val Phe Trp
                165                 170                 175

Leu Ser Ser Gly Ile Ser Leu Leu Thr Phe Leu Leu Leu Cys Phe Gly
            180                 185                 190

Arg Thr Lys Ser Pro Thr Gln Val Ala Arg Tyr Glu Asn Lys Ala Glu
        195                 200                 205

Glu Glu His Asp Ala Asp Lys Pro Ser Phe Lys Glu Ile Ile Ser Val
    210                 215                 220

Phe Lys Leu Lys Gln Leu Trp Glu Leu Val Phe Phe Ile Ile Phe Ser
225                 230                 235                 240

Gly Ser Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Gln Phe Phe
                245                 250                 255

Thr Gln Phe Phe Lys Thr Ala Ala Gln Gly Asn Thr Ala Tyr Gly Ile
            260                 265                 270

Leu Asn Ser Ile Glu Val Phe Leu Glu Ala Ile Met Met Ala Ile Val
        275                 280                 285

Pro Trp Ile Met Lys Lys Ile Gly Val Arg Lys Thr Leu Leu Ile Gly
    290                 295                 300

Val Thr Ile Met Phe Leu Arg Ile Gly Leu Cys Gly Leu Val Val Ser
305                 310                 315                 320

Pro Val Gly Ile Ser Ile Val Lys Leu Phe His Ala Pro Glu Thr Ala
                325                 330                 335

Ile Phe Ala Leu Ala Met Phe Arg Tyr Leu Thr Leu His Phe Asp Thr
            340                 345                 350

Arg Leu Ser Ala Thr Met Tyr Met Val Val Gly Gln Ile Ala Gly Gln
        355                 360                 365

Ile Gly Gln Ile Ile Leu Ser Thr Pro Leu Gly Met Leu His Asp Arg
    370                 375                 380

Ile Gly Tyr Arg Ala Thr Phe Leu Val Ile Ser Leu Ile Val Ile Cys
385                 390                 395                 400

Ala Ala Val Tyr Ala Phe Val Ile Leu Arg Lys Asp Asn Gln Glu Val
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Asp Gly Gln Pro Leu Glu Asn Asn
            420
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<210> 87
<211> 1323
<212> DNA
<213> Lactobacillus ruminis

<400> 87
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ttctttgctg gctggggcat ctggtggtca ttcttccaga tctggctgac aaccaagcag 180

gggttcaccg gagcccaggt tggcgagata tactccttca actcggcgtt ctcactgatt 240

gccaaccttg tttacagcaa cattcaggac aggctcggcc tcaaacgcaa ccttttgatc 300

ttctgcgcct gcctgcaggt gttcctcggg cccttcttca cgttcctctt cgtgccgatg 360

cttcatgcca accttgaact cggcgctctg atcggttcat gctacctgac gcttgcctat 420

ctttccgcat ccccgatgtt cgaggcactg acggaacgtg caagccgccg cttcaactat 480

cagtatgggt cagcgcgtgc ctggggctcg ttcggatatg ccgtatccgc cttgcttgca 540

ggattcgtct tcacaatcaa tccgtcgctg ctgttctgga tcggctctgc catcgctgtt 600

gtccttcttc tcctgctttt gttctggaac cctgtccgca acaaggagac ggttgccaga 660

tttgaaaatg aaatggtcag ggaacgtgag aactccaagc ctgggtcaag ggacttcctc 720

aatgtcttca aggttcgcag cctttgggaa atcgccattt tccttgtctt cagcggtaca 780

ttctacacga ttttcgatca gcagatgttt cctcagttct tcactcagtt cttcaagacc 840

caggcaatgg gcgatcacat gtatgggatc ctgaactcgg ttgaggtgtt cctcgaagca 900

ctcatgatgg gcctggttcc gcttctcatg aagaagatcg gcgtccgccg cacgattctt 960

gtcggcgtga cgttcatgtt catcagaatc ggtggctgcg gtctgattac gaaccctctt 1020

ggcgtttcaa tgatcaagct tctccatgcg cctgaaacgg ccattttctg cgtcgtaatg 1080

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cacatcggct atcagccgac cttcctggta atcgccggca tcgtattctg cgccggcatc 1260

tacggcttat tcatcattcg aagggatgat caggaagtaa acggagagag gctgtctgaa 1320

taa 1323

<210> 88
<211> 440
<212> PRT
<213> Lactobacillus ruminis

<400> 88

Met Met Pro Ile Ser Asp Asn Trp Lys Gly Ile Leu Phe Met Asn Asp
1 5 10 15

Met Asn Lys Ser Gly Arg Met Ser Gln Leu Lys Asn Pro Phe Phe Thr
20 25 30

```
Ser Asn Ala Thr Asn Ile Leu Met Phe Phe Ala Gly Trp Gly Ile Trp
        35                  40                  45

Trp Ser Phe Phe Gln Ile Trp Leu Thr Thr Lys Gln Gly Phe Thr Gly
    50                  55                  60

Ala Gln Val Gly Glu Ile Tyr Ser Phe Asn Ser Ala Phe Ser Leu Ile
65                  70                  75                  80

Ala Asn Leu Val Tyr Ser Asn Ile Gln Asp Arg Leu Gly Leu Lys Arg
                85                  90                  95

Asn Leu Leu Ile Phe Cys Ala Cys Leu Gln Val Phe Leu Gly Pro Phe
            100                 105                 110

Phe Thr Phe Leu Phe Val Pro Met Leu His Ala Asn Leu Glu Leu Gly
        115                 120                 125

Ala Leu Ile Gly Ser Cys Tyr Leu Thr Leu Ala Tyr Leu Ser Ala Ser
    130                 135                 140

Pro Met Phe Glu Ala Leu Thr Glu Arg Ala Ser Arg Arg Phe Asn Tyr
145                 150                 155                 160

Gln Tyr Gly Ser Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Val Ser
                165                 170                 175

Ala Leu Leu Ala Gly Phe Val Phe Thr Ile Asn Pro Ser Leu Leu Phe
            180                 185                 190

Trp Ile Gly Ser Ala Ile Ala Val Val Leu Leu Leu Leu Leu Leu Phe
        195                 200                 205

Trp Asn Pro Val Arg Asn Lys Glu Thr Val Ala Arg Phe Glu Asn Glu
    210                 215                 220

Met Val Arg Glu Arg Glu Asn Ser Lys Pro Gly Ser Arg Asp Phe Leu
225                 230                 235                 240

Asn Val Phe Lys Val Arg Ser Leu Trp Glu Ile Ala Ile Phe Leu Val
                245                 250                 255

Phe Ser Gly Thr Phe Tyr Thr Ile Phe Asp Gln Gln Met Phe Pro Gln
            260                 265                 270

Phe Phe Thr Gln Phe Phe Lys Thr Gln Ala Met Gly Asp His Met Tyr
        275                 280                 285

Gly Ile Leu Asn Ser Val Glu Val Phe Leu Glu Ala Leu Met Met Gly
    290                 295                 300
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Leu Val Pro Leu Leu Met Lys Lys Ile Gly Val Arg Arg Thr Ile Leu
305 310 315 320

Val Gly Val Thr Phe Met Phe Ile Arg Ile Gly Gly Cys Gly Leu Ile
325 330 335

Thr Asn Pro Leu Gly Val Ser Met Ile Lys Leu Leu His Ala Pro Glu
340 345 350

Thr Ala Ile Phe Cys Val Val Met Phe Arg Tyr Tyr Thr Leu His Tyr
355 360 365

Asp Pro Arg Val Ser Ala Thr Ile Asn Ile Val Thr Gly Ile Ala Gly
370 375 380

Ser Phe Gly Gln Ile Leu Leu Ser Thr Pro Leu Gly Leu Leu Arg Asp
385 390 395 400

His Ile Gly Tyr Gln Pro Thr Phe Leu Val Ile Ala Gly Ile Val Phe
405 410 415

Cys Ala Gly Ile Tyr Gly Leu Phe Ile Ile Arg Arg Asp Asp Gln Glu
420 425 430

Val Asn Gly Glu Arg Leu Ser Glu
435 440

<210> 89
<211> 1242
<212> DNA
<213> Yersinia frederiksenii

<400> 89
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aaaggtaccg aaacaggggc gacttttttcc gccattgcct taacggcact ttgcgctcaa 180

ccgctttatg gcgtgataca agataagttg gggctaaaaa aacatctttt atgggccatt 240

ggtattttgc tgctgatcag tggccctttt tttatttatg tttatgcccc tttattgcgt 300

gtcaacatgc tggttggtgc cgttaccggt ggcttatata tggggatgac gttctttgcc 360

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ggtaaagccc gtatgtgggg atcgctgggg tgggcgggtg caacctttt tgctggcatg 480

ttgtttaata ttaatcccaa cattaatttc tggatggcat cggcatcggc cgcgatattt 540

ttactgttgt tgtggcactt acatgaagtt aaaacagcgg ctatggggca gttggaatac 600

ggtaagaata gtgccctgac actgagtgat acattgtcac tgtttcgtat gccgcgtttc 660

tgggcgctgg tggtatttgt caccggtgtg agcgtttata acgtctatga ccagcaattt 720

ccggtctatt tctcctctct atttactgac cgacgccacg gcaatgaaat gtacggcttt 780

cttaattcac tacaggtatt cctagaggct ggtggtatgt tcctcgcgcc ttttctggtt 840

aaccgtattg gcgcgaaaaa gggcttactg ctgagcggat taatcatggc aatgcgcata 900

ttgggttcag ggttggcaca agatgcagtc accatctcat tgatgaagtt attacatgca 960

gtggagttgc ctattttgct cattgcgatg tttaagtata tcgccgccaa tttcgacccg 1020

cgtttgtcag ccacgcttta tctggtggga tttcagttta ttacccaagt ctatgccagc 1080

gtattttcgc cgttggcagg taaaggctat gacctgatcg ggttcgctga tacctatctg 1140

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tcgcgtacgg atgatccttc cctacaatta accactaagt ga 1242

<210> 90
<211> 413
<212> PRT
<213> Yersinia frederiksenii

<400> 90

Met Lys His Ser Val Arg Asn Gln Tyr Leu Ile Leu Ser Gly Leu Leu
1 5 10 15

Phe Thr Phe Phe Phe Thr Trp Ser Ser Ala Phe Ser Leu Phe Ser Ile
20 25 30

Trp Leu Asn Gln Tyr Val Gly Leu Lys Gly Thr Glu Thr Gly Ala Thr
35 40 45

Phe Ser Ala Ile Ala Leu Thr Ala Leu Cys Ala Gln Pro Leu Tyr Gly
50 55 60

Val Ile Gln Asp Lys Leu Gly Leu Lys Lys His Leu Leu Trp Ala Ile
65 70 75 80

Gly Ile Leu Leu Leu Ile Ser Gly Pro Phe Phe Ile Tyr Val Tyr Ala
85 90 95

Pro Leu Leu Arg Val Asn Met Leu Val Gly Ala Val Thr Gly Gly Leu
100 105 110

Tyr Met Gly Met Thr Phe Phe Ala Gly Ile Gly Ala Leu Glu Ser Tyr
115 120 125

Thr Glu Arg Val Ser Arg Ile Ser Gly Phe Glu Phe Gly Lys Ala Arg
130 135 140

Met Trp Gly Ser Leu Gly Trp Ala Gly Ala Thr Phe Phe Ala Gly Met
145 150 155 160

Leu Phe Asn Ile Asn Pro Asn Ile Asn Phe Trp Met Ala Ser Ala Ser
165 170 175

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Ala Ala Ile Phe Leu Leu Leu Leu Trp His Leu His Glu Val Lys Thr
            180                 185                 190

Ala Ala Met Gly Gln Leu Glu Tyr Gly Lys Asn Ser Ala Leu Thr Leu
        195                 200                 205

Ser Asp Thr Leu Ser Leu Phe Arg Met Pro Arg Phe Trp Ala Leu Val
    210                 215                 220

Val Phe Val Thr Gly Val Ser Val Tyr Asn Val Tyr Asp Gln Gln Phe
225                 230                 235                 240

Pro Val Tyr Phe Ser Ser Leu Phe Thr Asp Arg Arg His Gly Asn Glu
                245                 250                 255

Met Tyr Gly Phe Leu Asn Ser Leu Gln Val Phe Leu Glu Ala Gly Gly
            260                 265                 270

Met Phe Leu Ala Pro Phe Leu Val Asn Arg Ile Gly Ala Lys Lys Gly
        275                 280                 285

Leu Leu Leu Ser Gly Leu Ile Met Ala Met Arg Ile Leu Gly Ser Gly
    290                 295                 300

Leu Ala Gln Asp Ala Val Thr Ile Ser Leu Met Lys Leu Leu His Ala
305                 310                 315                 320

Val Glu Leu Pro Ile Leu Leu Ile Ala Met Phe Lys Tyr Ile Ala Ala
                325                 330                 335

Asn Phe Asp Pro Arg Leu Ser Ala Thr Leu Tyr Leu Val Gly Phe Gln
            340                 345                 350

Phe Ile Thr Gln Val Tyr Ala Ser Val Phe Ser Pro Leu Ala Gly Lys
        355                 360                 365

Gly Tyr Asp Leu Ile Gly Phe Ala Asp Thr Tyr Leu Ile Met Gly Gly
    370                 375                 380

Ile Val Leu Gly Leu Thr Ala Ile Ser Cys Phe Met Leu Arg Gly Glu
385                 390                 395                 400

Ser Arg Thr Asp Asp Pro Ser Leu Gln Leu Thr Thr Lys
                405                 410
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<210> 91
<211> 1260
<212> DNA
<213> Serratia proteamaculans

<400> 91
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aaagggactg aaaccgggct gatcttcgcg gcaatgtcga tcatggcgtt gtgcgcccaa 180

ccgctgtacg gctttattca ggacaaactt gggctgcgta agcacctgct gctgtttgtc 240

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cttaattcgc tgcaggtgtt tctggaggcc ggtggcatgt tcctggcccc gctgctggtt 840

aaccgcattg gcataaagca aagcctgttg ctggccagca gcgtgatggc gctgcgcatg 900

gtcggttccg gctttgccag cggcgccctg atgatttccg ccatgaaact gctgcacgcc 960

gtagaattgc caatcctgct ggtggcgatg ttcaagtaca tcaccacccg tttcgacagc 1020

cgcctgtcct ccacgctgta cctggtgggc ttccagttta tcagccaaat tgtcgccggt 1080

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accgtcgcca gtgcgcctca atttcaatcc acgttaaaat caagtgagcc aacccaatga 1260

<210> 92
<211> 419
<212> PRT
<213> Serratia proteamaculans

<400> 92

Met Asn Arg Glu Thr Lys Lys Tyr Tyr Val Leu Leu Ser Gly Leu Leu
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Phe Phe Phe Phe Phe Thr Trp Ser Ser Ser Phe Ser Leu Ile Ser Ile
20 25 30

Trp Leu Asn Gln Lys Ile Gly Leu Lys Gly Thr Glu Thr Gly Leu Ile
35 40 45

Phe Ala Ala Met Ser Ile Met Ala Leu Cys Ala Gln Pro Leu Tyr Gly
50 55 60

Phe Ile Gln Asp Lys Leu Gly Leu Arg Lys His Leu Leu Leu Phe Val
65 70 75 80

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Gly Val Leu Leu Leu Leu Thr Gly Pro Phe Phe Ile Tyr Val Tyr Ala
                85                  90                  95

Pro Leu Leu Gln Ser Asn Leu Val Val Gly Ala Leu Val Gly Gly Val
            100                 105                 110

Phe Val Ser Leu Ala Phe Asn Ala Gly Ile Gly Ala Leu Glu Ser Tyr
        115                 120                 125

Thr Glu Arg Val Ser Arg Ile Val Gly Phe Glu Phe Gly Arg Ala Arg
    130                 135                 140

Met Trp Gly Ser Leu Gly Trp Ala Ser Ala Thr Phe Phe Ala Gly Phe
145                 150                 155                 160

Asn Tyr Asn Ile Asp Pro Asn Ile Asn Phe Trp Ile Ala Ser Ala Ser
                165                 170                 175

Ala Ala Val Phe Leu Leu Leu Leu Trp Gln Val Arg Glu Leu Lys Pro
            180                 185                 190

Asn Ala Met Ala Gly Leu Glu Tyr Gly Lys Pro Glu Asn Leu Lys Leu
        195                 200                 205

Gln Asp Ala Leu Ala Leu Leu Arg Leu Pro Gly Phe Trp Ala Leu Val
    210                 215                 220

Val Phe Val Leu Gly Thr Ser Ile Tyr Gly Val Phe Asp Gln Gln Phe
225                 230                 235                 240

Pro Val Tyr Phe Ala Ser Gln Phe Pro Thr His Glu Glu Gly Asn Arg
                245                 250                 255

Met Tyr Gly Phe Leu Asn Ser Leu Gln Val Phe Leu Glu Ala Gly Gly
            260                 265                 270

Met Phe Leu Ala Pro Leu Leu Val Asn Arg Ile Gly Ile Lys Gln Ser
        275                 280                 285

Leu Leu Leu Ala Ser Ser Val Met Ala Leu Arg Met Val Gly Ser Gly
    290                 295                 300

Phe Ala Ser Gly Ala Leu Met Ile Ser Ala Met Lys Leu Leu His Ala
305                 310                 315                 320

Val Glu Leu Pro Ile Leu Leu Val Ala Met Phe Lys Tyr Ile Thr Thr
                325                 330                 335

Arg Phe Asp Ser Arg Leu Ser Ser Thr Leu Tyr Leu Val Gly Phe Gln
            340                 345                 350
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Phe Ile Ser Gln Ile Val Ala Gly Phe Leu Ala Pro Leu Ala Gly Tyr
355 360 365

Gly Tyr Asp Arg Ile Gly Phe Ala Asp Thr Tyr Leu Leu Met Gly Cys
370 375 380

Ala Val Ala Gly Thr Thr Leu Ile Ser Cys Phe Leu Leu Arg Gly Glu
385 390 395 400

Thr Val Ala Ser Ala Pro Gln Phe Gln Ser Thr Leu Lys Ser Ser Glu
405 410 415

Pro Thr Gln

<210> 93
<211> 1239
<212> DNA
<213> Escherichia coli

<400> 93
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aaagcatcgg aaaccggcat tatttttca gtattatccg tctccgcgct cttcgcgcag 180

gtctgttatg gctttattca ggaccgactt ggtctgcgca aacatttgtt atggtttatc 240

accgcgttgt tgatcctctc cggcccggct tatctgcttt ttagttattt gctgagcgtt 300

aatattctgc tgggcagcgt attcgggggc ttatttatcg ggctgacgtt taatgggggt 360

atcggcgttc tggagtccta taccgagcgc gtcgcgcgtc aaagtacctt tgagtttggg 420

cgggcacgca tgtgggggtc tctgggctgg gcagttgcca cgtttttgc cgggttactg 480

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tgcctcctgg cccgattaaa ggtggccgcg ccggcaagca tggagaaact cgaaattggc 600

gctaaaaaag tttctctgga agacgccctg cgtctgctta ctctgccgcg cttctgggca 660

ctgatattct tcgtggtcgg aacctgcatt tacggcgtat acgatcagca attcccggtc 720

tatttctcat cacagttccc gacattacgc gaagggaacg agatgtttgg ctatttaaac 780

tctttccagg tctttctcga ggccgcaggt atgttttgtg cgccgtggct ggttaatcgc 840

attggtgcta aaaatggtct gatattcgca ggaatggtga tggcgctgcg catgattact 900

tcagggctgg tggaaggccc cctgcttatc tccattacca aactgcttca cgcggtcgaa 960

ctgccaatat tgttagtcgc catatttaaa tacaacagtc tgaatttcga caaacgtctc 1020

tcctccacca tttatctggt gggatttgcc tgcaccagct ccgtcattgg taccgtattg 1080

tccccgctgg caggctttag ctatgagaga tttggcttcg cccaatccta tctgatcatg 1140

ggcatcatgg tgttcagcac cacgtttatt tccattttcc ttttgcgctc aactaaatcc 1200

tcatctgagc catcttttct gcagcaaaaa gctgtgtaa 1239

<210> 94
<211> 412
<212> PRT
<213> Escherichia coli

<400> 94

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Met Lys Lys Arg Pro Thr Arg Ser Tyr Met Leu Leu Ser Ala Leu Leu
1               5                   10                  15

Phe Phe Phe Phe Val Thr Trp Ser Ser Ser Ser Ser Leu Leu Ser Ile
            20                  25                  30

Trp Leu His Gln Glu Val Gly Leu Lys Ala Ser Glu Thr Gly Ile Ile
        35                  40                  45

Phe Ser Val Leu Ser Val Ser Ala Leu Phe Ala Gln Val Cys Tyr Gly
    50                  55                  60

Phe Ile Gln Asp Arg Leu Gly Leu Arg Lys His Leu Leu Trp Phe Ile
65                  70                  75                  80

Thr Ala Leu Leu Ile Leu Ser Gly Pro Ala Tyr Leu Leu Phe Ser Tyr
                85                  90                  95

Leu Leu Ser Val Asn Ile Leu Leu Gly Ser Val Phe Gly Gly Leu Phe
            100                 105                 110

Ile Gly Leu Thr Phe Asn Gly Gly Ile Gly Val Leu Glu Ser Tyr Thr
        115                 120                 125

Glu Arg Val Ala Arg Gln Ser Thr Phe Glu Phe Gly Arg Ala Arg Met
    130                 135                 140

Trp Gly Ser Leu Gly Trp Ala Val Ala Thr Phe Phe Ala Gly Leu Leu
145                 150                 155                 160

Phe Asn Ile Asn Pro Asp Leu Asn Phe Leu Val Ala Ser Cys Ser Gly
                165                 170                 175

Leu Ile Phe Phe Cys Leu Leu Ala Arg Leu Lys Val Ala Ala Pro Ala
            180                 185                 190

Ser Met Glu Lys Leu Glu Ile Gly Ala Lys Lys Val Ser Leu Glu Asp
        195                 200                 205

Ala Leu Arg Leu Leu Thr Leu Pro Arg Phe Trp Ala Leu Ile Phe Phe
    210                 215                 220

Val Val Gly Thr Cys Ile Tyr Gly Val Tyr Asp Gln Gln Phe Pro Val
225                 230                 235                 240
```

Tyr Phe Ser Ser Gln Phe Pro Thr Leu Arg Glu Gly Asn Glu Met Phe
245 250 255

Gly Tyr Leu Asn Ser Phe Gln Val Phe Leu Glu Ala Ala Gly Met Phe
260 265 270

Cys Ala Pro Trp Leu Val Asn Arg Ile Gly Ala Lys Asn Gly Leu Ile
275 280 285

Phe Ala Gly Met Val Met Ala Leu Arg Met Ile Thr Ser Gly Leu Val
290 295 300

Glu Gly Pro Leu Leu Ile Ser Ile Thr Lys Leu Leu His Ala Val Glu
305 310 315 320

Leu Pro Ile Leu Leu Val Ala Ile Phe Lys Tyr Asn Ser Leu Asn Phe
325 330 335

Asp Lys Arg Leu Ser Ser Thr Ile Tyr Leu Val Gly Phe Ala Cys Thr
340 345 350

Ser Ser Val Ile Gly Thr Val Leu Ser Pro Leu Ala Gly Phe Ser Tyr
355 360 365

Glu Arg Phe Gly Phe Ala Gln Ser Tyr Leu Ile Met Gly Ile Met Val
370 375 380

Phe Ser Thr Thr Phe Ile Ser Ile Phe Leu Leu Arg Ser Thr Lys Ser
385 390 395 400

Ser Ser Glu Pro Ser Phe Leu Gln Gln Lys Ala Val
405 410

<210> 95
<211> 1236
<212> DNA
<213> Bacillus licheniformis

<400> 95
atgaaaagct caaacagtct gtattggaaa ctaagcgcct atttttttctt tttctttttt 60

acttggtctt ccagctattc tttatttgcg atttggttag ggcaagaaat caatttgaac 120

gggtccgcga cgggcattat cttttctgta aacgctatct ttactttgtg catgcagcct 180

ttgtacggtt ttatctccga taagctcggg ctgaagaaaa acatattatt tatgatcagt 240

ttgctgctcg tatttacggg tccctttttat attttcgtct acggaccgct tttgcaatac 300

aacgtctttc ttggggctat cgtcggggga atttatttgg gaactgcttt tctcgccgga 360

atcggtgcga ttgaaacctt tattgaaaag gtcagccgca aatatcaatt tgaatatgga 420

agaacaagga tgtgggggtc cctcggctgg gctgcggcga catttttgc aggtcagctg 480

ttcaatatcg atccgaatat caacttctgg gttgcgtccg cctcagcaat catattggtg 540

gccattattg tttccgtaaa aattgagatg acagatgatg aaaaggaaag agcagactcg 600

gtcggattaa aagacgtagg agggcttttt ctcttaaaag atttctggtt tttgatgctg 660

tacgtgatcg gcgtaacatg cgtgtacggc gtctatgacc agcagttccc gctttactac 720

gcttccttat ttccgactgc ggccttgggg aaccaaatat ttggatacct taattcattc 780

caagtattta ttgaagcggg catgatgttt cttgcgcctt tcatcgtcaa taagctcggt 840

cctaaaaaaa gcttgatttt agcggggctg ttaatggctt tccggattat cggttccgga 900

cttgtcagcg gaccggtcgg aatttcatcg atgaaactca ttcatgcttt agaattgccg 960

attatgctga ttgcgatgtt taaatatttg gcgactaatt ttgataatcg tctttcatcc 1020

gtactttatc ttgtcggctt tcaattcgca tcccaggtag gcacgtcgat tttttcgccg 1080

cttgcgggag gtttatacga cagcatcgga tttcgccaca cttatctcat catgggagca 1140

atggtccttt gttttaccat tatttcgatt tttaccttgc tagactcaaa gaaagatgtt 1200

gaatttgctc aaaatctaca aagcaatcat atatag 1236

<210> 96
<211> 411
<212> PRT
<213> Bacillus licheniformis

<400> 96

Met Lys Ser Ser Asn Ser Leu Tyr Trp Lys Leu Ser Ala Tyr Phe Phe
1 5 10 15

Phe Phe Phe Phe Thr Trp Ser Ser Ser Tyr Ser Leu Phe Ala Ile Trp
20 25 30

Leu Gly Gln Glu Ile Asn Leu Asn Gly Ser Ala Thr Gly Ile Ile Phe
35 40 45

Ser Val Asn Ala Ile Phe Thr Leu Cys Met Gln Pro Leu Tyr Gly Phe
50 55 60

Ile Ser Asp Lys Leu Gly Leu Lys Lys Asn Ile Leu Phe Met Ile Ser
65 70 75 80

Leu Leu Leu Val Phe Thr Gly Pro Phe Tyr Ile Phe Val Tyr Gly Pro
85 90 95

Leu Leu Gln Tyr Asn Val Phe Leu Gly Ala Ile Val Gly Gly Ile Tyr
100 105 110

Leu Gly Thr Ala Phe Leu Ala Gly Ile Gly Ala Ile Glu Thr Phe Ile
115 120 125

Glu Lys Val Ser Arg Lys Tyr Gln Phe Glu Tyr Gly Arg Thr Arg Met
130 135 140

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Trp Gly Ser Leu Gly Trp Ala Ala Ala Thr Phe Phe Ala Gly Gln Leu
145                 150                 155                 160

Phe Asn Ile Asp Pro Asn Ile Asn Phe Trp Val Ala Ser Ala Ser Ala
                165                 170                 175

Ile Ile Leu Val Ala Ile Ile Val Ser Val Lys Ile Glu Met Thr Asp
            180                 185                 190

Asp Glu Lys Glu Arg Ala Asp Ser Val Gly Leu Lys Asp Val Gly Gly
        195                 200                 205

Leu Phe Leu Leu Lys Asp Phe Trp Phe Leu Met Leu Tyr Val Ile Gly
    210                 215                 220

Val Thr Cys Val Tyr Gly Val Tyr Asp Gln Gln Phe Pro Leu Tyr Tyr
225                 230                 235                 240

Ala Ser Leu Phe Pro Thr Ala Ala Leu Gly Asn Gln Ile Phe Gly Tyr
                245                 250                 255

Leu Asn Ser Phe Gln Val Phe Ile Glu Ala Gly Met Met Phe Leu Ala
            260                 265                 270

Pro Phe Ile Val Asn Lys Leu Gly Pro Lys Lys Ser Leu Ile Leu Ala
        275                 280                 285

Gly Leu Leu Met Ala Phe Arg Ile Ile Gly Ser Gly Leu Val Ser Gly
    290                 295                 300

Pro Val Gly Ile Ser Ser Met Lys Leu Ile His Ala Leu Glu Leu Pro
305                 310                 315                 320

Ile Met Leu Ile Ala Met Phe Lys Tyr Leu Ala Thr Asn Phe Asp Asn
                325                 330                 335

Arg Leu Ser Ser Val Leu Tyr Leu Val Gly Phe Gln Phe Ala Ser Gln
            340                 345                 350

Val Gly Thr Ser Ile Phe Ser Pro Leu Ala Gly Gly Leu Tyr Asp Ser
        355                 360                 365

Ile Gly Phe Arg His Thr Tyr Leu Ile Met Gly Ala Met Val Leu Cys
    370                 375                 380

Phe Thr Ile Ile Ser Ile Phe Thr Leu Leu Asp Ser Lys Lys Asp Val
385                 390                 395                 400

Glu Phe Ala Gln Asn Leu Gln Ser Asn His Ile
                405                 410
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<210> 97
<211> 1290
<212> DNA
<213> Pseudomonas fluorescens

<400> 97
atgcagtttg ccgccaaacg cgagtactgg cttatcagtg gtttgttgtt tttcttcttc 60

ttttcgtggt catccagcta ttcattgttt tctatctggc tgcatcgagt cattggcttg 120

aatggcacgg aaaccggctt cattttcgcc gccaacgcta ttgcggcgct gctggttcaa 180

cccttctacg gcgcccttca agaccgcctc gggctgtcca aaaagcttct ggtgtggatt 240

ggcatcctgc tgtgtgccgc ggccccgttt gcaatttatg tctacgccgg cctgttggcg 300

cagaacgtga tgctcggcgc gttggtcggt gcggcgttcc tggcgctggc gatgctggca 360

ggcgttgggg tgatcgagtc gtacaccgag cgcttgtcgc ggcatgcagg attcgagttt 420

ggaaccaccc gaatgtgggg gtcgttgggc tgggccagcg cgacgggcgt ggtcggcgtg 480

gtgttcaaca tcgatcctga cattgcgttt tacatgagca gcctcgccgg catcgtgttt 540

ttgctgatcc tgttccgtct ggacctcgac cggttggccc agccggcagt gcaggcgggc 600

gcggttgtcc accccgtgcg cctgaacgat ctctggaagt tgctggcact cccgcggttc 660

tgggctttca gcctttacct gacgggggta tgcgggatct acatgatcta cgagcaacag 720

tttccggtgt atttctcctc gtttttcccg accccggagg aggggacccg tgcctatggc 780

tacctgaact cgtctcaggt actggtcgag gcggtcctga tgctgcttgc accctgggtg 840

gtcagccgca caggcgccaa atacgggctg attctggccg gcagcatcat gttcgtgcgc 900

atccttgggt cggggctggt aacgcaggct tgggccatcg ccgcctgcaa gatgttgcac 960

gccttggaag tgcccatctt gctggtctcg atattcaaat acatttcgct caactttgac 1020

tctcggctgt ccgcctcgat ctacttggtg gggttccagt tcgcccagca actgaccgcc 1080

atgttgctgt caccgctggt gggctacggc tacgaccatt tcggtttctc cagcgtctac 1140

gtactgatgg caggcctggt cggcgcttgc ctgctgcttt catggacctt gttgcgcaag 1200

gaccccgtgc gtgacgcctc tcaagtcggg gctggcgatt cacggcagct tcccgccatc 1260

gcgccatccg cccctcgtta tgaaccctag 1290

<210> 98
<211> 429
<212> PRT
<213> Pseudomonas fluorescens

<400> 98

Met Gln Phe Ala Ala Lys Arg Glu Tyr Trp Leu Ile Ser Gly Leu Leu
1 5 10 15

Phe Phe Phe Phe Phe Ser Trp Ser Ser Ser Tyr Ser Leu Phe Ser Ile
20 25 30

Trp Leu His Arg Val Ile Gly Leu Asn Gly Thr Glu Thr Gly Phe Ile
35 40 45

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Phe Ala Ala Asn Ala Ile Ala Ala Leu Leu Val Gln Pro Phe Tyr Gly
    50                  55                  60

Ala Leu Gln Asp Arg Leu Gly Leu Ser Lys Lys Leu Leu Val Trp Ile
65                  70                  75                  80

Gly Ile Leu Leu Cys Ala Ala Ala Pro Phe Ala Ile Tyr Val Tyr Ala
                85                  90                  95

Gly Leu Leu Ala Gln Asn Val Met Leu Gly Ala Leu Val Gly Ala Ala
            100                 105                 110

Phe Leu Ala Leu Ala Met Leu Ala Gly Val Gly Val Ile Glu Ser Tyr
        115                 120                 125

Thr Glu Arg Leu Ser Arg His Ala Gly Phe Glu Phe Gly Thr Thr Arg
    130                 135                 140

Met Trp Gly Ser Leu Gly Trp Ala Ser Ala Thr Gly Val Val Gly Val
145                 150                 155                 160

Val Phe Asn Ile Asp Pro Asp Ile Ala Phe Tyr Met Ser Ser Leu Ala
                165                 170                 175

Gly Ile Val Phe Leu Leu Ile Leu Phe Arg Leu Asp Leu Asp Arg Leu
            180                 185                 190

Ala Gln Pro Ala Val Gln Ala Gly Ala Val Val His Pro Val Arg Leu
        195                 200                 205

Asn Asp Leu Trp Lys Leu Leu Ala Leu Pro Arg Phe Trp Ala Phe Ser
    210                 215                 220

Leu Tyr Leu Thr Gly Val Cys Gly Ile Tyr Met Ile Tyr Glu Gln Gln
225                 230                 235                 240

Phe Pro Val Tyr Phe Ser Ser Phe Phe Pro Thr Pro Glu Glu Gly Thr
                245                 250                 255

Arg Ala Tyr Gly Tyr Leu Asn Ser Ser Gln Val Leu Val Glu Ala Val
            260                 265                 270

Leu Met Leu Leu Ala Pro Trp Val Val Ser Arg Thr Gly Ala Lys Tyr
        275                 280                 285

Gly Leu Ile Leu Ala Gly Ser Ile Met Phe Val Arg Ile Leu Gly Ser
    290                 295                 300

Gly Leu Val Thr Gln Ala Trp Ala Ile Ala Ala Cys Lys Met Leu His
305                 310                 315                 320
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Ala Leu Glu Val Pro Ile Leu Leu Val Ser Ile Phe Lys Tyr Ile Ser
325 330 335

Leu Asn Phe Asp Ser Arg Leu Ser Ala Ser Ile Tyr Leu Val Gly Phe
340 345 350

Gln Phe Ala Gln Gln Leu Thr Ala Met Leu Leu Ser Pro Leu Val Gly
355 360 365

Tyr Gly Tyr Asp His Phe Gly Phe Ser Ser Val Tyr Val Leu Met Ala
370 375 380

Gly Leu Val Gly Ala Cys Leu Leu Leu Ser Trp Thr Leu Leu Arg Lys
385 390 395 400

Asp Pro Val Arg Asp Ala Ser Gln Val Gly Ala Gly Asp Ser Arg Gln
405 410 415

Leu Pro Ala Ile Ala Pro Ser Ala Pro Arg Tyr Glu Pro
420 425

<210> 99
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for variant sucrose transporter

<400> 99
atggcactga atattccatt cagaaatgcg tactatcgtt ttgcatccag ttactcattt 60

ctcttttta tttcctggtc gctgtggtgg tcgttatacg ctatttggct gaaaggacat 120

ctagggttga cagggacgga attaggtaca ctttattcgg tcaaccagtt taccagcatt 180

ctatttatga tgttctacgg catcgttcag gataaactcg gtctgaagaa accgctcatc 240

tggtgtatga gtttcatcct ggtcttgacc ggaccgttta tgatttacgt ttatgaaccg 300

ttactgcaaa gcaatttttc tgtaggtcta attctggggg cgctattttt tggcttgggg 360

tatctggcgg gatgcggttt gcttgatagc ttcaccgaaa aaatggcgcg aaattttcat 420

ttcgaatatg gaacagcgcg cgcctgggga tcttttggct atgctattgg cgcgttcttt 480

gccggcatat tttttagtat cagtccccat atcaacttct ggttggtctc gctatttggc 540

gctgtattta tgatgatcaa catgcgtttt aaagataagg atcaccagtg cgtagcggca 600

gatgcgggag gggtaaaaaa agaggatttt atcgcagttt tcaaggatcg aaacttctgg 660

gttttcgtca tatttattgt ggggacgtgg tctttctata acatttttga tcaacaactt 720

tttcctgtct tttattcagg tttattcgaa tcacacgatg taggaacgcg cctgtatggt 780

tatctcaact cattccaggt ggtactcgaa gcgctgtgca tggcgattat tcctttcttt 840

gtgaatcggg tagggccaaa aaatgcatta cttatcggag ttgtgattat ggcgttggcg 900

atcctttcct gcgcgctgtt cgttaacccc tggattattt cattagtgaa gttgttacat 960

gccattgagg ttccactttg tgtcatatcc gtcttcaaat acagcgtggc aaactttgat 1020

aagcgcctgt cgtcgacgat ctttctgatt ggttttcaaa ttgccagttc gcttgggatt 1080

gtgctgcttt caacgccgac tgggatactc tttgaccacg caggctacca gacagttttc 1140

ttcgcaattt cgggtattgt ctgcctgatg ttgctatttg gcattttctt cttgagtaaa 1200

aaacgcgagc aaatagttat ggaaacgcct gtaccttcag caatatag 1248

<210> 100
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant sucrose transporter

<400> 100

Met Ala Leu Asn Ile Pro Phe Arg Asn Ala Tyr Tyr Arg Phe Ala Ser
1 5 10 15

Ser Tyr Ser Phe Leu Phe Phe Ile Ser Trp Ser Leu Trp Trp Ser Leu
20 25 30

Tyr Ala Ile Trp Leu Lys Gly His Leu Gly Leu Thr Gly Thr Glu Leu
35 40 45

Gly Thr Leu Tyr Ser Val Asn Gln Phe Thr Ser Ile Leu Phe Met Met
50 55 60

Phe Tyr Gly Ile Val Gln Asp Lys Leu Gly Leu Lys Lys Pro Leu Ile
65 70 75 80

Trp Cys Met Ser Phe Ile Leu Val Leu Thr Gly Pro Phe Met Ile Tyr
85 90 95

Val Tyr Glu Pro Leu Leu Gln Ser Asn Phe Ser Val Gly Leu Ile Leu
100 105 110

Gly Ala Leu Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Leu
115 120 125

Asp Ser Phe Thr Glu Lys Met Ala Arg Asn Phe His Phe Glu Tyr Gly
130 135 140

Thr Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Gly Ala Phe Phe
145 150 155 160

Ala Gly Ile Phe Phe Ser Ile Ser Pro His Ile Asn Phe Trp Leu Val
165 170 175

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Ser Leu Phe Gly Ala Val Phe Met Met Ile Asn Met Arg Phe Lys Asp
            180                 185                 190

Lys Asp His Gln Cys Val Ala Ala Asp Ala Gly Gly Val Lys Lys Glu
        195                 200                 205

Asp Phe Ile Ala Val Phe Lys Asp Arg Asn Phe Trp Val Phe Val Ile
    210                 215                 220

Phe Ile Val Gly Thr Trp Ser Phe Tyr Asn Ile Phe Asp Gln Gln Leu
225                 230                 235                 240

Phe Pro Val Phe Tyr Ser Gly Leu Phe Glu Ser His Asp Val Gly Thr
                245                 250                 255

Arg Leu Tyr Gly Tyr Leu Asn Ser Phe Gln Val Val Leu Glu Ala Leu
            260                 265                 270

Cys Met Ala Ile Ile Pro Phe Phe Val Asn Arg Val Gly Pro Lys Asn
        275                 280                 285

Ala Leu Leu Ile Gly Val Val Ile Met Ala Leu Ala Ile Leu Ser Cys
    290                 295                 300

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
305                 310                 315                 320

Ala Ile Glu Val Pro Leu Cys Val Ile Ser Val Phe Lys Tyr Ser Val
                325                 330                 335

Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile Phe Leu Ile Gly Phe
            340                 345                 350

Gln Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
        355                 360                 365

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
    370                 375                 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
385                 390                 395                 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
                405                 410                 415
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<210> 101
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<223> coding squence for variant sucrose transporter

<400> 101
atggcactga atattccatt cagaaatgcg tactatcgtt ttgcatccag ttactcattt 60

ctcttttta tttcctggtc gctgtggtgg tcgttatacg ctatttggct gaaaggacat 120

ctagggttga cagggacgga attaggtaca ctttattcgg tcaaccagtt taccagcatt 180

ctatttatga tgttctacgg catcgttcag gataaactcg gtctgaagaa accgctcatc 240

tggtgtatga gtttcatcct ggtcttgacc ggaccgttta tgatttacgt ttatgaaccg 300

ttactgcaaa gcaatttttc tgtaggtcta attctggggg cgctattttt tggcttgggg 360

tatctggcgg gatgcggttt gcttgatagc ttcaccgaaa aaatggcgcg aaattttcat 420

ttcgaatatg gaacagcgcg cgcctgggga tcttttggct atgctattgg cgcgttcttt 480

gccggcatat tttttagtat cagtccccat atcaacttct ggttggtctc gctatttggc 540

gctgtattta tgatgatcaa catgcgtttt aaagataagg atcaccagtg cgtagcggca 600

gatgcgggag gggtaaaaaa agaggatttt atcgcagttt tcaaggatcg aaacttctgg 660

gttttcgtca tatttattgt ggggacgtgg tctttctata acatttttga tcaacaactt 720

tttcctgtct tttattcagg tttattcgaa tcacacgatg taggaacgcg cctgtatggt 780

tatctcaact cattccaggt ggtactcgaa gcgctgtgca tggcgattat tcctttcttt 840

gtgaatcggg tagggccaaa aaatgcatta cttatcggag ttgtgattat ggcgttgctg 900

atcctttcct gcgcgctgtt cgttaacccc tggattattt cattagtgaa gttgttacat 960

gccattgagg ttccactttg tgtcatatcc gtcttcaaat acagcgtggc aaactttgat 1020

aagcgcctgt cgtcgacgat ctttctgatt ggttttcaaa ttgccagttc gcttgggatt 1080

gtgctgcttt caacgccgac tgggatactc tttgaccacg caggctacca gacagttttc 1140

ttcgcaattt cgggtattgt ctgcctgatg ttgctatttg gcattttctt cttgagtaaa 1200

aaacgcgagc aaatagttat ggaaacgcct gtaccttcag caatatag 1248

<210> 102
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant sucrose transporter

<400> 102

Met Ala Leu Asn Ile Pro Phe Arg Asn Ala Tyr Tyr Arg Phe Ala Ser
1 5 10 15

Ser Tyr Ser Phe Leu Phe Phe Ile Ser Trp Ser Leu Trp Trp Ser Leu
20 25 30

Tyr Ala Ile Trp Leu Lys Gly His Leu Gly Leu Thr Gly Thr Glu Leu
35 40 45

Gly Thr Leu Tyr Ser Val Asn Gln Phe Thr Ser Ile Leu Phe Met Met
50 55 60

```
Phe Tyr Gly Ile Val Gln Asp Lys Leu Gly Leu Lys Lys Pro Leu Ile
65                  70                  75                  80

Trp Cys Met Ser Phe Ile Leu Val Leu Thr Gly Pro Phe Met Ile Tyr
                85                  90                  95

Val Tyr Glu Pro Leu Leu Gln Ser Asn Phe Ser Val Gly Leu Ile Leu
            100                 105                 110

Gly Ala Leu Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Leu
        115                 120                 125

Asp Ser Phe Thr Glu Lys Met Ala Arg Asn Phe His Phe Glu Tyr Gly
    130                 135                 140

Thr Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Gly Ala Phe Phe
145                 150                 155                 160

Ala Gly Ile Phe Phe Ser Ile Ser Pro His Ile Asn Phe Trp Leu Val
                165                 170                 175

Ser Leu Phe Gly Ala Val Phe Met Met Ile Asn Met Arg Phe Lys Asp
            180                 185                 190

Lys Asp His Gln Cys Val Ala Ala Asp Ala Gly Gly Val Lys Lys Glu
        195                 200                 205

Asp Phe Ile Ala Val Phe Lys Asp Arg Asn Phe Trp Val Phe Val Ile
    210                 215                 220

Phe Ile Val Gly Thr Trp Ser Phe Tyr Asn Ile Phe Asp Gln Gln Leu
225                 230                 235                 240

Phe Pro Val Phe Tyr Ser Gly Leu Phe Glu Ser His Asp Val Gly Thr
                245                 250                 255

Arg Leu Tyr Gly Tyr Leu Asn Ser Phe Gln Val Val Leu Glu Ala Leu
            260                 265                 270

Cys Met Ala Ile Ile Pro Phe Phe Val Asn Arg Val Gly Pro Lys Asn
        275                 280                 285

Ala Leu Leu Ile Gly Val Val Ile Met Ala Leu Leu Ile Leu Ser Cys
    290                 295                 300

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
305                 310                 315                 320

Ala Ile Glu Val Pro Leu Cys Val Ile Ser Val Phe Lys Tyr Ser Val
                325                 330                 335
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Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile Phe Leu Ile Gly Phe
340 345 350

Gln Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
355 360 365

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
370 375 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
385 390 395 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
405 410 415

<210> 103
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for variant sucrose transporter

<400> 103
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ctcttttta tttcctggtc gctgtggtgg tcgttatacg ctatttggct gaaaggacat 120

ctagggttga cagggacgga attaggtaca ctttattcgg tcaaccagtt taccagcatt 180

ctatttatga tgttctacgg catcgttcag gataaactcg gtctgaagaa accgctcatc 240

tggtgtatga gtttcatcct ggtcttgacc ggaccgttta tgatttacgt ttatgaaccg 300

ttactgcaaa gcaatttttc tgtaggtcta attctggggg cgctattttt tggcttgggg 360

tatctggcgg gatgcggttt gcttgatagc ttcaccgaaa aaatggcgcg aaattttcat 420

ttcgaatatg gaacagcgcg cgcctgggga tcttttggct atgctattgg cgcgttcttt 480

gccggcatat tttttagtat cagtccccat atcaacttct ggttggtctc gctatttggc 540

gctgtattta tgatgatcaa catgcgtttt aaagataagg atcaccagtg cgtagcggca 600

gatgcgggag gggtaaaaaa agaggatttt atcgcagttt tcaaggatcg aaacttctgg 660

gttttcgtca tatttattgt ggggacgtgg tctttctata acatttttga tcaacaactt 720

tttcctgtct tttattcagg tttattcgaa tcacacgatg taggaacgcg cctgtatggt 780

tatctcaact cattccaggt ggtactcgaa gcgctgtgca tggcgattat tcctttcttt 840

gtgaatcggg tagggccaaa aaatgcatta cttatcggag ttgtgattat ggcgttggcg 900

atcctttcct gcgcgctgtt cgttaacccc tggattattt cattagtgaa gttgttacat 960

gccattgagg ttccactttg tgtcatatcc gtcttcaaat acagcgtggc aaactttgat 1020

aagcgcctgt cgtcgacgat ctttctgatt ggttttcaca ttgccagttc gcttgggatt 1080

gtgctgcttt caacgccgac tgggatactc tttgaccacg caggctacca gacagttttc 1140

ttcgcaattt cgggtattgt ctgcctgatg ttgctatttg gcattttctt cttgagtaaa 1200

aaacgcgagc aaatagttat ggaaacgcct gtaccttcag caatatag 1248

<210> 104
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant sucrose transporter

<400> 104

Met Ala Leu Asn Ile Pro Phe Arg Asn Ala Tyr Tyr Arg Phe Ala Ser
1 5 10 15

Ser Tyr Ser Phe Leu Phe Phe Ile Ser Trp Ser Leu Trp Trp Ser Leu
20 25 30

Tyr Ala Ile Trp Leu Lys Gly His Leu Gly Leu Thr Gly Thr Glu Leu
35 40 45

Gly Thr Leu Tyr Ser Val Asn Gln Phe Thr Ser Ile Leu Phe Met Met
50 55 60

Phe Tyr Gly Ile Val Gln Asp Lys Leu Gly Leu Lys Lys Pro Leu Ile
65 70 75 80

Trp Cys Met Ser Phe Ile Leu Val Leu Thr Gly Pro Phe Met Ile Tyr
85 90 95

Val Tyr Glu Pro Leu Leu Gln Ser Asn Phe Ser Val Gly Leu Ile Leu
100 105 110

Gly Ala Leu Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Leu
115 120 125

Asp Ser Phe Thr Glu Lys Met Ala Arg Asn Phe His Phe Glu Tyr Gly
130 135 140

Thr Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Gly Ala Phe Phe
145 150 155 160

Ala Gly Ile Phe Phe Ser Ile Ser Pro His Ile Asn Phe Trp Leu Val
165 170 175

Ser Leu Phe Gly Ala Val Phe Met Met Ile Asn Met Arg Phe Lys Asp
180 185 190

Lys Asp His Gln Cys Val Ala Ala Asp Ala Gly Gly Val Lys Lys Glu
195 200 205

Asp Phe Ile Ala Val Phe Lys Asp Arg Asn Phe Trp Val Phe Val Ile
210 215 220

Phe Ile Val Gly Thr Trp Ser Phe Tyr Asn Ile Phe Asp Gln Gln Leu
225 230 235 240

Phe Pro Val Phe Tyr Ser Gly Leu Phe Glu Ser His Asp Val Gly Thr
245 250 255

Arg Leu Tyr Gly Tyr Leu Asn Ser Phe Gln Val Val Leu Glu Ala Leu
260 265 270

Cys Met Ala Ile Ile Pro Phe Phe Val Asn Arg Val Gly Pro Lys Asn
275 280 285

Ala Leu Leu Ile Gly Val Val Ile Met Ala Leu Ala Ile Leu Ser Cys
290 295 300

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
305 310 315 320

Ala Ile Glu Val Pro Leu Cys Val Ile Ser Val Phe Lys Tyr Ser Val
325 330 335

Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile Phe Leu Ile Gly Phe
340 345 350

His Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
355 360 365

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
370 375 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
385 390 395 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
405 410 415

<210> 105
<211> 1248
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for variant sucrose transporter

<400> 105
atggcactga atattccatt cagaaatgcg tactatcgtt ttgcatccag ttactcattt 60

ctctttttta tttcctggtc gctgtggtgg tcgttatacg ctatttggct gaaaggacat 120

ctagggttga cagggacgga attaggtaca ctttattcgg tcaaccagtt taccagcatt 180

ccatttatga tgttctacgg catcgttcag gataaactcg gtctgaagaa accgctcatc 240

tggtgtatga gtttcatcct ggtcttgacc ggaccgttta tgatttacgt ttatgaaccg 300

ttactgcaaa gcaatttttc tgtaggtcta attctggggg cgctattttt tggcttgggg 360

tatctggcgg gatgcggttt gcttgatagc ttcaccgaaa aaatggcgcg aaattttcat 420

ttcgaatatg gaacagcgcg cgcctgggga tcttttggct atgctattgg cgcgttcttt 480

gccggcatat tttttagtat cagtccccat atcaacttct ggttggtctc gctatttggc 540

gctgtattta tgatgatcaa catgcgtttt aaagataagg atcaccagtg cgtagcggca 600

gatgcgggag gggtaaaaaa agaggatttt atcgcagttt tcaaggatcg aaacttctgg 660

gttttcgtca tatttattgt ggggacgtgg tctttctata acatttttga tcaacaactt 720

tttcctgtct tttattcagg tttattcgaa tcacacgatg taggaacgcg cctgtatggt 780

tatctcaact cattccaggt ggtactcgaa gcgctgtgca tggcgattat tcctttcttt 840

gtgaatcggg tagggccaaa aaatgcatta cttatcggag ttgtgattat ggcgttggcg 900

atcctttcct gcgcgctgtt cgttaacccc tggattattt cattagtgaa gttgttacat 960

gccattgcgg ttccactttg tgtcatatcc gtcttcaaat acagcgtggc aaactttgat 1020

aagcgcctgt cgtcgacgat ctttctgatt ggttttcaca ttgccagttc gcttgggatt 1080

gtgctgcttt caacgccgac tgggatactc tttgaccacg caggctacca gacagttttc 1140

ttcgcaattt cgggtattgt ctgcctgatg ttgctatttg gcattttctt cttgagtaaa 1200

aaacgcgagc aaatagttat ggaaacgcct gtaccttcag caatatag 1248

<210> 106
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant sucrose transporter

<400> 106

Met Ala Leu Asn Ile Pro Phe Arg Asn Ala Tyr Tyr Arg Phe Ala Ser
1 5 10 15

Ser Tyr Ser Phe Leu Phe Phe Ile Ser Trp Ser Leu Trp Trp Ser Leu
20 25 30

Tyr Ala Ile Trp Leu Lys Gly His Leu Gly Leu Thr Gly Thr Glu Leu
35 40 45

Gly Thr Leu Tyr Ser Val Asn Gln Phe Thr Ser Ile Pro Phe Met Met
50 55 60

Phe Tyr Gly Ile Val Gln Asp Lys Leu Gly Leu Lys Lys Pro Leu Ile
65 70 75 80

Trp Cys Met Ser Phe Ile Leu Val Leu Thr Gly Pro Phe Met Ile Tyr
85 90 95

```
Val Tyr Glu Pro Leu Leu Gln Ser Asn Phe Ser Val Gly Leu Ile Leu
            100                 105                 110

Gly Ala Leu Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Leu
        115                 120                 125

Asp Ser Phe Thr Glu Lys Met Ala Arg Asn Phe His Phe Glu Tyr Gly
    130                 135                 140

Thr Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Gly Ala Phe Phe
145                 150                 155                 160

Ala Gly Ile Phe Phe Ser Ile Ser Pro His Ile Asn Phe Trp Leu Val
                165                 170                 175

Ser Leu Phe Gly Ala Val Phe Met Met Ile Asn Met Arg Phe Lys Asp
            180                 185                 190

Lys Asp His Gln Cys Val Ala Ala Asp Ala Gly Gly Val Lys Lys Glu
        195                 200                 205

Asp Phe Ile Ala Val Phe Lys Asp Arg Asn Phe Trp Val Phe Val Ile
    210                 215                 220

Phe Ile Val Gly Thr Trp Ser Phe Tyr Asn Ile Phe Asp Gln Gln Leu
225                 230                 235                 240

Phe Pro Val Phe Tyr Ser Gly Leu Phe Glu Ser His Asp Val Gly Thr
                245                 250                 255

Arg Leu Tyr Gly Tyr Leu Asn Ser Phe Gln Val Val Leu Glu Ala Leu
            260                 265                 270

Cys Met Ala Ile Ile Pro Phe Phe Val Asn Arg Val Gly Pro Lys Asn
        275                 280                 285

Ala Leu Leu Ile Gly Val Val Ile Met Ala Leu Ala Ile Leu Ser Cys
    290                 295                 300

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
305                 310                 315                 320

Ala Ile Ala Val Pro Leu Cys Val Ile Ser Val Phe Lys Tyr Ser Val
                325                 330                 335

Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile Phe Leu Ile Gly Phe
            340                 345                 350

His Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
        355                 360                 365
```

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
370 375 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
385 390 395 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
405 410 415

<210> 107
<211> 1261
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for variant sucrose transporter

<400> 107
atgaaaatca atatgccgtt ctccaatgac aaataccgtt atagttcggg ctacctgctg 60

ttcttcttcg ctgcgtggtc cctgtggtgg agtttctacg caatctggct gaaaaacaaa 120

ctgggcctgt ccggcaccga actgggcatg ctgtatgctg ttaatcagtt tttctccatg 180

ctgttcatgc tggtctacgg ctttctgcaa gataaactgg gcacccgtaa acatctgatt 240

tggctgatgg gcattgtgat cacgctgtca ggtccgttcc tgatctatgt ttacgaaccg 300

ctgctgacct cgaactttaa actgggcatg gcactgggtg ctattttctt tggtctgggt 360

tatctggcag gttgcggcct ggtggaatct tttgtggaaa aagtttctcg taaattcaac 420

ttcgaatttg gcaccgcacg tctgtggggc tctctgggtt acgcggccgg tacgttcgtt 480

ggcggtattt tctttagcat caacccgcac attaattttt ggtgtgtctc tgtgatgggc 540

gtcctgttcc tgctgatcaa cgtgctgttt aaaaccaata gtccggcacc gagctctgtg 600

aaaacccgtt ccccggaacc ggatgctctg acgcgcaaag acttcctgac catctttaaa 660

gatacgcagt tctggttttt cgttattttt gtggttggca cgtggagttt ctattccatc 720

tacgaccagc aaatgttccc ggtgttttat gcgagcctgt ttgatgaccc ggaactggcc 780

ccgcgtgttt atggttacct gaactctgtt caagtcttca tggaagcggt tggcatggcc 840

ctggtcccgt ttctgattaa tcgtatcggt ccgaaaagcg cactgctgct gggcggcacc 900

atcatggcat gcgcgattct gggttcagct ctgtttacgg atatctacat catctcgctg 960

atcaaaatgc tgcatgcgct ggaagtcccg ctgttcgtca tttcagtgtt caaattttcg 1020

gtggccaact ttgacaaacg cctgagttcc accatttacc tgatcggctt taatatcgcg 1080

tcatcgattg gtattatcgt gctgagtctg ccggttggca aactgttcga taaagttggt 1140

tatcaggaaa tttttctgat catggccagc atcgtcatta tcaccctgat tttcggctac 1200

tttagcctgt ctaaaaaaca tcaccagcaa aaaatgggta acgaactggt gacggaataa 1260

c 1261

<210> 108
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant sucrose transporter

<400> 108

Met Lys Ile Asn Met Pro Phe Ser Asn Asp Lys Tyr Arg Tyr Ser Ser
1 5 10 15

Gly Tyr Leu Leu Phe Phe Phe Ala Ala Trp Ser Leu Trp Trp Ser Phe
20 25 30

Tyr Ala Ile Trp Leu Lys Asn Lys Leu Gly Leu Ser Gly Thr Glu Leu
35 40 45

Gly Met Leu Tyr Ala Val Asn Gln Phe Phe Ser Met Leu Phe Met Leu
50 55 60

Val Tyr Gly Phe Leu Gln Asp Lys Leu Gly Thr Arg Lys His Leu Ile
65 70 75 80

Trp Leu Met Gly Ile Val Ile Thr Leu Ser Gly Pro Phe Leu Ile Tyr
85 90 95

Val Tyr Glu Pro Leu Leu Thr Ser Asn Phe Lys Leu Gly Met Ala Leu
100 105 110

Gly Ala Ile Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Val
115 120 125

Glu Ser Phe Val Glu Lys Val Ser Arg Lys Phe Asn Phe Glu Phe Gly
130 135 140

Thr Ala Arg Leu Trp Gly Ser Leu Gly Tyr Ala Ala Gly Thr Phe Val
145 150 155 160

Gly Gly Ile Phe Phe Ser Ile Asn Pro His Ile Asn Phe Trp Cys Val
165 170 175

Ser Val Met Gly Val Leu Phe Leu Leu Ile Asn Val Leu Phe Lys Thr
180 185 190

Asn Ser Pro Ala Pro Ser Ser Val Lys Thr Arg Ser Pro Glu Pro Asp
195 200 205

Ala Leu Thr Arg Lys Asp Phe Leu Thr Ile Phe Lys Asp Thr Gln Phe
210 215 220

Trp Phe Phe Val Ile Phe Val Val Gly Thr Trp Ser Phe Tyr Ser Ile
225 230 235 240

Tyr Asp Gln Gln Met Phe Pro Val Phe Tyr Ala Ser Leu Phe Asp Asp
245 250 255

Pro Glu Leu Ala Pro Arg Val Tyr Gly Tyr Leu Asn Ser Val Gln Val
260 265 270

Phe Met Glu Ala Val Gly Met Ala Leu Val Pro Phe Leu Ile Asn Arg
275 280 285

Ile Gly Pro Lys Ser Ala Leu Leu Leu Gly Gly Thr Ile Met Ala Cys
290 295 300

Ala Ile Leu Gly Ser Ala Leu Phe Thr Asp Ile Tyr Ile Ile Ser Leu
305 310 315 320

Ile Lys Met Leu His Ala Leu Glu Val Pro Leu Phe Val Ile Ser Val
325 330 335

Phe Lys Phe Ser Val Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile
340 345 350

Tyr Leu Ile Gly Phe Asn Ile Ala Ser Ser Ile Gly Ile Ile Val Leu
355 360 365

Ser Leu Pro Val Gly Lys Leu Phe Asp Lys Val Gly Tyr Gln Glu Ile
370 375 380

Phe Leu Ile Met Ala Ser Ile Val Ile Ile Thr Leu Ile Phe Gly Tyr
385 390 395 400

Phe Ser Leu Ser Lys Lys His His Gln Gln Lys Met Gly Asn Glu Leu
405 410 415

Val Thr Glu

<210> 109
<211> 1261
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for variant sucrose transporter

<400> 109
atgaaaatca atatgccgtt ctccaatgac aaataccgtt atagttcggg ctacctgctg 60

ttcttcttcg ctgcgtggtc cctgtggtgg agtttctacg caatctggct gaaaaacaaa 120

ctgggcctgt ccggcaccga actgggcatg ctgtatgctg ttaatcagtt tttctccatg 180

ctgttcatgc tggtctacgg ctttctgcaa gataaactgg gcacccgtaa acatctgatt 240

tggctgatgg gcattgtgat cacgctgtca ggtccgttcc tgatctatgt ttacgaaccg 300

ctgctgacct cgaactttaa actgggcatg gcactgggtg ctattttctt tggtctgggt 360

tatctggcag gttgcggcct ggtggaatct tttgtggaaa aagtttctcg taaattcaac 420

ttcgaatttg gcaccgcacg tctgtggggc tctctgggtt acgcggccgg tacgttcgtt 480

ggcggtattt tctttagcat caacccgcac attaattttt ggtgtgtctc tgtgatgggc 540

gtcctgttcc tgctgatcaa cgtgctgttt aaaaccaata gtccggcacc gagctctgtg 600

aaaacccgtt ccccggaacc ggatgctctg acgcgcaaag acttcctgac catctttaaa 660

gatacgcagt tctggttttt cgttattttt gtggttggca cgtggagttt ctattccatc 720

tacgaccagc aaatgttccc ggtgttttat gcgagcctgt ttgatgaccc ggaactggcc 780

ccgcgtgttt atggttacct gaactctgtt caagtcttca tggaagcggt tggcatggcc 840

ctggtcccgt ttctgattaa tcgtatcggt ccgaaaagcg cactgctgct gggcggcacc 900

atcatggcat gcctgattct gggttcagct ctgtttacgg atatctacat catctcgctg 960

atcaaaatgc tgcatgcgct ggaagtcccg ctgttcgtca tttcagtgtt caaattttcg 1020

gtggccaact ttgacaaacg cctgagttcc accatttacc tgatcggctt taatatcgcg 1080

tcatcgattg gtattatcgt gctgagtctg ccggttggca aactgttcga taaagttggt 1140

tatcaggaaa tttttctgat catggccagc atcgtcatta tcaccctgat tttcggctac 1200

tttagcctgt ctaaaaaaca tcaccagcaa aaaatgggta acgaactggt gacggaataa 1260

c 1261

<210> 110
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant sucrose transporter

<400> 110

Met Lys Ile Asn Met Pro Phe Ser Asn Asp Lys Tyr Arg Tyr Ser Ser
1 5 10 15

Gly Tyr Leu Leu Phe Phe Phe Ala Ala Trp Ser Leu Trp Trp Ser Phe
20 25 30

Tyr Ala Ile Trp Leu Lys Asn Lys Leu Gly Leu Ser Gly Thr Glu Leu
35 40 45

Gly Met Leu Tyr Ala Val Asn Gln Phe Phe Ser Met Leu Phe Met Leu
50 55 60

Val Tyr Gly Phe Leu Gln Asp Lys Leu Gly Thr Arg Lys His Leu Ile
65 70 75 80

Trp Leu Met Gly Ile Val Ile Thr Leu Ser Gly Pro Phe Leu Ile Tyr
85 90 95

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Val Tyr Glu Pro Leu Leu Thr Ser Asn Phe Lys Leu Gly Met Ala Leu
            100                 105                 110

Gly Ala Ile Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Val
        115                 120                 125

Glu Ser Phe Val Glu Lys Val Ser Arg Lys Phe Asn Phe Glu Phe Gly
    130                 135                 140

Thr Ala Arg Leu Trp Gly Ser Leu Gly Tyr Ala Ala Gly Thr Phe Val
145                 150                 155                 160

Gly Gly Ile Phe Phe Ser Ile Asn Pro His Ile Asn Phe Trp Cys Val
                165                 170                 175

Ser Val Met Gly Val Leu Phe Leu Leu Ile Asn Val Leu Phe Lys Thr
            180                 185                 190

Asn Ser Pro Ala Pro Ser Ser Val Lys Thr Arg Ser Pro Glu Pro Asp
        195                 200                 205

Ala Leu Thr Arg Lys Asp Phe Leu Thr Ile Phe Lys Asp Thr Gln Phe
    210                 215                 220

Trp Phe Phe Val Ile Phe Val Val Gly Thr Trp Ser Phe Tyr Ser Ile
225                 230                 235                 240

Tyr Asp Gln Gln Met Phe Pro Val Phe Tyr Ala Ser Leu Phe Asp Asp
                245                 250                 255

Pro Glu Leu Ala Pro Arg Val Tyr Gly Tyr Leu Asn Ser Val Gln Val
            260                 265                 270

Phe Met Glu Ala Val Gly Met Ala Leu Val Pro Phe Leu Ile Asn Arg
        275                 280                 285

Ile Gly Pro Lys Ser Ala Leu Leu Leu Gly Gly Thr Ile Met Ala Cys
    290                 295                 300

Leu Ile Leu Gly Ser Ala Leu Phe Thr Asp Ile Tyr Ile Ile Ser Leu
305                 310                 315                 320

Ile Lys Met Leu His Ala Leu Glu Val Pro Leu Phe Val Ile Ser Val
                325                 330                 335

Phe Lys Phe Ser Val Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile
            340                 345                 350

Tyr Leu Ile Gly Phe Asn Ile Ala Ser Ser Ile Gly Ile Ile Val Leu
        355                 360                 365
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Ser Leu Pro Val Gly Lys Leu Phe Asp Lys Val Gly Tyr Gln Glu Ile
370 375 380

Phe Leu Ile Met Ala Ser Ile Val Ile Ile Thr Leu Ile Phe Gly Tyr
385 390 395 400

Phe Ser Leu Ser Lys Lys His His Gln Gln Lys Met Gly Asn Glu Leu
405 410 415

Val Thr Glu

<210> 111
<211> 1339
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for variant sucrose transporter

<400> 111
atggcgtcag cgaccaaatc ggcgtggaaa aacccgtcct atctgcaatc ctcattcggc 60

atcttcatgt tcttctgttc gtggggcatt tggtggtcat ttttccagcg ttggctgatc 120

tcgggcgtgg gtctgacgaa cgccgaagtt ggcaccattt atagcatcaa ttctctggca 180

accctggtga ttatgtttgt gtacggcgtt attcaggatc aactgggtat caaacgtaaa 240

ctggttattg tggttagcgt catcgcggcc tgcgtgggtc cgtttgtcca gttcgtgtat 300

gcaccgatga ttctggcggg cggcaccacg cgttggatcg gtgctctgat tggttcaatc 360

gtgctgtcgg cgggctttat gagtggttgc tccctgttcg aagctgttac cgaacgttat 420

tctcgcaaat ttggcttcga atacggtcag agccgcgcct ggggctcttt tggttatgca 480

attgtggctc tgtgtgcggg ctttctgttc aacattaatc cgctgatcaa cttttgggtt 540

ggttcagcat tcggtccggg catgctgctg gtttacgctt tttgggtccc ggcggaacaa 600

aaagaagaac tgaaaaaaga aacggatccg aacgcagctc cgaccaatcc gtcgctgaaa 660

gaaatggttg cggtcctgaa aatgccgacg ctgtgggttc tgattgtctt tatgctgctg 720

accaacacgt tttataccgt gttcgaccag caaatgtttc cgacgtatta cgctaacctg 780

tttccgaccg aagaaatcgg caacgcgacc tacggcacgc tgaatggttt tcaggttttc 840

ctggaaagcg ccatgatggg tgtcgtgccg attatcatga agaaaattgg cgttcgtaat 900

gccctgctgc tgggtgcaac ggtcatgttt ctggcgatcg gcctgtgcgg tgtgttccat 960

gatccggtta ccattagtat cgtcaaactg tttcactcca ttgaagtgcc gctgttctgt 1020

ctgccggcgt ttcgttattt caccctgcat tttgacacga aactgagcgc caccctgtac 1080

atggttggct tccagattgc aagccaagtg ggtcaagtta tcttttctac gccgctgggc 1140

gccttccacg ataaaatggc acaaatcctg ccgaacaatg acatgggtag tcgtgtcacc 1200

ttttgggtga tttccgctat cgtgctgtgt gcgctgattt atggcttttt cgtcatcaaa 1260

catgatgacc aggaagtggg cggtgatccg ttctacaccg acaaacaact gcgccaaatg 1320

gaagcggcca aagcgtaac 1339

<210> 112
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant sucrose transporter

<400> 112

Met Ala Ser Ala Thr Lys Ser Ala Trp Lys Asn Pro Ser Tyr Leu Gln
1 5 10 15

Ser Ser Phe Gly Ile Phe Met Phe Phe Cys Ser Trp Gly Ile Trp Trp
20 25 30

Ser Phe Phe Gln Arg Trp Leu Ile Ser Gly Val Gly Leu Thr Asn Ala
35 40 45

Glu Val Gly Thr Ile Tyr Ser Ile Asn Ser Leu Ala Thr Leu Val Ile
50 55 60

Met Phe Val Tyr Gly Val Ile Gln Asp Gln Leu Gly Ile Lys Arg Lys
65 70 75 80

Leu Val Ile Val Val Ser Val Ile Ala Ala Cys Val Gly Pro Phe Val
85 90 95

Gln Phe Val Tyr Ala Pro Met Ile Leu Ala Gly Gly Thr Thr Arg Trp
100 105 110

Ile Gly Ala Leu Ile Gly Ser Ile Val Leu Ser Ala Gly Phe Met Ser
115 120 125

Gly Cys Ser Leu Phe Glu Ala Val Thr Glu Arg Tyr Ser Arg Lys Phe
130 135 140

Gly Phe Glu Tyr Gly Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr Ala
145 150 155 160

Ile Val Ala Leu Cys Ala Gly Phe Leu Phe Asn Ile Asn Pro Leu Ile
165 170 175

Asn Phe Trp Val Gly Ser Ala Phe Gly Pro Gly Met Leu Leu Val Tyr
180 185 190

Ala Phe Trp Val Pro Ala Glu Gln Lys Glu Glu Leu Lys Lys Glu Thr
195 200 205

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Asp Pro Asn Ala Ala Pro Thr Asn Pro Ser Leu Lys Glu Met Val Ala
    210                 215                 220

Val Leu Lys Met Pro Thr Leu Trp Val Leu Ile Val Phe Met Leu Leu
225                 230                 235                 240

Thr Asn Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Thr Tyr
                245                 250                 255

Tyr Ala Asn Leu Phe Pro Thr Glu Glu Ile Gly Asn Ala Thr Tyr Gly
            260                 265                 270

Thr Leu Asn Gly Phe Gln Val Phe Leu Glu Ser Ala Met Met Gly Val
        275                 280                 285

Val Pro Ile Ile Met Lys Lys Ile Gly Val Arg Asn Ala Leu Leu Leu
    290                 295                 300

Gly Ala Thr Val Met Phe Leu Ala Ile Gly Leu Cys Gly Val Phe His
305                 310                 315                 320

Asp Pro Val Thr Ile Ser Ile Val Lys Leu Phe His Ser Ile Glu Val
                325                 330                 335

Pro Leu Phe Cys Leu Pro Ala Phe Arg Tyr Phe Thr Leu His Phe Asp
            340                 345                 350

Thr Lys Leu Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser
        355                 360                 365

Gln Val Gly Gln Val Ile Phe Ser Thr Pro Leu Gly Ala Phe His Asp
    370                 375                 380

Lys Met Ala Gln Ile Leu Pro Asn Asn Asp Met Gly Ser Arg Val Thr
385                 390                 395                 400

Phe Trp Val Ile Ser Ala Ile Val Leu Cys Ala Leu Ile Tyr Gly Phe
                405                 410                 415

Phe Val Ile Lys His Asp Asp Gln Glu Val Gly Gly Asp Pro Phe Tyr
            420                 425                 430

Thr Asp Lys Gln Leu Arg Gln Met Glu Ala Ala Lys Ala
        435                 440                 445
```

<210> 113
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid

<400> 113
aggaattccc taggcgatct gtgctgtttg ccacggtatg cagcaccagc gcgagattat 60

gggctcgcac gctcgactgt cggacggggg cactggaacg agaagtcagg cgagccgtca 120

cgcccttgac tatgccacat cctgagcaaa taattcaacc actaaacaaa tcaaccgcgt 180

ttcccggagg taaccaagct tgcccggatc cgcatgcgcg gccgcgtcga ctctagttta 240

aacccccggg tgatcgatag ctcttaatta agttgtttgc caatgtaatg ccgctgcacc 300

caggcatcaa ataaaacgaa aggctcagtc gaaagactgg gcctttcgtt ttatctgttg 360

tttgtcggtg aacgctctct actagagtca cactggctca ccttcgggtg ggcctttctg 420

cgtttataca gctgtcggta ccgccag 447

<210> 114
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> Plasmid

<400> 114
aggaattccc taggcgatct gtgctgtttg ccacggtatg cagcaccagc gcgagattat 60

gggctcgcac gctcgactgt cggacggggg cactggaacg agaagtcagg cgagccgtca 120

cgcccttgac gatgccacat cctgagcaaa taattcaacc actaaacaaa tcaaccgcgt 180

ttcccggagg taaccaagct tgcccggatc cgcatgcgcg gccgcgtcga ctctagttta 240

aacccccggg tgatcgatag ctcttaatta agttgtttgc caatgtaatg ccgctgcacc 300

caggcatcaa ataaaacgaa aggctcagtc gaaagactgg gcctttcgtt ttatctgttg 360

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gccttccacg ataaaatggc acaaatcctg ccgaacaatg acatgggtag tcgtgtcacc 1200

ttttgggtga tttccgctat cgtgctgtgt gcgctgattt atggcttttt cgtcatcaaa 1260

catgatgacc aggaagtggg cggtgatccg ttctacaccg acaaacaact gcgccaaatg 1320

gaagcggcca aagcgtaa 1338

<210> 127
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 127
gcaccatcat ggcatgcgcg attctgggtt cagctct 37

<210> 128
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 128
agagctgaac ccagaatcgc gcatgccatg atggtgc 37

<210> 129
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 129
caccatcatg gcatgcctga ttctgggttc agctct 36

<210> 130
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 130
agagctgaac ccagaatcag gcatgccatg atggtg 36

<210> 131
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 131
aacggtcatg tttctggcga tcggcctgtg cggtg 35

<210> 132
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 132
caccgcacag gccgatcgcc agaaacatga ccgtt 35

<210> 133
<211> 1476
<212> DNA
<213> Pseudomonas fluorescens

<400> 133
atgcacgctg cactgttaga gcaagcgcat cgcgctattg aaaaaaaact gcctgggcgg 60

ggtgatgtct atcgcctggc ctatcatctt gcgccgccgg tggggtggat gaatgacccg 120

aacggtctgg tttattttcg cggcgagtac catgtgttct accaacatca tccctattcg 180

gctcagtggg ggccgatgca ctggggccat gccaagagcc gtgacctggt gcactgggag 240

cacctgccca tcgcgctggc gccgggcgag gcctatgacc gcgacggttg cttttcaggg 300

tctgcggtgg tcatggacga cgtgttgtac ctgatttaca ccgggcatac ctggctgggt 360

gcgcccggtg acgagcggag cattcgccag gttcagtgcc tggccagcag caccgacggg 420

gttgcgttca gcaagcacgg gccggtgatc gatagggcgc ctgaaccggg catcatgcat 480

tttcgcgacc ccaaggtatg gcggcgagga gagcaatggt ggatggccct gggggcgcgc 540

caaggcgacg cccctcagct cctgctctat cgctcaggcg acctgcatca ctggacgtac 600

ctcaggtgcg cactgcaagg gcaacgagag tcggacggct atatgtggga gtgtcctgac 660

ctgttcgaac tcgatggctg tgatgtgttt ctctattcgc ctcaaggctt gaaccccagc 720

ggttatgaca actggaacaa gttccagaac agctatcgga tgggcctgct ggacgatcgc 780

ggatacttca gcgagggcgg tgagctgcgt gaactggatc atggtcacga tttctatgcg 840

gcgcagacct tgctggcgcc agacgggcga cgcctgttgt gggcttggat ggacatgtgg 900

gacagcccga tgccgagtca ggcgcaacac tggtgcggtg cgctgtcgct acctcgtgaa 960

ctgagccgca atggcgaacg gctacgcatg cggccggccc gcgagttggc agcgctacgc 1020

cagtcgcaac ggacactggc gatcggcgtg gtcgaatccg gcaattgcat actcgctgag 1080

cgaggggcgc tgctggaatt cgaactgacc ctggacctgg ctggtagcac ggctgagcgt 1140

ttcgggttgg cgctgcgttg tagtgaggat cggcaagagc ggaccctggt gtacttcgat 1200

gcgatggcgc ggcgtctggt gctggacagg caacactcgg gagcgggggt aagcggtgcg 1260

cgcagcgtgc cgatagccaa gggccaaatg cagatagcct tgcggatttt ccttgatcga 1320

tcctccattg aggtgtttgt cgatgacgga gcctatagct tgagcagtcg gatctaccct 1380

agccccgaca gcgtggcggt catggcgttt gcggtcaatg gtagcggtgg ttttggccaa 1440

gcgtcggtct ggcacctggc cgatctgcac ctgtga 1476

<210> 134
<211> 491
<212> PRT
<213> Pseudomonas fluorescens

<400> 134

Met His Ala Ala Leu Leu Glu Gln Ala His Arg Ala Ile Glu Lys Lys
1 5 10 15

Leu Pro Gly Arg Gly Asp Val Tyr Arg Leu Ala Tyr His Leu Ala Pro
20 25 30

Pro Val Gly Trp Met Asn Asp Pro Asn Gly Leu Val Tyr Phe Arg Gly
35 40 45

Glu Tyr His Val Phe Tyr Gln His His Pro Tyr Ser Ala Gln Trp Gly
50 55 60

```
Pro Met His Trp Gly His Ala Lys Ser Arg Asp Leu Val His Trp Glu
65                  70                  75                  80

His Leu Pro Ile Ala Leu Ala Pro Gly Glu Ala Tyr Asp Arg Asp Gly
                85                  90                  95

Cys Phe Ser Gly Ser Ala Val Val Met Asp Asp Val Leu Tyr Leu Ile
            100                 105                 110

Tyr Thr Gly His Thr Trp Leu Gly Ala Pro Gly Asp Glu Arg Ser Ile
        115                 120                 125

Arg Gln Val Gln Cys Leu Ala Ser Ser Thr Asp Gly Val Ala Phe Ser
    130                 135                 140

Lys His Gly Pro Val Ile Asp Arg Ala Pro Glu Pro Gly Ile Met His
145                 150                 155                 160

Phe Arg Asp Pro Lys Val Trp Arg Arg Gly Glu Gln Trp Trp Met Ala
                165                 170                 175

Leu Gly Ala Arg Gln Gly Asp Ala Pro Gln Leu Leu Leu Tyr Arg Ser
            180                 185                 190

Gly Asp Leu His His Trp Thr Tyr Leu Arg Cys Ala Leu Gln Gly Gln
        195                 200                 205

Arg Glu Ser Asp Gly Tyr Met Trp Glu Cys Pro Asp Leu Phe Glu Leu
    210                 215                 220

Asp Gly Cys Asp Val Phe Leu Tyr Ser Pro Gln Gly Leu Asn Pro Ser
225                 230                 235                 240

Gly Tyr Asp Asn Trp Asn Lys Phe Gln Asn Ser Tyr Arg Met Gly Leu
                245                 250                 255

Leu Asp Asp Arg Gly Tyr Phe Ser Glu Gly Gly Glu Leu Arg Glu Leu
            260                 265                 270

Asp His Gly His Asp Phe Tyr Ala Ala Gln Thr Leu Leu Ala Pro Asp
        275                 280                 285

Gly Arg Arg Leu Leu Trp Ala Trp Met Asp Met Trp Asp Ser Pro Met
    290                 295                 300

Pro Ser Gln Ala Gln His Trp Cys Gly Ala Leu Ser Leu Pro Arg Glu
305                 310                 315                 320

Leu Ser Arg Asn Gly Glu Arg Leu Arg Met Arg Pro Ala Arg Glu Leu
                325                 330                 335
```

```
Ala Ala Leu Arg Gln Ser Gln Arg Thr Leu Ala Ile Gly Val Val Glu
            340                 345                 350

Ser Gly Asn Cys Ile Leu Ala Glu Arg Gly Ala Leu Leu Glu Phe Glu
        355                 360                 365

Leu Thr Leu Asp Leu Ala Gly Ser Thr Ala Glu Arg Phe Gly Leu Ala
    370                 375                 380

Leu Arg Cys Ser Glu Asp Arg Gln Glu Arg Thr Leu Val Tyr Phe Asp
385                 390                 395                 400

Ala Met Ala Arg Arg Leu Val Leu Asp Arg Gln His Ser Gly Ala Gly
                405                 410                 415

Val Ser Gly Ala Arg Ser Val Pro Ile Ala Lys Gly Gln Met Gln Ile
            420                 425                 430

Ala Leu Arg Ile Phe Leu Asp Arg Ser Ser Ile Glu Val Phe Val Asp
        435                 440                 445

Asp Gly Ala Tyr Ser Leu Ser Ser Arg Ile Tyr Pro Ser Pro Asp Ser
    450                 455                 460

Val Ala Val Met Ala Phe Ala Val Asn Gly Ser Gly Gly Phe Gly Gln
465                 470                 475                 480

Ala Ser Val Trp His Leu Ala Asp Leu His Leu
                485                 490
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<210> 135
<211> 1479
<212> DNA
<213> Bacillus licheniformis

<400> 135

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atgaacagaa ttcagcaggc agaagaagca ttaaagaaag ccgggaaaaa agtgaatcgc       60

cgttaccgaa tgggctatca catgatgccc cgggcaaact ggataaatga tccaaacgga      120

cttattcaat ataaagggga gtatcatgtc ttttatcaac atcatccgta tgatgagaat      180

tgggggccga tgcattgggg ccatttgaag agcaaggatc ttattcactg ggagcacttg      240

ccggttgctt tagcgccggg agacgaattt gatgagagcg gctgtttctc aggaagcgca      300

gtcgaatata acggcgacct cgctttaatc tatactgggc ataatatgat agatgaagag      360

aaagacgatt tctaccaaac tcagaatata gcagtcagca aagacggtat cgtctttgaa      420

aaactgaaag aaaaccctgt tattgcagag ccgccggaag acagcgcacg tcactttcgc      480

gatccaaaag tatggaagca tcgtgagaac tggtatatgg tggtcggaaa ctcctcaaaa      540

gagaacgtcg ggcgggtcat cttataccgc tcgcctaact ttgtagattg ggagtacgta      600

ggcgttctcg cccaaagcga cggaaatctc ggctttatgt gggaatgtcc ggatttcttt      660
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gaactagacg gcaaacacat tttgctgatt tcccctcagg gtatagaggc tgatggtgaa 720

tcatatcaaa atctgtatca aacaggctat ttgattggag actatgatga agaaacgaat 780

gagtttgtac atggctcctt taaagagttg gatcacggcc acgactttta tgccgtgcaa 840

actttattgg atgacaaagg ccgcagaatt gcgattggct ggatggatat gtgggagtca 900

gagatgccga cgaaagcaga cggatggtgc ggggcattaa ctttgccgcg tgaattgacg 960

ttgaaggatg gtcacaaaat tttaatgaat cccgtcgagg agactaaatt acttcgtgga 1020

tcggaacatc atgagtgtga caatcaatcg atttccggca gctattttat aaagacagcc 1080

gaaaagcttc ttgaagtggt ggccgttttt gatttgacaa tttgcagtgc cgaaacggtt 1140

ggcttaaaga tccggggaat tgaacaggaa gaaacaacca tcaagtacag cttgattgat 1200

caaaagctga cgctcgactg ttcaaagtcc ggcaaagcga gggacggtgt gagaaacgta 1260

cggcttgaag cggatgagaa gctcactttg catctgtttc tcgacagatc gtctattgaa 1320

gtatttgcaa atcatggtga agcgacaatg acaagccgca tatatccgaa ggaaggaaga 1380

gcggggattg agctgttttc tgagaaaggc aacgtacggg ttgaagaatt cacttactgg 1440

acgttgaaag atatttggaa aggtgatgaa gccaaatga 1479

<210> 136
<211> 492
<212> PRT
<213> Bacillus licheniformis

<400> 136

Met Asn Arg Ile Gln Gln Ala Glu Glu Ala Leu Lys Lys Ala Gly Lys
1 5 10 15

Lys Val Asn Arg Arg Tyr Arg Met Gly Tyr His Met Met Pro Arg Ala
20 25 30

Asn Trp Ile Asn Asp Pro Asn Gly Leu Ile Gln Tyr Lys Gly Glu Tyr
35 40 45

His Val Phe Tyr Gln His His Pro Tyr Asp Glu Asn Trp Gly Pro Met
50 55 60

His Trp Gly His Leu Lys Ser Lys Asp Leu Ile His Trp Glu His Leu
65 70 75 80

Pro Val Ala Leu Ala Pro Gly Asp Glu Phe Asp Glu Ser Gly Cys Phe
85 90 95

Ser Gly Ser Ala Val Glu Tyr Asn Gly Asp Leu Ala Leu Ile Tyr Thr
100 105 110

Gly His Asn Met Ile Asp Glu Glu Lys Asp Asp Phe Tyr Gln Thr Gln
115 120 125

```
Asn Ile Ala Val Ser Lys Asp Gly Ile Val Phe Glu Lys Leu Lys Glu
    130                 135                 140

Asn Pro Val Ile Ala Glu Pro Pro Glu Asp Ser Ala Arg His Phe Arg
145                 150                 155                 160

Asp Pro Lys Val Trp Lys His Arg Glu Asn Trp Tyr Met Val Val Gly
                165                 170                 175

Asn Ser Ser Lys Glu Asn Val Gly Arg Val Ile Leu Tyr Arg Ser Pro
            180                 185                 190

Asn Phe Val Asp Trp Glu Tyr Val Gly Val Leu Ala Gln Ser Asp Gly
        195                 200                 205

Asn Leu Gly Phe Met Trp Glu Cys Pro Asp Phe Phe Glu Leu Asp Gly
    210                 215                 220

Lys His Ile Leu Leu Ile Ser Pro Gln Gly Ile Glu Ala Asp Gly Glu
225                 230                 235                 240

Ser Tyr Gln Asn Leu Tyr Gln Thr Gly Tyr Leu Ile Gly Asp Tyr Asp
                245                 250                 255

Glu Glu Thr Asn Glu Phe Val His Gly Ser Phe Lys Glu Leu Asp His
            260                 265                 270

Gly His Asp Phe Tyr Ala Val Gln Thr Leu Leu Asp Asp Lys Gly Arg
        275                 280                 285

Arg Ile Ala Ile Gly Trp Met Asp Met Trp Glu Ser Glu Met Pro Thr
    290                 295                 300

Lys Ala Asp Gly Trp Cys Gly Ala Leu Thr Leu Pro Arg Glu Leu Thr
305                 310                 315                 320

Leu Lys Asp Gly His Lys Ile Leu Met Asn Pro Val Glu Glu Thr Lys
                325                 330                 335

Leu Leu Arg Gly Ser Glu His His Glu Cys Asp Asn Gln Ser Ile Ser
            340                 345                 350

Gly Ser Tyr Phe Ile Lys Thr Ala Glu Lys Leu Leu Glu Val Val Ala
        355                 360                 365

Val Phe Asp Leu Thr Ile Cys Ser Ala Glu Thr Val Gly Leu Lys Ile
    370                 375                 380

Arg Gly Ile Glu Gln Glu Glu Thr Thr Ile Lys Tyr Ser Leu Ile Asp
385                 390                 395                 400
```

```
Gln Lys Leu Thr Leu Asp Cys Ser Lys Ser Gly Lys Ala Arg Asp Gly
                405                 410                 415

Val Arg Asn Val Arg Leu Glu Ala Asp Glu Lys Leu Thr Leu His Leu
            420                 425                 430

Phe Leu Asp Arg Ser Ser Ile Glu Val Phe Ala Asn His Gly Glu Ala
        435                 440                 445

Thr Met Thr Ser Arg Ile Tyr Pro Lys Glu Gly Arg Ala Gly Ile Glu
    450                 455                 460

Leu Phe Ser Glu Lys Gly Asn Val Arg Val Glu Glu Phe Thr Tyr Trp
465                 470                 475                 480

Thr Leu Lys Asp Ile Trp Lys Gly Asp Glu Ala Lys
                485                 490
```