

SEQUENCE LISTING

<110> Solar Foods

<120> STRAINS AND PROCESSES FOR SINGLE CELL PROTEIN OR BIOMASS PRODUCTION

<130> Solar002

<160> 59

<170> PatentIn version 3.5

<210> 1

<211> 1482

<212> DNA

<213> Unknown

<220>

<223> Novel strain

<400> 1

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 <213> Unknown

<220>
 <223> novel strain

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 <212> PRT
 <213> Unknown

<220>

<223> novel strain

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35 40 45

Pro Gln Ala Gly Val Asp Pro Val Glu Ala Ala Ala Val Ala Gly
50 55 60

Glu Ser Ser Thr Ala Thr Trp Thr Val Val Trp Thr Asp Arg Leu Thr
65 70 75 80

Ala Ala Asp Val Tyr Arg Ala Lys Ala Tyr Lys Val Glu Pro Val Pro
85 90 95

Gly Gln Glu Gly Gln Tyr Phe Cys Tyr Ile Ala Tyr Asp Leu Asp Leu
100 105 110

Phe Glu Glu Gly Ser Ile Ala Asn Leu Thr Ala Ser Ile Ile Gly Asn
115 120 125

Val Phe Ser Phe Lys Pro Leu Lys Ala Ala Arg Leu Glu Asp Met Arg
130 135 140

Leu Pro Val Ala Tyr Val Lys Thr Phe Arg Gly Pro Pro Thr Gly Ile
145 150 155 160

Val Val Glu Arg Glu Arg Leu Asp Lys Phe Gly Arg Pro Leu Leu Gly
165 170 175

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

Val Val Tyr Glu Ala Leu Lys Gly Gly Leu Asp Phe Val Lys Asp Asp
195 200 205

Glu Asn Ile Asn Ser Gln Pro Phe Met His Trp Arg Asp Arg Phe Leu
210 215 220

Tyr Cys Met Glu Ala Val Asn Lys Ala Gln Ala Glu Thr Gly Glu Val
225 230 235 240

Lys Gly His Tyr Leu Asn Ile Thr Ala Gly Thr Met Glu Glu Met Tyr
245 250 255

Arg Arg Ala Glu Phe Ala Lys Glu Leu Gly Ser Val Val Val Met Val
260 265 270

Asp Leu Ile Ile Gly Trp Thr Ala Ile Gln Ser Met Ser Asn Trp Cys
275 280 285

Arg Glu Asn Asp Met Ile Leu His Met His Arg Ala Gly His Gly Thr
290 295 300

Tyr Thr Arg Gln Lys Ser His Gly Val Ser Phe Arg Val Ile Ala Lys
305 310 315 320

Trp Leu Arg Leu Ala Gly Val Asp His Leu His Thr Gly Thr Ala Val
325 330 335

Gly Lys Leu Glu Gly Asp Pro Met Thr Val Gln Gly Phe Tyr Asn Val
340 345 350

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

Gly Ile His Ala Gly Gln Met His Gln Leu Ile Asp Leu Phe Gly Glu
385 390 395 400

Asp Val Val Leu Gln Phe Gly Gly Gly Thr Ile Gly His Pro Asp Gly
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Ile Gln Ala Gly Ala Thr Ala Asn Arg Val Ala Leu Glu Thr Met Ile
420 425 430

Leu Ala Arg Asn Glu Gly Arg Asp Ile Arg Asn Glu Gly Pro Glu Ile
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Leu Val Glu Ala Ala Lys Trp Cys Arg Pro Leu Arg Ala Ala Leu Asp
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Tyr Val Pro Thr Ala Ser Val Ala
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<212> DNA
<213> Unknown

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 <211> 134
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 5

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Thr Gln Ile Lys Ala Gln Val Gln Tyr Cys Leu Asp Gln Gly Trp Ala
 20 25 30

Val Ser Val Glu His Thr Asp Asp Pro His Pro Arg Asn Thr Tyr Trp
 35 40 45

Glu Met Trp Gly Pro Pro Met Phe Asp Leu Arg Asp Ala Ala Gly Val
 50 55 60

Phe Gly Glu Ile Glu Ala Cys Arg Ala Ala Asn Pro Glu His Tyr Val
 65 70 75 80

Arg Val Asn Ala Phe Asp Ser Ser Arg Gly Trp Glu Thr Ile Arg Leu
 85 90 95

Ser Phe Ile Val Gln Arg Pro Thr Val Glu Glu Gly Phe Arg Leu Asp
 100 105 110

Arg Thr Glu Gly Lys Gly Arg Asn Gln Ser Tyr Ala Met Arg Tyr Arg
 115 120 125

Ala Gln Phe Ala Pro Arg
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 <211> 1896
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

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<210> 7

<211> 631

<212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 7

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Val Val Ala Asp Ala Val Ala Ser Val Gly Gly Ala Arg Thr Arg Leu
 35 40 45

Met Asp Ile Val Gln Leu Ala Gln Gln Arg Leu Gly His Leu Ser Glu
 50 55 60

Glu Thr Met Ala Ala Ile Ala Ala Arg Leu Ala Ile Pro Pro Val Glu
 65 70 75 80

Val Ala Asp Met Val Ser Phe Tyr Ala Phe Leu Asn Arg Ala Pro Lys
 85 90 95

Gly Arg Tyr His Ile Arg Leu Ser Arg Ser Pro Ile Ser Leu Met Lys
 100 105 110

Gly Ala Glu Ala Val Ala Ala Ala Phe Cys Gln Ile Leu Gly Ile Ala
 115 120 125

Met Gly Glu Thr Ser Gln Asp Gly Asp Phe Thr Leu Glu Trp Thr Asn
 130 135 140

Asp Ile Gly Met Ala Asp Gln Glu Pro Ala Ala Leu Val Asn Gly Thr
 145 150 155 160

Val Met Thr Gln Leu Ala Pro Gly Asp Ala Ala Ile Ile Val Gly Arg
 165 170 175

Leu Arg Ala His His Ala Pro Asn Ala Leu Pro Leu Phe Pro Gly Ala
 180 185 190

Gly Val Ala Gly Ser Gly Leu Pro His Ala Arg Ile Arg Pro Ser Leu
 195 200 205

Val Met Pro Gly Gln Leu Leu Phe Arg Glu Asp His Thr Thr Pro Gly
 210 215 220

Ala Gly Ile Lys Ala Ala Leu Ala Leu Thr Pro Asp Glu Val Val Gln
 225 230 235 240

Lys Val Ser Ala Ala Arg Leu Arg Gly Arg Gly Ala Gly Phe Pro

245

250

255

Thr Gly Leu Lys Trp Lys Leu Cys Arg Gln Ser Pro Ala Thr Thr Arg
260 265 270

His Val Ile Cys Asn Ala Asp Glu Gly Glu Pro Gly Thr Phe Lys Asp
275 280 285

Arg Val Leu Leu Thr Gln Ala Pro His Leu Met Phe Asp Gly Met Thr
290 295 300

Ile Ala Gly Tyr Ala Leu Gly Ala Arg Glu Gly Val Val Tyr Leu Arg
305 310 315 320

Gly Glu Tyr Ala Tyr Leu Trp Glu Pro Leu His Ala Val Leu Arg Glu
325 330 335

Arg Tyr Gly Leu Gly Leu Ala Gly Ala Asn Ile Leu Gly His Ala Gly
340 345 350

Phe Asp Phe Asp Ile Arg Ile Gln Leu Gly Ala Gly Ala Tyr Ile Cys
355 360 365

Gly Glu Glu Ser Ala Leu Val Glu Ser Leu Glu Gly Lys Arg Gly Ser
370 375 380

Pro Arg Asp Arg Pro Pro Phe Pro Thr Val Arg Gly His Leu Gln Gln
385 390 395 400

Pro Thr Ala Val Asp Asn Val Glu Thr Phe Ala Cys Ala Ala Arg Ile
405 410 415

Leu Glu Asp Gly Val Glu Ala Phe Ala Gly Ile Gly Thr Pro Glu Ser
420 425 430

Ala Gly Thr Lys Leu Leu Ser Val Ser Gly Asp Cys Pro Arg Pro Gly
435 440 445

Val Tyr Glu Val Pro Phe Gly Leu Thr Val Asn Ala Leu Leu Asp Leu
450 455 460

Val Gly Ala Pro Asp Ala Ala Phe Val Gln Met Gly Gly Pro Ser Gly
465 470 475 480

Gln Cys Val Ala Pro Lys Asp Tyr Gly Arg Arg Ile Ala Phe Glu Asp
485 490 495

Leu Pro Thr Gly Gly Ser Val Met Val Phe Gly Pro Gly Arg Asp Val
500 505 510

Leu Ala Met Val Arg Glu Phe Ala Asp Phe Phe Ala Gly Glu Ser Cys
515 520 525

Gly Trp Cys Thr Pro Cys Arg Val Gly Thr Thr Leu Leu Lys Glu Glu
530 535 540

Leu Asp Lys Leu Leu Ala Asn Arg Ala Thr Leu Ala Asp Ile Arg Ala
545 550 555 560

Leu Glu Thr Leu Ala Thr Thr Val Ser Arg Thr Ser Arg Cys Gly Leu
565 570 575

Gly Gln Thr Ala Pro Asn Pro Ile Leu Ser Thr Met Arg Asn Leu Pro
580 585 590

Glu Ala Tyr Glu Ala Arg Leu Arg Pro Glu Asp Phe Leu Pro Trp Ala
595 600 605

Ser Leu Asp Glu Ala Leu Lys Pro Ala Ile Val Ile Gln Gly Arg Ala
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Pro Val Pro Glu Glu Glu Ala
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<211> 1491
<212> DNA
<213> Unknown

<220>
<223> novel strain

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<210> 9
<211> 496
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 9

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20 25 30

Arg Val Glu Gly His Gly Lys Val Thr Ile Arg Leu Asp Glu Ala Gly
35 40 45

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

Arg Phe Ile Gln Gly Arg Met Tyr Trp Glu Val Pro Leu Ile Ile Gln
65 70 75 80

Arg Leu Cys Gly Ile Cys Pro Val Ser His His Leu Ala Ala Ala Lys
85 90 95

Ala Met Asp Gln Val Ala Gly Val Asp Arg Val Pro Pro Thr Ala Glu
100 105 110

Lys Leu Arg Arg Leu Met His Tyr Gly Gln Val Leu Gln Ser Asn Ala
115 120 125

Leu His Ile Phe His Leu Ala Ser Pro Asp Leu Leu Phe Gly Phe Asp
130 135 140

Ala Pro Ala Glu Gln Arg Asn Ile Ile Ala Val Leu Gln Arg Tyr Pro
145 150 155 160

Glu Ile Gly Lys Trp Ala Ile Phe Ile Arg Lys Phe Gly Gln Glu Val
165 170 175

Ile Lys Ala Thr Gly Gly Arg Lys Ile His Pro Thr Ser Ala Ile Pro
180 185 190

Gly Gly Val Asn Gln Asn Leu Ala Val Glu Asp Arg Asp Ala Leu Arg
195 200 205

Ala Lys Val Gly Glu Ile Ile Ser Trp Cys Met Ala Ala Leu Asp His
210 215 220

His Lys Ala Tyr Val Ala Glu Asn Arg Ala Leu His Asp Ser Phe Ala
225 230 235 240

Ala Phe Pro Ser Ala Phe Met Ser Leu Val Gly Pro Asp Gly Gly Met
245 250 255

Asp Leu Tyr Asp Gly Thr Leu Arg Val Ile Asp Ala Glu Gly Ala Pro
260 265 270

Leu Ile Glu Gly Ala Pro Pro Ala Ser Tyr Arg Asp His Leu Ile Glu
275 280 285

Glu Val Arg Pro Trp Ser Tyr Leu Lys Phe Pro His Leu Arg Ala Phe
290 295 300

Gly Arg Asp Asp Gly Trp Tyr Arg Val Gly Pro Leu Ala Gln Val Asn
305 310 315 320

Cys Ala Ala Ser Ile Asp Thr Pro Arg Ala Glu Ala Ala Arg Arg Asp
325 330 335

Phe Met Ala Glu Gly Gly Gly Lys Pro Val His Ala Thr Leu Ala Tyr
340 345 350

His Trp Ala Arg Leu Ile Val Leu Val His Cys Ala Glu Lys Ile Glu
355 360 365

Gln Leu Leu Phe Asp Asp Asp Leu Gln Gly Cys Asp Leu Arg Ala Glu
370 375 380

Gly Thr Arg Arg Gly Glu Gly Val Ala Trp Ile Glu Ala Pro Arg Gly
385 390 395 400

Thr Leu Ile His His Tyr Glu Val Asp Glu Asn Asp Gln Val Arg Arg
405 410 415

Ala Asn Leu Ile Val Ser Thr Thr His Asn Asn Glu Ala Met Asn Arg
420 425 430

Ala Val Arg Gln Val Ala Lys Thr Asp Leu Ser Gly Arg Glu Ile Thr
435 440 445

Glu Gly Leu Leu Asn His Ile Glu Val Ala Ile Arg Ala Phe Asp Pro
450 455 460

Cys Leu Ser Cys Ala Thr His Ala Leu Gly Gln Met Pro Leu Ile Val
465 470 475 480

Thr Leu Glu Asp Ala Ser Gly Ala Glu Ile Ala Arg Gly Val Lys Glu
485 490 495

<210> 10
<211> 720
<212> DNA
<213> Unknown

<220>
<223> novel strain

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<210> 11
<211> 239
<212> PRT
<213> Unknown

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<400> 11

Met Ser Glu Thr Pro Phe Thr Phe Thr Val Asp Gly Ile Ala Val Pro
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Ala Thr Pro Gly Gln Ser Val Ile Glu Ala Cys Asp Ala Ala Gly Ile
20 25 30

Tyr Ile Pro Arg Leu Cys His His Pro Asp Leu Pro Pro Ala Gly His
35 40 45

Cys Arg Val Cys Thr Cys Ile Ile Asp Gly Arg Pro Ala Ser Ala Cys
50 55 60

Thr Met Pro Ala Ala Arg Gly Met Val Val Glu Asn Glu Thr Pro Ala
65 70 75 80

Leu Leu Ala Glu Arg Arg Thr Leu Ile Glu Met Leu Phe Ala Glu Gly
85 90 95

Asn His Phe Cys Gln Phe Cys Glu Ala Ser Gly Asp Cys Glu Leu Gln
100 105 110

Ala Leu Gly Tyr Leu Phe Gly Met Val Ala Pro Pro Phe Pro His Leu
115 120 125

Trp Pro Lys Arg Pro Val Asp Ala Ser His Pro Asp Ile Tyr Ile Asp
130 135 140

His Asn Arg Cys Ile Leu Cys Ser Arg Cys Val Arg Ala Ser Arg Thr
145 150 155 160

Leu Asp Gly Lys Ser Val Phe Gly Phe Glu Gly Arg Gly Ile Glu Met
165 170 175

His Leu Ala Val Thr Gly Gly His Leu Asp Asp Ser Ala Ile Ala Ala
180 185 190

Ala Asp Arg Ala Val Glu Met Cys Pro Val Gly Cys Ile Val Leu Lys
195 200 205

Arg Thr Gly Tyr Arg Thr Pro Tyr Gly Arg Arg Arg Tyr Asp Ala Ala
210 215 220

Pro Ile Gly Ser Asp Ile Thr Ala Arg Arg Gly Gly Ala Lys Asp
225 230 235

<210> 12
<211> 543
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 12
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ttcctggaca tggacgagcg catcgtcgag ctcatcgacc tggatggacct cgacgtctcg 120
cccctcgacg acaagaaaaa cttcaccggc atggttgaaa tcggcctggt ggaaggcggc 180
tgcgccgacg agcgccatgt gaaggtgctg cgcgagttcc gcgagaaatc ccgcatcctg 240

gtggcgggtgg gcgcctgcgc catcaccggc ggcatcccgg cattgcgcaa cctcgccggc 300
ctcgacgaat gcctgaggga agcctacctc accggcccca cggtggaagg cggcgggctc 360
attcccaacg acccgagct gccgctgctg ctggacaagg tctatccggt gcaggacttc 420
gtgaagatcg accatttcct gcccggtgc ccgccctcgg ccgacgccat ctgggcggct 480
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tga 543

<210> 13
<211> 180
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 13

Met Ala Lys Pro Lys Leu Ala Thr Cys Ala Leu Ala Gly Cys Phe Gly
1 5 10 15

Cys His Met Ser Phe Leu Asp Met Asp Glu Arg Ile Val Glu Leu Ile
20 25 30

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

Thr Gly Met Val Glu Ile Gly Leu Val Glu Gly Gly Cys Ala Asp Glu
50 55 60

Arg His Val Lys Val Leu Arg Glu Phe Arg Glu Lys Ser Arg Ile Leu
65 70 75 80

Val Ala Val Gly Ala Cys Ala Ile Thr Gly Gly Ile Pro Ala Leu Arg
85 90 95

Asn Leu Ala Gly Leu Asp Glu Cys Leu Arg Glu Ala Tyr Leu Thr Gly
100 105 110

Pro Thr Val Glu Gly Gly Gly Leu Ile Pro Asn Asp Pro Glu Leu Pro
115 120 125

Leu Leu Leu Asp Lys Val Tyr Pro Val Gln Asp Phe Val Lys Ile Asp
130 135 140

His Phe Leu Pro Gly Cys Pro Pro Ser Ala Asp Ala Ile Trp Ala Ala
145 150 155 160

Leu Lys Ala Leu Leu Thr Gly Thr Glu Pro His Leu Pro Tyr Pro Leu
165 170 175

Phe Lys Tyr Glu
180

<210> 14
 <211> 1013
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 14
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 tgctcgcgac gctgaaggcg gtgcgggcgg cgctggaaga gacctgttc ggcgcgctt 180
 tggaagaggt ggcgggcctg gacggcgccg ccgccgtgga ggcttggcgc gccaacggcc 240
 cggaagggga tttccgcctg ttcctggaga tcgccgccga cctggagctg gaccggctcg 300
 gccgcgcgca cgaccgttt ctctccttcg gcgcctacgc ccaggacgag gggcgcttt 360
 atggcgccgg caccttcgag gccgggacgg cgggagggct cgatcccaac gccatcaccg 420
 aggaccacgc cttcgccgc atggaggacc gcgcggcgcc ccatgcgccc ttgacggct 480
 ccaccttccc cgatgccgac gacaccgagg gctacacctg gtgcaaggcg ccgcgccttg 540
 ccggcctgcc cttcgagacc ggcgcttcg cccggcaggt ggtggcgggc catccgctcg 600
 cccgggacct cgtgacgcgg gaaggcggca ctgtgcgcag ccgcgtggtc ggccggctgc 660
 tggaaaccgc gcgcaccctg atcgccatgg agggctgggt gaaggaactg cggcccgaag 720
 ggccctggtg cgcccagggc cacctgcccc aggaaggccg gccttcggc ctcaccgagg 780
 cggcgcgagg ggcgctcggc cactggatgg tggtagagaa gggccgcatt gcccgctacc 840
 agatcatcgc cccaccacc tggaaattct ccccccgcga cggcgcgggc ctgcccggcc 900
 cgctggagac ggccctggtg ggcgcgcccg tgcggcaggg agagacgacg cccgtgagcg 960
 tgcagcacat cgtgcgtcc ttcgaccgt gcatggtctg cactgtgcat tga 1013

<210> 15
 <211> 485
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 15

Met Ser Ala Glu Thr Arg Arg Leu Val Val Gly Pro Phe Asn Arg Val
 1 5 10 15

Glu Gly Asp Leu Glu Val Arg Leu Asp Val Gln Asp Gly Arg Val Gln
 20 25 30

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

Glu Gly Arg Asp Pro Arg Asp Ala Leu Val Ile Ala Pro Arg Ile Cys

50

55

60

Gly Ile Cys Ser Val Ser Gln Ser His Ala Ala Ala Leu Ala Leu Ala
65 70 75 80

Gly Leu Gln Gly Ile Ala Pro Thr His Asp Gly Arg Ile Ala Thr Asn
85 90 95

Leu Ile Val Ala Ala Glu Asn Val Ala Asp His Leu Thr His Phe His
100 105 110

Val Phe Phe Met Pro Asp Phe Ala Arg Ala Val Tyr Glu Asp Arg Pro
115 120 125

Trp Phe Ala Gln Ala Ala Arg Arg Phe Lys Ala Asn Gln Gly Val Ser
130 135 140

Val Arg Arg Ala Leu Gln Thr Arg Ala Thr Leu Leu His Val Leu Gly
145 150 155 160

Thr Leu Ala Gly Arg Trp Pro His Thr Leu Ala Leu Gln Pro Gly Gly
165 170 175

Val Thr Arg Ser Ala Asp Gln His Asp Arg Met Arg Leu Leu Ala Thr
180 185 190

Leu Lys Ala Val Arg Ala Ala Leu Glu Glu Thr Leu Phe Gly Ala Pro
195 200 205

Leu Glu Glu Val Ala Ala Leu Asp Gly Ala Ala Ala Val Glu Ala Trp
210 215 220

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

Ala Asp Leu Glu Leu Asp Arg Leu Gly Arg Ala His Asp Arg Phe Leu
245 250 255

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

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

Glu Asp His Ala Phe Ala Arg Met Glu Asp Arg Ala Ala Pro His Ala
290 295 300

Pro Phe Asp Gly Ser Thr Phe Pro Asp Ala Asp Asp Thr Glu Gly Tyr
305 310 315 320

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

Ala Phe Ala Arg Gln Val Val Ala Gly His Pro Leu Ala Arg Asp Leu
340 345 350

Val Thr Arg Glu Gly Gly Thr Val Arg Ser Arg Val Val Gly Arg Leu
355 360 365

Leu Glu Thr Ala Arg Thr Leu Ile Ala Met Glu Gly Trp Val Lys Glu
370 375 380

Leu Arg Pro Glu Gly Pro Trp Cys Ala Gln Gly His Leu Pro Gln Glu
385 390 395 400

Gly Arg Ala Phe Gly Leu Thr Glu Ala Ala Arg Gly Ala Leu Gly His
405 410 415

Trp Met Val Val Glu Lys Gly Arg Ile Ala Arg Tyr Gln Ile Ile Ala
420 425 430

Pro Thr Thr Trp Asn Phe Ser Pro Arg Asp Gly Ala Gly Leu Pro Gly
435 440 445

Pro Leu Glu Thr Ala Leu Val Gly Ala Pro Val Arg Gln Gly Glu Thr
450 455 460

Thr Pro Val Ser Val Gln His Ile Val Arg Ser Phe Asp Pro Cys Met
465 470 475 480

Val Cys Thr Val His
485

<210> 16
<211> 858
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 16
acgggggagg aagcccgcg catcttcgac gccatccttg ccggcggttat cgtcctcgac 60
gccctgtgcg tggaaaggcg gctgctgcgc gggccgaacg gcaccgggcg cttccatgtg 120
ctggcgggca cggacacccc caccatcgac tgggcgcggc agctcgccgg catggcgcg 180
cacgtggtgg cggtgggcac ctgcgccgcc tatgggggcg tgacggcggc gggcatcaac 240
cccaccgatg cctgcggcct ccagttcgac ggacgccgga agggtggggc gctgggggcg 300
gacttccgct cccgctcggg gcttccggtc atcaatgtgg ccggctgccc caccatccc 360
aactgggtga cggaaacct gatgctgctc gcctgcggcc tgctgggcga ggccgacctc 420
gacgtctatg gccggcgcg cttctatgac gacctgctgg tgcatcacgg ctgcccgcgc 480
aacgaatact atgaatacaa ggcgagcgcc gagaagatga gcgacctcgg ctgcatgatg 540

```

gagcatctgg gctgcctcgg caccagggcc cagccgact gcaacacgcg cctttggaat      600
ggcgagggct cgtgcacccg cggcggctat gcctgcatca actgcacggc gccggaattc      660
gaggagccgg gccacgcctt cctggagacg cccaagatcg gcggcatccc catcggcctg      720
cccaccgaca tgcccaaggc ctggttcacg gccttgtcct ccctcgcaa ggcgggcgacg      780
ccggagcggc tgcgaagaa cgcggtgtcc gaccatgtgg tcacgccgcc cgccgtcaag      840
gacatcaagc ggcgatga                                           858

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<210> 17
 <211> 335
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 17

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Met Ser Thr Pro Phe Ser Val Leu Trp Leu Gln Ser Gly Gly Cys Gly
1           5           10           15

```

```

Gly Cys Thr Met Ser Leu Leu Cys Ala Glu Ala Pro Asp Leu Ala Thr
                20           25           30

```

```

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

```

```

Glu Glu Thr Gly Glu Glu Ala Arg Ala Ile Phe Asp Ala Ile Leu Ala
50           55           60

```

```

Gly Val Ile Val Leu Asp Ala Leu Cys Val Glu Gly Ala Leu Leu Arg
65           70           75           80

```

```

Gly Pro Asn Gly Thr Gly Arg Phe His Val Leu Ala Gly Thr Asp Thr
                85           90           95

```

```

Pro Thr Ile Asp Trp Ala Arg Gln Leu Ala Gly Met Ala Arg His Val
        100           105           110

```

```

Val Ala Val Gly Thr Cys Ala Ala Tyr Gly Gly Val Thr Ala Ala Gly
        115           120           125

```

```

Ile Asn Pro Thr Asp Ala Cys Gly Leu Gln Phe Asp Gly Arg Arg Lys
        130           135           140

```

```

Gly Gly Ala Leu Gly Ala Asp Phe Arg Ser Arg Ser Gly Leu Pro Val
145           150           155           160

```

```

Ile Asn Val Ala Gly Cys Pro Thr His Pro Asn Trp Val Thr Glu Thr
        165           170           175

```

```

Leu Met Leu Leu Ala Cys Gly Leu Leu Gly Glu Ala Asp Leu Asp Val
        180           185           190

```

Tyr Gly Arg Pro Arg Phe Tyr Ala Asp Leu Leu Val His His Gly Cys
195 200 205

Pro Arg Asn Glu Tyr Tyr Glu Tyr Lys Ala Ser Ala Glu Lys Met Ser
210 215 220

Asp Leu Gly Cys Met Met Glu His Leu Gly Cys Leu Gly Thr Gln Ala
225 230 235 240

His Ala Asp Cys Asn Thr Arg Leu Trp Asn Gly Glu Gly Ser Cys Thr
245 250 255

Arg Gly Gly Tyr Ala Cys Ile Asn Cys Thr Ala Pro Glu Phe Glu Glu
260 265 270

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

Gly Leu Pro Thr Asp Met Pro Lys Ala Trp Phe Ile Ala Leu Ser Ser
290 295 300

Leu Ala Lys Ala Ala Thr Pro Glu Arg Leu Arg Lys Asn Ala Val Ser
305 310 315 320

Asp His Val Val Thr Pro Pro Ala Val Lys Asp Ile Lys Arg Arg
325 330 335

<210> 18
<211> 870
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 18
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gtcatcacgg ccatgcgggg cattgcggcg gcgcgggcgc gggaggcgc gggtcggctc 120
gacggcatcc gcgcctatgc gcagaccatc gccgaggcca tcggccatgt gctcgccgtg 180
ctgcccgagg agggccgcgc ccggctctcc gggcaccggc atcggggcca tgcggtcatc 240
gccctgtgcg cggagcaggg ctttgccggc gtcttcaacg agcgggtgct ggacgaggcc 300
gcccggctgc tgaccggcgg ggcggggccg gccgagctgc tgctggtggg cgaccggggc 360
ctgatggtgg cccgcgagcg ggggctcgat gtctcctggt cggtgcccat ggtggcccat 420
gcgggccagg cctcggcgct ggcggaccgc atcagcgagg agctctaccg gcggatcgat 480
gcgggacggg tgacgcgggt gtcggtggtg caccgcgagc ccgccgcgtc cgccgccatc 540
gagacggtgg tgaaagtgtt ggtgccgttc gacttcgccc gcttccccct ggcgcgggtg 600
gcatccgccc cgctcatgac catgccgccg ccgcggctgc tggcccagct gtcggaggaa 660

tatgtgttcg ccgagctgtg cgaggcgctc accttgtcct tcgcggcgga gaacgaggcc 720
cgcatgcggg ccatgatcgc cgcccgcgcc aatgtggccg ataccctgga gggcctcgtc 780
ggccgcgccc ggccagatgcg ccaggaggag atcaccaacg agatcatcga gctggaaggc 840
ggcgccggca gcgcccggca tgcggattga 870

<210> 19
<211> 289
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 19

Met Thr Glu Arg Leu Ser Asp Val Asn Ala Arg Ile Ala Ser Val Arg
1 5 10 15

Gln Leu Ser Ser Val Ile Thr Ala Met Arg Gly Ile Ala Ala Ala Arg
20 25 30

Ala Arg Glu Ala Arg Gly Arg Leu Asp Gly Ile Arg Ala Tyr Ala Gln
35 40 45

Thr Ile Ala Glu Ala Ile Gly His Val Leu Ala Val Leu Pro Glu Glu
50 55 60

Ala Arg Ala Arg Ser Ser Gly His Arg His Arg Gly His Ala Val Ile
65 70 75 80

Ala Leu Cys Ala Glu Gln Gly Phe Ala Gly Val Phe Asn Glu Arg Val
85 90 95

Leu Asp Glu Ala Ala Arg Leu Leu Thr Gly Gly Ala Gly Pro Ala Glu
100 105 110

Leu Leu Leu Val Gly Asp Arg Gly Leu Met Val Ala Arg Glu Arg Gly
115 120 125

Leu Asp Val Ser Trp Ser Val Pro Met Val Ala His Ala Gly Gln Ala
130 135 140

Ser Ala Leu Ala Asp Arg Ile Ser Glu Glu Leu Tyr Arg Arg Ile Asp
145 150 155 160

Ala Gly Arg Val Thr Arg Val Ser Val Val His Ala Glu Pro Ala Ala
165 170 175

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

Ala Arg Phe Pro Leu Ala Arg Val Ala Ser Ala Pro Leu Met Thr Met
195 200 205

Pro Pro Pro Arg Leu Leu Ala Gln Leu Ser Glu Glu Tyr Val Phe Ala
210 215 220

Glu Leu Cys Glu Ala Leu Thr Leu Ser Phe Ala Ala Glu Asn Glu Ala
225 230 235 240

Arg Met Arg Ala Met Ile Ala Ala Arg Ala Asn Val Ala Asp Thr Leu
245 250 255

Glu Gly Leu Val Gly Arg Ala Arg Gln Met Arg Gln Glu Glu Ile Thr
260 265 270

Asn Glu Ile Ile Glu Leu Glu Gly Gly Ala Gly Ser Ala Arg His Ala
275 280 285

Asp

<210> 20
<211> 1536
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 20
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gggacgcgcc tttccagca atcccaatcg gtgggcccgg tggaggagat ggccgacggc 120
atgccccgcg tctccggcct gccgatgtg cggctcgac agcttctcac cttcgagggc 180
ggccagaccg gctatgccct caccctcgat cgcaccgaga tcgccgtggg gctgctggat 240
gacgcctccg gcgtggaggc gggcgcccgg gtgttcggca ccggcgagggt ggtgaagggtg 300
ccggtggggc cggggctgct gggccgcatc gtcgaccccc tcggccggcc catggaccgc 360
tccgagccgg tggtagcgca ggcgcacat cccatcgagc ggccggcgcc ggccatcatc 420
gcccgcgacc tggctctgca gccggttcag accggcacgc tggtagtgga tgcgctgttc 480
tccctcggcc ggggccagcg cgagctcatc atcggcgacc gggctaccgg caagaccgcc 540
atcgcggtgg acaccatcat cagccagaag cattcggaca tcgtgtgcat ctacgtggcg 600
gtgggccagc gcgccgccgc cgtggagcgg gtggtggagg cggtagcgcg ccacggggcg 660
atcgagcgct gcatcttctg gtctgcctcg gccgccgcct cgccagggct gcaatggatc 720
gcgccgttcg ccggcatgac catggcggaa tatttccgcg acaacggcca gcatgcgctc 780
atcatcatcg atgatctcac caagcatgcg gccacccatc gcgagctggc gctgctcacc 840
cacgagccgc cgggccgcga ggcctatccc ggcgacatct tctatgtgca cgccgcctt 900
ctggagcggg ccgccaagct ctccgccgag ctgggcgggtg gctcgctcac ggccctgccc 960
atcgcggaga cggacgcggg aaacctctcc gcctatatcc ccaccaacct catctccatc 1020

accgatgggc agatcgtgct ggatttcgcg ctgttcgcg ccaaccagcg cccggcggtg 1080
gatgtgggcc tctccgtgag ccgggtgggc ggcaaggcgc agcatccgc gcttcgggcc 1140
gtgtccgggc gcatccggct cgattattcc cagttcctgg agctggaaat gttcaccgc 1200
ttcgcgccga tcaccgatac ccgctgaag gcgcagatca cccggggcga gcgcattccgc 1260
gcgctgctca cccagccgcg cttttccacc ctgcgccttc aggacgaggt ggcgctgctg 1320
gccgcgctgg cggagggggg gttcgacact ttggccccgg ggctgatggg cgccgtgctg 1380
gcccgcattc cggcccagct ggatgcgcag gtgaaggacg tggcctcggc cctcgccgag 1440
ggcaagggtg tggaggaggg cttgcacgcc cgtctcgtgg cggccgtgcg ggccgtcgcg 1500
gcggacgtgg ccgcgaccgc gaaggccggg ccgtga 1536

<210> 21
<211> 511
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 21

Met Ser Thr Gly Ala Gln Ala Ser Glu Asp Trp Leu Thr Arg Ser Arg
1 5 10 15

Ala Ala Leu Ala Gly Thr Arg Leu Ser Gln Gln Ser Gln Ser Val Gly
20 25 30

Arg Val Glu Glu Met Ala Asp Gly Ile Ala Arg Val Ser Gly Leu Pro
35 40 45

Asp Val Arg Leu Asp Glu Leu Leu Thr Phe Glu Gly Gly Gln Thr Gly
50 55 60

Tyr Ala Leu Thr Leu Asp Arg Thr Glu Ile Ala Val Val Leu Leu Asp
65 70 75 80

Asp Ala Ser Gly Val Glu Ala Gly Ala Arg Val Phe Gly Thr Gly Glu
85 90 95

Val Val Lys Val Pro Val Gly Pro Gly Leu Leu Gly Arg Ile Val Asp
100 105 110

Pro Leu Gly Arg Pro Met Asp Arg Ser Glu Pro Val Val Ala Gln Ala
115 120 125

His His Pro Ile Glu Arg Pro Ala Pro Ala Ile Ile Ala Arg Asp Leu
130 135 140

Val Ser Gln Pro Val Gln Thr Gly Thr Leu Val Val Asp Ala Leu Phe
145 150 155 160

Ser Leu Gly Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Ala Thr
 165 170 175

Gly Lys Thr Ala Ile Ala Val Asp Thr Ile Ile Ser Gln Lys His Ser
 180 185 190

Asp Ile Val Cys Ile Tyr Val Ala Val Gly Gln Arg Ala Ala Ala Val
 195 200 205

Glu Arg Val Val Glu Ala Val Arg Ala His Gly Ala Ile Glu Arg Cys
 210 215 220

Ile Phe Val Val Ala Ser Ala Ala Ala Ser Pro Gly Leu Gln Trp Ile
 225 230 235 240

Ala Pro Phe Ala Gly Met Thr Met Ala Glu Tyr Phe Arg Asp Asn Gly
 245 250 255

Gln His Ala Leu Ile Ile Ile Asp Asp Leu Thr Lys His Ala Ala Thr
 260 265 270

His Arg Glu Leu Ala Leu Leu Thr His Glu Pro Pro Gly Arg Glu Ala
 275 280 285

Tyr Pro Gly Asp Ile Phe Tyr Val His Ala Arg Leu Leu Glu Arg Ala
 290 295 300

Ala Lys Leu Ser Ala Glu Leu Gly Gly Gly Ser Leu Thr Ala Leu Pro
 305 310 315 320

Ile Ala Glu Thr Asp Ala Gly Asn Leu Ser Ala Tyr Ile Pro Thr Asn
 325 330 335

Leu Ile Ser Ile Thr Asp Gly Gln Ile Val Leu Asp Ser Arg Leu Phe
 340 345 350

Ala Ala Asn Gln Arg Pro Ala Val Asp Val Gly Leu Ser Val Ser Arg
 355 360 365

Val Gly Gly Lys Ala Gln His Pro Ala Leu Arg Ala Val Ser Gly Arg
 370 375 380

Ile Arg Leu Asp Tyr Ser Gln Phe Leu Glu Leu Glu Met Phe Thr Arg
 385 390 395 400

Phe Gly Gly Ile Thr Asp Thr Arg Val Lys Ala Gln Ile Thr Arg Gly
 405 410 415

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

Leu Gln Asp Glu Val Ala Leu Leu Ala Ala Leu Ala Glu Gly Val Phe

435

440

445

Asp Thr Leu Ala Pro Gly Leu Met Gly Ala Val Arg Ala Arg Ile Pro
 450 455 460

Ala Gln Leu Asp Ala Gln Val Lys Asp Val Ala Ser Ala Leu Ala Glu
 465 470 475 480

Gly Lys Val Leu Glu Glu Gly Leu His Ala Arg Leu Val Ala Ala Val
 485 490 495

Arg Ala Val Ala Ala Asp Val Ala Ala Thr Ala Lys Ala Gly Pro
 500 505 510

<210> 22
 <211> 741
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 22
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 ctcttgagcc gcttctgtt caagccggtg gcgcaggtca tcgcgcagcg ccgtgccgag 120
 atcgagaagc tgggtggagga tgcgcgcgcc gccaaaggccg ccgccgaggc cgagcgggac 180
 acggcgaagg cggaggaggc gcgccttgcc gccgagcgcg gcgcccgcac ggcggcggtc 240
 gccaaaggagg cggaggcgca gaaggcggca ttgctggccg ccgccaagac cgaggccgag 300
 gccctgcacg cggccgcgga agcggccatc gtccggggcg gggcgagcga ggaggaagcc 360
 gccgccgacc gcgccagccg ccttgccgtg gacatcgccg ccaagctgct ggaccggctg 420
 cccgacgacg cccgggtcgc gggcttcatc gatggcctcg ccgaggggct tgaagccctg 480
 cccgaggcga gccgggcggg gatcggcgtc gacggcgcg cagtgcgcgt gacggccgcg 540
 cgcgccctta tgccggcgga ggaggaggcc tgccgcacgc ggctctccca ggcgctgggc 600
 cgtccggtga cgctggccgt gaccatcgac ccgcccctca tcgccgcctt ggagatggag 660
 acgccccacg cgggtggtgcg caattccttc aaggccgac tcgaccgcgt caccgcggcg 720
 ctaccccatc atgggacctg a 741

<210> 23
 <211> 246
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 23

Met Gln Ile Asp Trp Trp Thr Leu Gly Leu Gln Thr Val Asn Val Leu
 1 5 10 15

Val Leu Ile Trp Leu Leu Ser Arg Phe Leu Phe Lys Pro Val Ala Gln
 20 25 30

Val Ile Ala Gln Arg Arg Ala Glu Ile Glu Lys Leu Val Glu Asp Ala
 35 40 45

Arg Ala Ala Lys Ala Ala Ala Glu Ala Glu Arg Asp Thr Ala Lys Ala
 50 55 60

Glu Glu Ala Arg Leu Ala Ala Glu Arg Gly Ala Arg Met Ala Ala Val
 65 70 75 80

Ala Lys Glu Ala Glu Ala Gln Lys Ala Ala Leu Leu Ala Ala Ala Lys
 85 90 95

Thr Glu Ala Glu Ala Leu His Ala Ala Ala Glu Ala Ala Ile Val Arg
 100 105 110

Ala Arg Ala Ser Glu Glu Glu Ala Ala Ala Asp Arg Ala Ser Arg Leu
 115 120 125

Ala Val Asp Ile Ala Ala Lys Leu Leu Asp Arg Leu Pro Asp Asp Ala
 130 135 140

Arg Val Ala Gly Phe Ile Asp Gly Leu Ala Glu Gly Leu Glu Ala Leu
 145 150 155 160

Pro Glu Ala Ser Arg Ala Val Ile Gly Val Asp Gly Ala Pro Val Arg
 165 170 175

Val Thr Ala Ala Arg Ala Leu Met Pro Ala Glu Glu Glu Ala Cys Arg
 180 185 190

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

Ile Asp Pro Ala Leu Ile Ala Gly Leu Glu Met Glu Thr Pro His Ala
 210 215 220

Val Val Arg Asn Ser Phe Lys Ala Asp Leu Asp Arg Val Thr Ala Ala
 225 230 235 240

Leu Thr His His Gly Thr
 245

<210> 24
 <211> 243
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 24

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gggccggccc tgggagaggg ccgggagggtg gccgcggcca tggacgcat cgcccgcag      120
ccggaggcgg ccggaacctt gtcgcgcacg ctcttcgtcg gcctcgccat gatcgagacc      180
atggcgatct actgcctggt gatcgcgctc ctgggtctct tcgccaatcc gttcgtgaag      240
tga                                                                    243
```

<210> 25
<211> 80
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 25

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

```
Phe Gly Ala Ile Gly Pro Ala Leu Gly Glu Gly Arg Ala Val Ala Ala
          20          25          30
```

```
Ala Met Asp Ala Ile Ala Arg Gln Pro Glu Ala Ala Gly Thr Leu Ser
          35          40          45
```

```
Arg Thr Leu Phe Val Gly Leu Ala Met Ile Glu Thr Met Ala Ile Tyr
          50          55          60
```

```
Cys Leu Val Ile Ala Leu Leu Val Leu Phe Ala Asn Pro Phe Val Lys
65          70          75          80
```

<210> 26
<211> 699
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 26

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ccggtggtgg tcacctggct catcatggcc gccttcattg ggctggcgcg gctcatcacc      120
cggaagcttt ccaccgatcc caccgggacc caggcggcgg tggaaacggt gctgaccgcc      180
atcgattccc agatcgccga caccatgcag gccgatcccg cgccttatcg cgcgctcatc      240
ggcaccatct tcctttatgt gctggtggcc aactggctct cgctcatccc gggcatcgag      300
ccgcccacgg cgcatatcga gaccgatcgc gcgctcgctt tcatcgtgtt cgccgccacc      360
atcgggttcg ggttgaagac aaggggtgtg aagggtatc tcgccacatt cgccgaaccc      420
tcctgggtga tgatcccgt caatgtggtg gagcagatca cccggacctt ctcgctcatc      480
gtgcgcctgt tcggcaacat catgagcggg gtgttcgtgg tcggcatcat cctgtccctc      540
gccgggtcgc tggtgcccat cccctcatg gcgctcgatc tcctgaccgg cgccgtgcag      600
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gcctacatct tcgcggtgct ggctgcgtg ttcacggcg cggccattgg cgaggcgccg 660

gcaaagcccc aatcgaagga gccagggaac acatcatga 699

<210> 27

<211> 232

<212> PRT

<213> Unknown

<220>

<223> novel strain

<400> 27

Met Gly Ser Pro Leu Ile Leu Glu Pro Leu Phe His Ile Gly Pro Val
1 5 10 15

Pro Ile Thr Ala Pro Val Val Val Thr Trp Leu Ile Met Ala Ala Phe
20 25 30

Ile Gly Leu Ala Arg Leu Ile Thr Arg Lys Leu Ser Thr Asp Pro Thr
35 40 45

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

Ile Ala Asp Thr Met Gln Ala Asp Pro Ala Pro Tyr Arg Ala Leu Ile
65 70 75 80

Gly Thr Ile Phe Leu Tyr Val Leu Val Ala Asn Trp Ser Ser Leu Ile
85 90 95

Pro Gly Ile Glu Pro Pro Thr Ala His Ile Glu Thr Asp Ala Ala Leu
100 105 110

Ala Phe Ile Val Phe Ala Ala Thr Ile Gly Phe Gly Leu Lys Thr Arg
115 120 125

Gly Val Lys Gly Tyr Leu Ala Thr Phe Ala Glu Pro Ser Trp Val Met
130 135 140

Ile Pro Leu Asn Val Val Glu Gln Ile Thr Arg Thr Phe Ser Leu Ile
145 150 155 160

Val Arg Leu Phe Gly Asn Ile Met Ser Gly Val Phe Val Val Gly Ile
165 170 175

Ile Leu Ser Leu Ala Gly Leu Leu Val Pro Ile Pro Leu Met Ala Leu
180 185 190

Asp Leu Leu Thr Gly Ala Val Gln Ala Tyr Ile Phe Ala Val Leu Ala
195 200 205

Cys Val Phe Ile Gly Ala Ala Ile Gly Glu Ala Pro Ala Lys Pro Gln

210

215

220

Ser Lys Glu Pro Gly Lys Thr Ser
225 230

<210> 28
<211> 456
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 28
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gcggatttcc tgaccgttct ggaggcctgc gtggtgcgct tcaaggatgg ggccgacggc 180
gtgcattatt gtgctctcag tgggtggcgtg ctgtcggtcg aggagggccg gcgcatcgcc 240
atgcctgcc gtcagggcac ggtgagcgac gacctggtcg ccctggaagg ggcggtggac 300
gccatgcgtt cggcggagag cgatgccgac aagcggggcc gggtggagca gatgcgcctt 360
catgcccacg ccgtgcgcca gtcctgcac tatctgcggc ccggccgggc cggcggcgtg 420
gcgccggccg ccgcgccgga ggagggggccg tcatga 456

<210> 29
<211> 151
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 29

Met Ser Ala Pro Leu His Leu Thr Ile Thr Thr Pro Ala Ala Val Leu
1 5 10 15

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

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

Ala Cys Val Val Arg Phe Lys Asp Gly Ala Asp Gly Val His Tyr Cys
50 55 60

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

Ile Ala Cys Arg Gln Gly Thr Val Ser Asp Asp Leu Val Ala Leu Glu
85 90 95

Gly Ala Val Asp Ala Met Arg Ser Ala Glu Ser Asp Ala Asp Lys Arg
100 105 110

Ala Arg Val Glu Gln Met Arg Leu His Ala His Ala Val Arg Gln Leu
 115 120 125

Leu His Tyr Leu Arg Pro Gly Arg Ala Gly Gly Val Ala Pro Ala Ala
 130 135 140

Ala Pro Glu Glu Gly Pro Ser
 145 150

<210> 30
 <211> 1494
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 30
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 gccgtgcgcg gcgcggtgat cgacatcgcc ttgtcccagc ctccgctgcc gccgctggac 120
 gacgcccttc tcatcaccga cggccggggc ggcacggtgc tgggtgaggt gcagagccat 180
 atggatcggc acacggtgcg cgccatcgcc cttcaggcca ccaccggcct cagccggggg 240
 ctggaggcgg cgcggtggg cgggccggtg aagggtgccg tgggagacca tgtgctcggc 300
 cgctctctgg atgtcaccgg cgccatcggc gacaaggcg gcccgctgcc ggccgacgtg 360
 cccacgcggc cgatccacca cgcgccgcca tccttcgccg cgcaggcgcg cacgtccgat 420
 ctgtttcgca ccggcatcaa ggtcatcgac ctcttgccg ccctcgcca gggcggcaag 480
 gcggccatgt tcggcggggc ggcgtgggc aagaccgtgc tggatgatga gctgatccac 540
 gccatggtgg cgagctacaa gggcatctcg gtgtttgccg gcgtggggga gcgctccgc 600
 gagggccacg agatgctgct ggacatgacc gattccggcg tgctcgaccg caccgttctg 660
 gtctatggcc agatgaacga gcccccggg gcccgctggc gggtgcccat gacggcgctg 720
 accatcgccg aatatttccg cgacgagaag caccagaac tcctgctgct gatggacaac 780
 atcttcgct tcgtccaggc gggggcggag gtctccggcc ttttgggccc tccgccctcc 840
 cgggtgggat accagccgac gctggcgagc gaggtggcgg cgctccagga acgcatcacc 900
 tccgtgggcg aggctcggg gaccgccatc gaggcgtct acgtgccggc ggatgacttc 960
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 gccatggcgg cggagggcat gtatccggcg gtggacccca tctcctcctc gtcggtgctg 1080
 ctcgaccgc tcatcgtggg ggacgagcat gcgcgcgtcg ccaacgaggt gcgccggacc 1140
 atcgagcatt atcgcgagct tcaggatgtg atctcgtgc tgggcatgga ggaattgggc 1200
 accgaggatc gccgcatcgt ggagcgggcg cgccggctcc agcgcttcct caccagccc 1260
 ttcacggtca ccgaggcctt caccggcgtg cccggccgct cgggtggccat cgccgacacc 1320
 atcgccggct gcaggatgat cctgtccggc gcctgcgacg actggcagga aagcgccctc 1380

tacatggtgg gcaccatcga cgaggcccg cagaaggagg aggccgctcg cgccaaggcg 1440

gggcagggcg ccccgccgg gacggcagcc gagacggcgg aggccgcccc gtga 1494

<210> 31
<211> 497
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 31

Met Ala Ala Ala Asp Glu Glu Ala Gln Ser Ala Ala Gly Pro Ala Ser
1 5 10 15

Gly Arg Val Val Ala Val Arg Gly Ala Val Ile Asp Ile Ala Phe Ala
20 25 30

Gln Pro Pro Leu Pro Pro Leu Asp Asp Ala Leu Leu Ile Thr Asp Gly
35 40 45

Arg Gly Gly Thr Val Leu Val Glu Val Gln Ser His Met Asp Arg His
50 55 60

Thr Val Arg Ala Ile Ala Leu Gln Ala Thr Thr Gly Leu Ser Arg Gly
65 70 75 80

Leu Glu Ala Ala Arg Val Gly Gly Pro Val Lys Val Pro Val Gly Asp
85 90 95

His Val Leu Gly Arg Leu Leu Asp Val Thr Gly Ala Ile Gly Asp Lys
100 105 110

Gly Gly Pro Leu Pro Ala Asp Val Pro Thr Arg Pro Ile His His Ala
115 120 125

Pro Pro Ser Phe Ala Ala Gln Gly Gly Thr Ser Asp Leu Phe Arg Thr
130 135 140

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

Ala Ala Met Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Val Met
165 170 175

Glu Leu Ile His Ala Met Val Ala Ser Tyr Lys Gly Ile Ser Val Phe
180 185 190

Ala Gly Val Gly Glu Arg Ser Arg Glu Gly His Glu Met Leu Leu Asp
195 200 205

Met Thr Asp Ser Gly Val Leu Asp Arg Thr Val Leu Val Tyr Gly Gln
210 215 220

Met Asn Glu Pro Pro Gly Ala Arg Trp Arg Val Pro Met Thr Ala Leu
 225 230 235 240

Thr Ile Ala Glu Tyr Phe Arg Asp Glu Lys His Gln Asn Val Leu Leu
 245 250 255

Leu Met Asp Asn Ile Phe Arg Phe Val Gln Ala Gly Ala Glu Val Ser
 260 265 270

Gly Leu Leu Gly Arg Pro Pro Ser Arg Val Gly Tyr Gln Pro Thr Leu
 275 280 285

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

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

Thr Asp Pro Ala Val Thr Thr Ile Ala Ala His Val Asp Ser Met Val
 325 330 335

Val Leu Ser Arg Ala Met Ala Ala Glu Gly Met Tyr Pro Ala Val Asp
 340 345 350

Pro Ile Ser Ser Ser Ser Val Leu Leu Asp Pro Leu Ile Val Gly Asp
 355 360 365

Glu His Ala Arg Val Ala Asn Glu Val Arg Arg Thr Ile Glu His Tyr
 370 375 380

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

Thr Glu Asp Arg Arg Ile Val Glu Arg Ala Arg Arg Leu Gln Arg Phe
 405 410 415

Leu Thr Gln Pro Phe Thr Val Thr Glu Ala Phe Thr Gly Val Pro Gly
 420 425 430

Arg Ser Val Ala Ile Ala Asp Thr Ile Ala Gly Cys Arg Met Ile Leu
 435 440 445

Ser Gly Ala Cys Asp Asp Trp Gln Glu Ser Ala Leu Tyr Met Val Gly
 450 455 460

Thr Ile Asp Glu Ala Arg Gln Lys Glu Glu Ala Ala Arg Ala Lys Ala
 465 470 475 480

Gly Gln Gly Ala Pro Ala Gly Thr Ala Ala Glu Thr Ala Glu Ala Ala
 485 490 495

Pro

<210> 32
<211> 1437
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 32
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gacgggcatc tgccggcgat tctcaacgag atcgagacca ccaaccaggg caaccggctg 120
gtgctcgaag tggctcagca tctcggcgag aacaccgtgc gctgcatcgc catggatgcc 180
actgaaggcc tgggtcgtgg ccaggagggt gccgacaccg atgcgcccac ccagggtccc 240
gtgggcgccc ccaccctcgg ccgcatcatg aacgtgatcg gcgagccggt ggacgagctg 300
ggccccatcg agggcgaagc gctgcgcggc atccatcagc cggccccctc ctatgcggag 360
caggccacgg aagctgagat cctcgtcacc ggcatcaagg tggatgatct gctggcgccc 420
tattccaagg gcggcaaggt gggcctgttc ggcgcgccg gcgtgggcaa gaccgtgctc 480
atcatggagc tgatcaacaa cgtggccaag gcgcacggcg gctattccgt gttcgccggc 540
gtgggtgagc gcacccgcga gggcaacgac ctctaccacg agatgatcga gtccaacgtg 600
aacaaggacc cgcacgagaa caatggctcg gcggccggtt ccaagtgcgc cctgggtctat 660
ggccagatga acgagccgcc cggcgcccg gcccgcggtg ccctcaccgg cctcaccgtc 720
gccgagcatt tccgcgacca gggccaggac gtgctgttct tcgtggacaa catcttccgc 780
ttcaccaggg cgggctccga ggtgtcggcg cttctcggcc gcatcccctc ggcgggtgggc 840
taccagccga cgctggccac cgacatgggc cagctgcagg agcgcatcac caccaccacc 900
aagggtcca tcacctcgtt gcaggccatc tacgtgccgg cggacgatct gaccgatccg 960
gcgccggccg cctccttcgc ccatctggac gccaccacgg tgctgtcgcg ctccatcgcg 1020
gagaagggca tctaccggc ggtggatccg ctggactcca cctcgcgcat gctgtctccc 1080
gccatcctcg gcgacgagca ctacaacacc gcgcgccagg tgcagcagac cctgcagcgc 1140
tacaaggcgc tccaggacat catcgccatc ctgggcatgg acgaactctc cgaagaggac 1200
aagctcaccg tggcccgcg ccgcaagatc gagcgcttcc tctcccagcc cttccacgtg 1260
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ttcaagggcc tggatggacg caagtacgac tacctgccc agcaggcctt ctacatggtg 1380
ggcaccatcg aagaagccat cgagaagggc aagaagctgg cggccgaggc ggcctga 1437

<210> 33
<211> 478
<212> PRT
<213> Unknown

<220>

<223> novel strain

<400> 33

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

Asp Val Gln Phe Asp Gly His Leu Pro Ala Ile Leu Asn Ala Ile Glu
20 25 30

Thr Thr Asn Gln Gly Asn Arg Leu Val Leu Glu Val Ala Gln His Leu
35 40 45

Gly Glu Asn Thr Val Arg Cys Ile Ala Met Asp Ala Thr Glu Gly Leu
50 55 60

Val Arg Gly Gln Glu Val Ala Asp Thr Asp Ala Pro Ile Gln Val Pro
65 70 75 80

Val Gly Ala Ala Thr Leu Gly Arg Ile Met Asn Val Ile Gly Glu Pro
85 90 95

Val Asp Glu Leu Gly Pro Ile Glu Gly Glu Ala Leu Arg Gly Ile His
100 105 110

Gln Pro Ala Pro Ser Tyr Ala Glu Gln Ala Thr Glu Ala Glu Ile Leu
115 120 125

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

Gly Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu
145 150 155 160

Ile Met Glu Leu Ile Asn Asn Val Ala Lys Ala His Gly Gly Tyr Ser
165 170 175

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

His Glu Met Ile Glu Ser Asn Val Asn Lys Asp Pro His Glu Asn Asn
195 200 205

Gly Ser Ala Ala Gly Ser Lys Cys Ala Leu Val Tyr Gly Gln Met Asn
210 215 220

Glu Pro Pro Gly Ala Arg Ala Arg Val Ala Leu Thr Gly Leu Thr Val
225 230 235 240

Ala Glu His Phe Arg Asp Gln Gly Gln Asp Val Leu Phe Phe Val Asp
245 250 255

Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Ala Leu Leu

260

265

270

Gly Arg Ile Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Thr Asp
 275 280 285

Met Gly Gln Leu Gln Glu Arg Ile Thr Thr Thr Thr Lys Gly Ser Ile
 290 295 300

Thr Ser Val Gln Ala Ile Tyr Val Pro Ala Asp Asp Leu Thr Asp Pro
 305 310 315 320

Ala Pro Ala Ala Ser Phe Ala His Leu Asp Ala Thr Thr Val Leu Ser
 325 330 335

Arg Ser Ile Ala Glu Lys Gly Ile Tyr Pro Ala Val Asp Pro Leu Asp
 340 345 350

Ser Thr Ser Arg Met Leu Ser Pro Ala Ile Leu Gly Asp Glu His Tyr
 355 360 365

Asn Thr Ala Arg Gln Val Gln Gln Thr Leu Gln Arg Tyr Lys Ala Leu
 370 375 380

Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp
 385 390 395 400

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

Pro Phe His Val Ala Glu Val Phe Thr Gly Ser Pro Gly Lys Leu Val
 420 425 430

Asp Leu Ala Asp Thr Ile Lys Gly Phe Lys Gly Leu Val Asp Gly Lys
 435 440 445

Tyr Asp Tyr Leu Pro Glu Gln Ala Phe Tyr Met Val Gly Thr Ile Glu
 450 455 460

Glu Ala Ile Glu Lys Gly Lys Lys Leu Ala Ala Glu Ala Ala
 465 470 475

<210> 34
 <211> 876
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 34
 atggcgagtc tgaaggacct gagaaaccgc attgcctcgg tgaaggcgac gcagaagatc 60
 accaaggcga tgcagatggt cgccgcggcg aagctgcgtc gcgccaggc ggcggctgaa 120
 gcggcccgctc cctatgcgga acgcatggag acgggtgctcg gaaatcttgc ctccggcatg 180

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gtggtgggcg cgcaggcgcc tgttctcatg accgggacgg gcaagagcga caccacctg      240
ctgctggtgt gcaccggcga gcgcggcctg tgcggcgcct tcaactcgtc catcgtgcgc      300
ttcgcccgcg agcgggcgca gctgctgctg gccgagggca agaaggtgaa aatcctgtgc      360
gtgggccgca agggccacga gcagctgcgc cgcattctacc cggacaacat catcgacgtg      420
gtggacctgc gcgcggtgcg caacatcggc ttcaaggagg ccgacgccat cgcccgaag      480
gtgctggccc tgctcgatga aggcgcattc gacgtctgca cgctcttcta ctcccacttc      540
aggagcgtga tcgcccaggt gccgacggcc cagcagctca ttccggccac cttcgacgag      600
cggccggccg tcgccgatgc gccggtctat gaatatgagc cggaggagga ggagatcctc      660
gccgagctgc tgccgcgcaa cgtggcggtg cagatcttca aggccctcct cgagaaccag      720
gcttctttct atggctccca gatgagcgcc atggacaacg ccacgcgcaa tgcgggcgag      780
atgatcaaga agcagacgct cacctacaac cgtacccgcc aggccatgat cacgaaggaa      840
ctcatcgaga tcatctccgg cgccgaggcc gtctga      876

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<210> 35
 <211> 291
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 35

Met Ala Ser Leu Lys Asp Leu Arg Asn Arg Ile Ala Ser Val Lys Ala
1 5 10 15

Thr Gln Lys Ile Thr Lys Ala Met Gln Met Val Ala Ala Ala Lys Leu
20 25 30

Arg Arg Ala Gln Ala Ala Ala Glu Ala Ala Arg Pro Tyr Ala Glu Arg
35 40 45

Met Glu Thr Val Leu Gly Asn Leu Ala Ser Gly Met Val Val Gly Ala
50 55 60

Gln Ala Pro Val Leu Met Thr Gly Thr Gly Lys Ser Asp Thr His Leu
65 70 75 80

Leu Leu Val Cys Thr Gly Glu Arg Gly Leu Cys Gly Ala Phe Asn Ser
85 90 95

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

Gly Lys Lys Val Lys Ile Leu Cys Val Gly Arg Lys Gly His Glu Gln
115 120 125

Leu Arg Arg Ile Tyr Pro Asp Asn Ile Ile Asp Val Val Asp Leu Arg

130135140

Ala Val Arg Asn Ile Gly Phe Lys Glu Ala Asp Ala Ile Ala Arg Lys
145150155160

Val Leu Ala Leu Leu Asp Glu Gly Ala Phe Asp Val Cys Thr Leu Phe
165170175

Tyr Ser His Phe Arg Ser Val Ile Ala Gln Val Pro Thr Ala Gln Gln
180185190

Leu Ile Pro Ala Thr Phe Asp Glu Arg Pro Ala Val Ala Asp Ala Pro
195200205

Val Tyr Glu Tyr Glu Pro Glu Glu Glu Glu Ile Leu Ala Glu Leu Leu
210215220

Pro Arg Asn Val Ala Val Gln Ile Phe Lys Ala Leu Leu Glu Asn Gln
225230235240

Ala Ser Phe Tyr Gly Ser Gln Met Ser Ala Met Asp Asn Ala Thr Arg
245250255

Asn Ala Gly Glu Met Ile Lys Lys Gln Thr Leu Thr Tyr Asn Arg Thr
260265270

Arg Gln Ala Met Ile Thr Lys Glu Leu Ile Glu Ile Ile Ser Gly Ala
275280285

Glu Ala Val
290

<210> 36<211> 1530<212> DNA<213> Unknown

<220><223> novel strain

<400> 36atggacattc gagccgctga aatctctgcc atcctgaaag agcagatcca gaatttcggc60caggaggcgg aagtctccga ggtgggtcag gttctgtccg tgggtgacgg catcgcgcg120gtctacggcc tcgacaacgt ccaggcgggc gagatggtcg agttcgagaa cggcacgcgc180ggcatggcgc tgaacctcga gtcgacaat gtcggcatcg tgatcttcgg ttccgaccgc240gagatcaagg aaggccagac cgtcaagcgg accggcgcca tcgtggacgc ccccgtcggc300aagggcctgc tcggccgctg cgtggacgct ctcggcaacc cgatcgacgg caagggcccgc360atcatgttca ccgagcgtcg ccgggtcgac gtgaaggcgc cgggcatcat cccgcgcaag420tcgggtgcacg agcccatgca gaccggcctg aaggccatcg atgcgctcat ccccatcggc480cgcgggccagc gcgagctcat catcggcgac cgccagaccg gcaagaccgc cgtggcgctc540

gactcgatcc tgaaccagaa gcccataaac cagggcgacg acgagaaggc caagctctac 600
 tgcgtctatg tcgcggtggg ccagaagcgt tccactgtcg cgcagttcgt gaaggtgctc 660
 gaggagcacg gcgcgctgga atattccatc gtcgtcgccg ccaccgcctc ggacgcggcc 720
 cccatgcagt tcctggcgcc gttcaccggc accgccatgg gcgagtattt ccgcgacaac 780
 ggcatgcacg ccctcatcat ccatgatgac ctgtccaagc aggccgtggc ctaccgccag 840
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 aaggcgatga agcaggtggc cggcaagatc aaggcgagc tcgccagta tcgcgagctg 1200
 gcggccttcg cccagttcgg ttcggacctg gacgcggcca cccagaagct gctgaaccgc 1260
 ggcgcccgcc tcaccgagct gctgaagcag agccagttct cggccctcaa ggtggaggag 1320
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 gtgcgcgagt tcgagcaggg tctgtcctg tcgtgcgct cgcagcatcc ggagatcctg 1440
 gacgccatcc gcacgtccaa ggagctttcc aaggacaccg ccgagaagct gacgaaggcc 1500
 atcgacgcct tcgccaagag cttctcctga 1530

<210> 37
 <211> 509
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 37

Met Asp Ile Arg Ala Ala Glu Ile Ser Ala Ile Leu Lys Glu Gln Ile
 1 5 10 15

Gln Asn Phe Gly Gln Glu Ala Glu Val Ser Glu Val Gly Gln Val Leu
 20 25 30

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

Ala Gly Glu Met Val Glu Phe Glu Asn Gly Thr Arg Gly Met Ala Leu
 50 55 60

Asn Leu Glu Leu Asp Asn Val Gly Ile Val Ile Phe Gly Ser Asp Arg
 65 70 75 80

Glu Ile Lys Glu Gly Gln Thr Val Lys Arg Thr Gly Ala Ile Val Asp
 85 90 95

Ala Pro Val Gly Lys Gly Leu Leu Gly Arg Val Val Asp Ala Leu Gly
100 105 110

Asn Pro Ile Asp Gly Lys Gly Pro Ile Met Phe Thr Glu Arg Arg Arg
115 120 125

Val Asp Val Lys Ala Pro Gly Ile Ile Pro Arg Lys Ser Val His Glu
130 135 140

Pro Met Gln Thr Gly Leu Lys Ala Ile Asp Ala Leu Ile Pro Ile Gly
145 150 155 160

Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr
165 170 175

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

Asp Asp Glu Lys Ala Lys Leu Tyr Cys Val Tyr Val Ala Val Gly Gln
195 200 205

Lys Arg Ser Thr Val Ala Gln Phe Val Lys Val Leu Glu Glu His Gly
210 215 220

Ala Leu Glu Tyr Ser Ile Val Val Ala Ala Thr Ala Ser Asp Ala Ala
225 230 235 240

Pro Met Gln Phe Leu Ala Pro Phe Thr Gly Thr Ala Met Gly Glu Tyr
245 250 255

Phe Arg Asp Asn Gly Met His Ala Leu Ile Ile His Asp Asp Leu Ser
260 265 270

Lys Gln Ala Val Ala Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro
275 280 285

Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg
290 295 300

Leu Leu Glu Arg Ala Ala Lys Leu Asn Asp Glu His Gly Ala Gly Ser
305 310 315 320

Leu Thr Ala Leu Pro Val Ile Glu Thr Gln Ala Asn Asp Val Ser Ala
325 330 335

Tyr Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Ile Phe Leu
340 345 350

Glu Ser Asp Leu Phe Tyr Gln Gly Ile Arg Pro Ala Val Asn Val Gly
355 360 365

Leu Ser Val Ser Arg Val Gly Ser Ser Ala Gln Ile Lys Ala Met Lys
370 375 380

Gln Val Ala Gly Lys Ile Lys Gly Glu Leu Ala Gln Tyr Arg Glu Leu
385 390 395 400

Ala Ala Phe Ala Gln Phe Gly Ser Asp Leu Asp Ala Ala Thr Gln Lys
405 410 415

Leu Leu Asn Arg Gly Ala Arg Leu Thr Glu Leu Leu Lys Gln Ser Gln
420 425 430

Phe Ser Pro Leu Lys Val Glu Glu Gln Val Ala Val Ile Tyr Ala Gly
435 440 445

Thr Asn Gly Tyr Leu Asp Pro Leu Pro Val Ser Lys Val Arg Glu Phe
450 455 460

Glu Gln Gly Leu Leu Leu Ser Leu Arg Ser Gln His Pro Glu Ile Leu
465 470 475 480

Asp Ala Ile Arg Thr Ser Lys Glu Leu Ser Lys Asp Thr Ala Glu Lys
485 490 495

Leu Thr Lys Ala Ile Asp Ala Phe Ala Lys Ser Phe Ser
500 505

<210> 38
<211> 555
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 38
gtggcggaaa cgatcgtgtc aggcattggcg ggacgctatg cgaccgcgct gttcgagctg 60
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ctggccgaga gcgcggatct ggcgcggtg gtcaagagcc cggctttcac cgccgagcag 180
cagctcggcg cgatggcggc cattctcgat caagcaggca ttccggcct tgcgggcaaa 240
ttcgtgaagc tgggtggcgca gaaccgccgc ctgttcgcac tgccgcgcat gattgccgaa 300
tacgccgtcc tgggtggccc gaagaagggc gagacctcgg cgagcgtgac cgttgccacc 360
cccctgagcg atgagcatct ggccacgctc aaggcggccc tggctgaaaa gaccggcaag 420
gacgtgaagc tcgacgtcac cgtcgatccg tccatcctcg gtggtctcat cgtgaagctc 480
ggctcgcgca tggtcgatgc ttccctgaag accaaactca attctatccg gcatgcgatg 540
aaagaggtcc gctga 555

<210> 39
<211> 184
<212> PRT

<213> Unknown

<220>

<223> novel strain

<400> 39

Met Ala Glu Thr Ile Val Ser Gly Met Ala Gly Arg Tyr Ala Thr Ala
1 5 10 15

Leu Phe Glu Leu Ala Asp Glu Ala Gly Ala Ile Asp Ser Val Gln Ala
20 25 30

Asp Leu Asp Arg Leu Ser Gly Leu Leu Ala Glu Ser Ala Asp Leu Ala
35 40 45

Arg Leu Val Lys Ser Pro Val Phe Thr Ala Glu Gln Gln Leu Gly Ala
50 55 60

Met Ala Ala Ile Leu Asp Gln Ala Gly Ile Ser Gly Leu Ala Gly Lys
65 70 75 80

Phe Val Lys Leu Val Ala Gln Asn Arg Arg Leu Phe Ala Leu Pro Arg
85 90 95

Met Ile Ala Glu Tyr Ala Val Leu Val Ala Arg Lys Lys Gly Glu Thr
100 105 110

Ser Ala Ser Val Thr Val Ala Thr Pro Leu Ser Asp Glu His Leu Ala
115 120 125

Thr Leu Lys Ala Ala Leu Ala Glu Lys Thr Gly Lys Asp Val Lys Leu
130 135 140

Asp Val Thr Val Asp Pro Ser Ile Leu Gly Gly Leu Ile Val Lys Leu
145 150 155 160

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

Arg His Ala Met Lys Glu Val Arg
180

<210> 40

<211> 492

<212> DNA

<213> Unknown

<220>

<223> novel strain

<400> 40

atgaccgaaa tggaactggc tgagctctgg gtcgccatcg ccttcctggt tttcgtaggc 60

ctcctgatct atgcgggcgc ccaccgcgc atcgtctccg ccctggattc ccgcggctcg 120

cgcctgcct cggaactgga ggaggcccg cggtcaagg aagaggccca gaagctggtg 180

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gccgaattca agcgcaagca gcgcgaggcc gaggccgagg ccgaatccat cgtcaccggc      240
gccaaggccg aggccgagcg cctcgccgcc gaggccaagg cgaagatcga ggatttcgtc      300
acccgccgca ccaagatggc cgaggacaag atcgcccagg ccgagcatca ggctctggcg      360
gacgtgaagt ccattcgccgc cgaggcggcg gccaaaggcg ccgaggtgat cctcggcgcc      420
caggccaccg gcgcggtggc ggagcgtctg ctgtcgggcg ccatctccga ggtcaagacc      480
aagctcaact ga                                                              492

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<210> 41
 <211> 163
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 41

Met Thr Glu Met Glu Leu Ala Glu Leu Trp Val Ala Ile Ala Phe Leu
1 5 10 15

Val Phe Val Gly Leu Leu Ile Tyr Ala Gly Ala His Arg Ala Ile Val
20 25 30

Ser Ala Leu Asp Ser Arg Gly Ser Arg Ile Ala Ser Glu Leu Glu Glu
35 40 45

Ala Arg Arg Leu Lys Glu Glu Ala Gln Lys Leu Val Ala Glu Phe Lys
50 55 60

Arg Lys Gln Arg Glu Ala Glu Ala Glu Ala Glu Ser Ile Val Thr Gly
65 70 75 80

Ala Lys Ala Glu Ala Glu Arg Leu Ala Ala Glu Ala Lys Ala Lys Ile
85 90 95

Glu Asp Phe Val Thr Arg Arg Thr Lys Met Ala Glu Asp Lys Ile Ala
100 105 110

Gln Ala Glu His Gln Ala Leu Ala Asp Val Lys Ser Ile Ala Ala Glu
115 120 125

Ala Ala Ala Lys Ala Ala Glu Val Ile Leu Gly Ala Gln Ala Thr Gly
130 135 140

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

Lys Leu Asn

<210> 42

<211> 729
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 42
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 atgcccgtcg cgggcgtggc cgagctgag acttctcccg ctccggcggc agtggcgag 120
 gccgatcatg cggtgccac cgaggcggcc ggccagggca ccgccgatgc ggcccatgcc 180
 gccgcgccgg gcgaggccgc ccatggtggc gcggccaagc acgaaacca tttcccgccc 240
 ttcgacggca ccaccttcgc ctcccagttg ctgtggctcg ccgtcacctt cggcctgctt 300
 tactacctca tgagcaaggt cacgtgccg cgcatcggcc gcatacctgga agagcgccac 360
 gaccgcatcg ccgatgatct ggaggaagcc tccaagcatc gcgccgagag cgaggccgcc 420
 cagcgggcct atgagaaggc gctgagcgag gcccgcgga agggccattc catcgccgcg 480
 gaaacccgcg accgccttgc gccccacgcc gacaccaacc gcaaggcgct ggagagcgag 540
 ctcaccgcca agctgcaggc ggccgaggag cgcatcgcca ccaccaagag cgaagccctc 600
 acccatgtgc gcggcatcgc ggtggacgcc acccaatcca tcgtctccac cctcatcggc 660
 gtcgcgcccc cggcggccga cgtggaaaaa gcggtggacg gcgccctgtc ccagcacggc 720
 caggcctga 729

<210> 43
 <211> 242
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 43

Met Met Ile Ala Trp Lys Arg Thr Phe Ala Val Val Thr Phe Gly Ala
 1 5 10 15

Ala Leu Met Ala Met Pro Val Ala Gly Val Val Ala Ala Glu Thr Ser
 20 25 30

Pro Ala Pro Ala Ala Val Ala Gln Ala Asp His Ala Val Pro Thr Glu
 35 40 45

Ala Ala Gly Gln Gly Thr Ala Asp Ala Ala His Ala Ala Ala Pro Gly
 50 55 60

Glu Ala Ala His Gly Gly Ala Ala Lys His Glu Thr His Phe Pro Pro
 65 70 75 80

Phe Asp Gly Thr Thr Phe Ala Ser Gln Leu Leu Trp Leu Ala Val Thr
 85 90 95

Phe Gly Leu Leu Tyr Tyr Leu Met Ser Lys Val Thr Leu Pro Arg Ile
100 105 110

Gly Arg Ile Leu Glu Glu Arg His Asp Arg Ile Ala Asp Asp Leu Glu
115 120 125

Glu Ala Ser Lys His Arg Ala Glu Ser Glu Ala Ala Gln Arg Ala Tyr
130 135 140

Glu Lys Ala Leu Ser Glu Ala Arg Ala Lys Ala His Ser Ile Ala Ala
145 150 155 160

Glu Thr Arg Asp Arg Leu Ala Ala His Ala Asp Thr Asn Arg Lys Ala
165 170 175

Leu Glu Ser Glu Leu Thr Ala Lys Leu Gln Ala Ala Glu Glu Arg Ile
180 185 190

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

Asp Ala Thr Gln Ser Ile Val Ser Thr Leu Ile Gly Val Ala Pro Ala
210 215 220

Ala Ala Asp Val Glu Lys Ala Val Asp Gly Ala Leu Ser Gln His Gly
225 230 235 240

Gln Ala

<210> 44
<211> 228
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 44
atggaagcgg aagctggaag gttcatcggg gccggcctcg cctgcctcgg catgggtctc 60
gctggcgctcg gcgtcggtaa catcttcggg aacttcctct ccggcgccct gcgcaaccgg 120
tccgctgccg acggccagtt cgcccgcgcc ttcacggcgc ccgccctcgc ggaaggtctc 180
ggcatcttct cgctggctgt tgcgctcgtc ctgctgttcg tggcctga 228

<210> 45
<211> 75
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 45

Met Glu Ala Glu Ala Gly Lys Phe Ile Gly Ala Gly Leu Ala Cys Leu

1					5					10					15				
Gly	Met	Gly	Leu	Ala	Gly	Val	Gly	Val	Gly	Asn	Ile	Phe	Gly	Asn	Phe				
			20					25					30						
Leu	Ser	Gly	Ala	Leu	Arg	Asn	Pro	Ser	Ala	Ala	Asp	Gly	Gln	Phe	Ala				
		35					40					45							
Arg	Ala	Phe	Ile	Gly	Ala	Ala	Leu	Ala	Glu	Gly	Leu	Gly	Ile	Phe	Ser				
	50					55					60								
Leu	Val	Val	Ala	Leu	Val	Leu	Leu	Phe	Val	Ala									
65					70					75									

<210>	46
<211>	753
<212>	DNA
<213>	Unknown

<220>
<223> novel strain

[illegible]

<210>	47
<211>	250
<212>	PRT
<213>	Unknown

<220>
<223> novel strain

<400> 47

Met Thr Val Asp Pro Ile His Gln Phe Glu Ile Lys Arg Tyr Val Asp
1 5 10 15

Leu Leu Asn Val Gly Gly Val Gln Phe Ser Phe Thr Asn Ala Thr Val
 20 25 30

Phe Met Ile Gly Ile Val Leu Val Ile Phe Phe Phe Leu Thr Phe Ala
 35 40 45

Thr Arg Gly Arg Thr Leu Val Pro Gly Arg Met Gln Ser Ala Ala Glu
 50 55 60

Leu Ser Tyr Glu Phe Ile Ala Lys Met Val Arg Asp Ala Ala Gly Ser
 65 70 75 80

Glu Gly Met Val Phe Phe Pro Phe Val Phe Ser Leu Phe Met Phe Val
 85 90 95

Leu Val Ala Asn Val Leu Gly Leu Ile Pro Tyr Thr Phe Thr Val Thr
 100 105 110

Ala His Leu Ile Val Thr Ala Ala Leu Ala Ala Thr Val Ile Leu Thr
 115 120 125

Val Ile Ile Tyr Gly Phe Val Arg His Gly Thr His Phe Leu His Leu
 130 135 140

Phe Val Pro Ser Gly Val Pro Gly Phe Leu Leu Pro Phe Leu Val Val
 145 150 155 160

Ile Glu Val Val Ser Phe Leu Ser Arg Pro Ile Ser Leu Ser Leu Arg
 165 170 175

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

Phe Phe Val Val Gly Leu Ala Ser Ala Gly Ala Ile Gly Trp Phe Gly
 195 200 205

Ala Thr Leu Pro Phe Phe Met Ile Val Ala Leu Thr Ala Leu Glu Leu
 210 215 220

Leu Val Ala Val Leu Gln Ala Tyr Val Phe Ala Val Leu Thr Ser Ile
 225 230 235 240

Tyr Leu Asn Asp Ala Ile His Pro Gly His
 245 250

<210> 48
 <211> 390
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 48

atgtccgagc cgaatgatcc atcccgagg gacggtgcga aggcgaaaga cgagacgcag 60
gactcccggc ccggtgaggc ggatcttgct cggcgccctcg atgcgctcgg cacctccatc 120
ggtcagggtca agtccagaag cggggagccc gcggcgacgc cgcgcaagga cacctcctcg 180
gcctccggcg cggccctggc gtttcggctg ggcgccgagt ttgtttcagg cgtgctgggtg 240
ggctcgctca tcggctacgg gttggattat gcgtttgcga tttcgccctg ggggctgatc 300
gccttcacgc tgatcggctt tgccgccggc gtcctgaaca tgctgcgcgt ggcgaacagc 360
gatgccaagc gccacagcgc ggacaggtga 390

<210> 49
<211> 129
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 49

Met Ser Glu Pro Asn Asp Pro Ser Arg Arg Asp Gly Ala Lys Ala Lys
1 5 10 15

Asp Glu Thr Gln Asp Ser Arg Pro Gly Glu Ala Asp Leu Ala Arg Arg
20 25 30

Leu Asp Ala Leu Gly Thr Ser Ile Gly Gln Val Lys Ser Arg Ser Gly
35 40 45

Glu Pro Ala Ala Thr Pro Arg Lys Asp Thr Ser Ser Ala Ser Gly Ala
50 55 60

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

Gly Ser Leu Ile Gly Tyr Gly Leu Asp Tyr Ala Phe Ala Ile Ser Pro
85 90 95

Trp Gly Leu Ile Ala Phe Thr Leu Ile Gly Phe Ala Ala Gly Val Leu
100 105 110

Asn Met Leu Arg Val Ala Asn Ser Asp Ala Lys Arg His Ser Ala Asp
115 120 125

Arg

<210> 50
<211> 1929
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 50

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atgagttcgc tctccgccac tattcaacag gtcttcaacg agccgggctg cgcgaagaac      60
cagaataagt ccgaggcgga gaagaagaag ggctgcacca agcagctgca acccggcgga      120
gcggccggcg gctgcgcgtt cgacggcgcg aagatcgcg tccagccctt gaccgacgtc      180
gcccacctgg tgcacggccc catcgctgc gaaggcaatt cctgggacaa tcgtggcgcc      240
aagtcctccg gctcgaacat ctggcgccacc ggcttcacca cggacatcaa cgaaaccgac      300
gtggtgttcg gcggcgagaa gcgtctgttc aagtccatca aggaaatcat cgagaagtac      360
gacccgccgg ccgtcttcgt ctatcagacc tgcgtcccg ccatgatcgg cgacgacatc      420
gacgcggtgt gcaaggcggc cagggagaag ttcggaaagc cggtgatccc gatcaattcc      480
cccggttcg tggggccgaa gaatctcggc aacaagctcg ccggcgaggc gtcctcgac      540
catgtgatcg gcaccgagga gcccgattac acgacggcct acgacatcaa catcatcggc      600
gaataacaat tctccggcga gttgtggcag gtgaagccgc tgctggacga gctgggcatc      660
cgcatcctcg cctgcatctc ggcgacggg aagtacaagg atgtggcgtc ctcccaccgc      720
gccaaggcgg cgatgatggt gtgctccaag gccatgatca acgtggccc caagatggag      780
gagcgctacg acatcccctt cttcgaaggc tccttctacg gcatcgagga tagctccgat      840
tccctgcgcg agattgcgcg catgctcatc gagaaggcg ccgatccgga gctgatggac      900
cgcaccgagg cgctgattga gcgggaagag aagaaggcgt gggacgcat cgccgcctac      960
aagccccgct tcaaggacaa gaagggtgct ctcatcaccg gcggcgtgaa atcctggtcg     1020
gtggtggcag cgctccagga agccggcctc gaactggtgg gcacctcggg gaagaagtcc     1080
accaaggagg acaaggagcg catcaaggaa ctgatgggccc aggacgcca catgatcgac     1140
gacatgacgc cccgcgaaat gtacaagatg ctgaaggacg ccaaggcgga catcatgctc     1200
tcgggcgggc gctcgcaatt catcgcgctc aaggccgcca tgccctggct cgacatcaac     1260
caggagcgcc accacgccta tatgggctat gtgggcatgg tgaagctggt cgaggagatc     1320
gacaaggcgc tctacaatcc cgtgtgggaa cagggtgcga agcccgcctc gtgggaaaat     1380
ccggaagaca cctggcaggc ccgtgcgctc gccgaaatgg aggcggaggc cgccgcgctc     1440
gccgccgatc cgggtgcgcg ggaagagggtg cgccgggtcca agaagatctg caattgcaag     1500
agcgtcgacc tcggaaccat tgaggacgcc atcaaggctc acgcgctgac caccgtggag     1560
ggtgtgcgag agcacaccaa tgacctggga ggctgcggag cctgcagcgg gcggatcgag     1620
gagatcttcg aggccgtggg cggtgtcgcc gccccgcctc ccgaggaggc cgccccgtct     1680
ccgcaggaga tcgcgcccga tccgctcgct gcggaggaaa agcgccgcgc caagaaggcc     1740
tgccgctgca aggaggtagc ggtcggcacc attgaggatg ccatccgcgc caagggtctg     1800
cgaaacatcg cggaggtgcg tgcggccacc gatgccaaca ccggctgcgg caattgccag     1860
gagcgggtgg agggcatcct cgaccgggtt ctgcgcgagg cggcctcaga actccaggcg     1920
gcggaatag                                     1929

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<210> 51

<211> 642
<212> PRT
<213> Unknown

<220>
<223> novel strain

<400> 51

Met Ser Ser Leu Ser Ala Thr Ile Gln Gln Val Phe Asn Glu Pro Gly
1 5 10 15

Cys Ala Lys Asn Gln Asn Lys Ser Glu Ala Glu Lys Lys Lys Gly Cys
20 25 30

Thr Lys Gln Leu Gln Pro Gly Gly Ala Ala Gly Gly Cys Ala Phe Asp
35 40 45

Gly Ala Lys Ile Ala Leu Gln Pro Leu Thr Asp Val Ala His Leu Val
50 55 60

His Gly Pro Ile Ala Cys Glu Gly Asn Ser Trp Asp Asn Arg Gly Ala
65 70 75 80

Lys Ser Ser Gly Ser Asn Ile Trp Arg Thr Gly Phe Thr Thr Asp Ile
85 90 95

Asn Glu Thr Asp Val Val Phe Gly Gly Glu Lys Arg Leu Phe Lys Ser
100 105 110

Ile Lys Glu Ile Ile Glu Lys Tyr Asp Pro Pro Ala Val Phe Val Tyr
115 120 125

Gln Thr Cys Val Pro Ala Met Ile Gly Asp Asp Ile Asp Ala Val Cys
130 135 140

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

Pro Gly Phe Val Gly Pro Lys Asn Leu Gly Asn Lys Leu Ala Gly Glu
165 170 175

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

Ala Tyr Asp Ile Asn Ile Ile Gly Glu Tyr Asn Leu Ser Gly Glu Leu
195 200 205

Trp Gln Val Lys Pro Leu Leu Asp Glu Leu Gly Ile Arg Ile Leu Ala
210 215 220

Cys Ile Ser Gly Asp Gly Lys Tyr Lys Asp Val Ala Ser Ser His Arg
225 230 235 240

Ala Lys Ala Ala Met Met Val Cys Ser Lys Ala Met Ile Asn Val Ala
245 250 255

Arg Lys Met Glu Glu Arg Tyr Asp Ile Pro Phe Phe Glu Gly Ser Phe
260 265 270

Tyr Gly Ile Glu Asp Ser Ser Asp Ser Leu Arg Glu Ile Ala Arg Met
275 280 285

Leu Ile Glu Lys Gly Ala Asp Pro Glu Leu Met Asp Arg Thr Glu Ala
290 295 300

Leu Ile Glu Arg Glu Glu Lys Lys Ala Trp Asp Ala Ile Ala Ala Tyr
305 310 315 320

Lys Pro Arg Phe Lys Asp Lys Lys Val Leu Leu Ile Thr Gly Gly Val
325 330 335

Lys Ser Trp Ser Val Val Ala Ala Leu Gln Glu Ala Gly Leu Glu Leu
340 345 350

Val Gly Thr Ser Val Lys Lys Ser Thr Lys Glu Asp Lys Glu Arg Ile
355 360 365

Lys Glu Leu Met Gly Gln Asp Ala His Met Ile Asp Asp Met Thr Pro
370 375 380

Arg Glu Met Tyr Lys Met Leu Lys Asp Ala Lys Ala Asp Ile Met Leu
385 390 395 400

Ser Gly Gly Arg Ser Gln Phe Ile Ala Leu Lys Ala Ala Met Pro Trp
405 410 415

Leu Asp Ile Asn Gln Glu Arg His His Ala Tyr Met Gly Tyr Val Gly
420 425 430

Met Val Lys Leu Val Glu Glu Ile Asp Lys Ala Leu Tyr Asn Pro Val
435 440 445

Trp Glu Gln Val Arg Lys Pro Ala Pro Trp Glu Asn Pro Glu Asp Thr
450 455 460

Trp Gln Ala Arg Ala Leu Ala Glu Met Glu Ala Glu Ala Ala Ala Leu
465 470 475 480

Ala Ala Asp Pro Val Arg Ala Glu Glu Val Arg Arg Ser Lys Lys Ile
485 490 495

Cys Asn Cys Lys Ser Val Asp Leu Gly Thr Ile Glu Asp Ala Ile Lys
500 505 510

Ala His Ala Leu Thr Thr Val Glu Gly Val Arg Glu His Thr Asn Ala

515

520

525

Ser Gly Gly Cys Gly Ala Cys Ser Gly Arg Ile Glu Glu Ile Phe Glu
530 535 540

Ala Val Gly Val Val Ala Ala Pro Pro Pro Ala Glu Ala Ala Pro Ser
545 550 555 560

Pro Gln Glu Ile Ala Pro Asp Pro Leu Ala Ala Glu Glu Lys Arg Arg
565 570 575

Ala Lys Lys Ala Cys Gly Cys Lys Glu Val Ala Val Gly Thr Ile Glu
580 585 590

Asp Ala Ile Arg Ala Lys Gly Leu Arg Asn Ile Ala Glu Val Arg Ala
595 600 605

Ala Thr Asp Ala Asn Thr Gly Cys Gly Asn Cys Gln Glu Arg Val Glu
610 615 620

Gly Ile Leu Asp Arg Val Leu Ala Glu Ala Ala Ser Glu Leu Gln Ala
625 630 635 640

Ala Glu

<210> 52
<211> 1503
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 52
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gaagagggtcc tcaagggtcta tcccgagaag accgccaagc gccgcgcaa gcacctgaac 120
gtccacgaag ccggcaagtc cgactgcggc gtgaagtcca acatcaagtc catcccgggc 180
gtgatgacca tccgcggttg cgcttatgcc ggctccaagg gtgtggtgtg ggggtcccatc 240
aaggacatga tccacatctc ccacggcccc gtgggctgcg gccagtatag ctgggccgccc 300
cgccgcaact actatatcgg cagcaccggc atcgacacct tcgtgacgat gcagttcacc 360
tccgacttcc aggagaagga catcgtcttc ggccggcgaca agaagctcgc caagatcatg 420
gacgagatcc aggagctggt cccgctgaac aacggcatca ccgttcagtc cgagtgcacc 480
atcggcctca tcggcgacga catcgaggcc gtctccaagc agaagtccaa ggagtatgag 540
ggcaagacca tcgtgccggt gcgctgcgag ggcttcgcg gcgtgtccca gtccctgggc 600
caccacatcg ccaacgacgc catccgcgat tgggtgttcg acaagatcgc gcccgacgcc 660
gagccgcgct ttgagccgac cccgtacgac gtcgcatca tcggcgacta caatatcggt 720
ggtgacgcct ggtcgtcccc tatcctcctg gaggagatgg gcctgcgcgt gatcgcccag 780

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tgggtccggcg acggttcgct cgctgagctg gaggccaccc cgaaggccaa gctcaacgtg      840
ctgcactgct accgctccat gaactacatc tcgcgccaca tggaagagaa gtacgggtatc      900
ccgtgggtgcg agtacaactt cttcggtcct tccaagatcg ccgagtcctt gcgcaagatc      960
gccagctact tcgacgacaa gatcaaggaa ggcgcgggagc gcgtcatcgc caagtatcag     1020
ccgctcatgg atgcggtgat cgcgaagtat cgtccccgcc tcgagggcaa gaccgtgatg     1080
ctgtacgtgg gcggcctgcg tccccgtcac gtcacggcg cctacgagga cctgggcatg     1140
gaagtggctg gcacgggcta cgagttcgcc cataacgacg actaccagcg caccgcccag     1200
cactacgtca aggatggcac catcatctat gacgacgtga ccggctacga gttcgagaag     1260
ttcgtcgaga agatccagcc ggacctggtc ggttcgggca tcaaggaaaa gtacgtcttc     1320
cagaagatgg gcgtgccgtt ccgccagatg cactcctggg actactcggg cccgtaccac     1380
ggctatgacg gcttcgcat cttcgcgcg gacatggaca tggccatcaa cagccccgtg     1440
tggaagatga cccaggctcc gtggaagagc gtccccaagc cgacgatgct cgcggctgaa     1500
tga                                                                    1503

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<210> 53
 <211> 500
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 53

Met Ser Val Ala Gln Ser Gln Ser Val Ala Glu Ile Lys Ala Arg Asn
1 5 10 15

Lys Glu Leu Ile Glu Glu Val Leu Lys Val Tyr Pro Glu Lys Thr Ala
20 25 30

Lys Arg Arg Ala Lys His Leu Asn Val His Glu Ala Gly Lys Ser Asp
35 40 45

Cys Gly Val Lys Ser Asn Ile Lys Ser Ile Pro Gly Val Met Thr Ile
50 55 60

Arg Gly Cys Ala Tyr Ala Gly Ser Lys Gly Val Val Trp Gly Pro Ile
65 70 75 80

Lys Asp Met Ile His Ile Ser His Gly Pro Val Gly Cys Gly Gln Tyr
85 90 95

Ser Trp Ala Ala Arg Arg Asn Tyr Tyr Ile Gly Thr Thr Gly Ile Asp
100 105 110

Thr Phe Val Thr Met Gln Phe Thr Ser Asp Phe Gln Glu Lys Asp Ile
115 120 125

Val Phe Gly Gly Asp Lys Lys Leu Ala Lys Ile Met Asp Glu Ile Gln
130 135 140

Glu Leu Phe Pro Leu Asn Asn Gly Ile Thr Val Gln Ser Glu Cys Pro
145 150 155 160

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

Lys Glu Tyr Glu Gly Lys Thr Ile Val Pro Val Arg Cys Glu Gly Phe
180 185 190

Arg Gly Val Ser Gln Ser Leu Gly His His Ile Ala Asn Asp Ala Ile
195 200 205

Arg Asp Trp Val Phe Asp Lys Ile Ala Pro Asp Ala Glu Pro Arg Phe
210 215 220

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

Gly Asp Ala Trp Ser Ser Arg Ile Leu Leu Glu Glu Met Gly Leu Arg
245 250 255

Val Ile Ala Gln Trp Ser Gly Asp Gly Ser Leu Ala Glu Leu Glu Ala
260 265 270

Thr Pro Lys Ala Lys Leu Asn Val Leu His Cys Tyr Arg Ser Met Asn
275 280 285

Tyr Ile Ser Arg His Met Glu Glu Lys Tyr Gly Ile Pro Trp Cys Glu
290 295 300

Tyr Asn Phe Phe Gly Pro Ser Lys Ile Ala Glu Ser Leu Arg Lys Ile
305 310 315 320

Ala Ser Tyr Phe Asp Asp Lys Ile Lys Glu Gly Ala Glu Arg Val Ile
325 330 335

Ala Lys Tyr Gln Pro Leu Met Asp Ala Val Ile Ala Lys Tyr Arg Pro
340 345 350

Arg Leu Glu Gly Lys Thr Val Met Leu Tyr Val Gly Gly Leu Arg Pro
355 360 365

Arg His Val Ile Gly Ala Tyr Glu Asp Leu Gly Met Glu Val Val Gly
370 375 380

Thr Gly Tyr Glu Phe Ala His Asn Asp Asp Tyr Gln Arg Thr Ala Gln
385 390 395 400

His Tyr Val Lys Asp Gly Thr Ile Ile Tyr Asp Asp Val Thr Gly Tyr
405 410 415

Glu Phe Glu Lys Phe Val Glu Lys Ile Gln Pro Asp Leu Val Gly Ser
420 425 430

Gly Ile Lys Glu Lys Tyr Val Phe Gln Lys Met Gly Val Pro Phe Arg
435 440 445

Gln Met His Ser Trp Asp Tyr Ser Gly Pro Tyr His Gly Tyr Asp Gly
450 455 460

Phe Ala Ile Phe Ala Arg Asp Met Asp Met Ala Ile Asn Ser Pro Val
465 470 475 480

Trp Lys Met Thr Gln Ala Pro Trp Lys Ser Val Pro Lys Pro Thr Met
485 490 495

Leu Ala Ala Glu
500

<210> 54
<211> 1377
<212> DNA
<213> Unknown

<220>
<223> novel strain

<400> 54
atggccaccg tttccgtctc caagaaggcc tgcgcggtca acccctcaa gatgagccag 60
ccggtgggac gcgcgctcgc cttcatgggc gtgcgcaagg ccatgccgct gctgcacggc 120
tcgcagggct gcacctcctt cggcctgggtg ctgttcgtgc gccacttcaa ggaagccatc 180
cccatgcaga ccaccgccat gagcgagggtg gcgacgggtc tggcgggcct tgagaatgtg 240
gagcaggcca ttctcaacat ctacaatcgc accaagccgg agatcatcgg catctgctcc 300
accggcgtca ccgagaccaa gggcgatgat gtcgacggct acatcaagct gatccgggac 360
aagtatcccc agctggccga cttcccgctg gtctatgtct ccacccccga tttcaaggac 420
gccttccagg acggttggga gaagaccgtg gcgaagatgg tggaggcgct ggtgaagccc 480
gccgccgaca agcagaagga caagaccgc gtcaacgtcc tgcccggtg ccacctcacg 540
cccggcgatc tggatgagat gcggaccatc ttcgaggatt tcgggctcac accctatttc 600
ctgccggatc tggccggctc gctggatggg catatccccg aggacttctc gccaccacc 660
atcggcggca tcggcatcga tgagatcgcc accatgggag aggcggccca caccatctgc 720
atcggcgcg c agatgcgccg ggccggcgag gccatggaga agaagaccgg cattcccttc 780
aagctgttcg agcgctgtg cggcctggag gcgaacgac cttcatcat gcacctgtcg 840
cagatctccg gccggccggt gccggtgaag tatcgccggc agcggggcca gctggtggat 900
gccatgctgg acggccactt ccatctgggc ggtcgcaagg tggccatggg ggccggagccg 960

gacctgtctt acgacgtggg ctctttcctg cactgagatgg gcgcccacat cttttccgcg 1020
 gtcaccacca cccagtcgcc ggtgctggcg cgctgcctg ccgaggaggt gcttatcggc 1080
 gacctggagg atctggagac ccaggcgaag gcgcgcggat gcgatctcct gctcacccat 1140
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 atgtttgacc ggctgggggc ggggcatctg ttgtcggtgg gctatcgcgg caccgcgcac 1260
 ctcatcttcc atctcgcaa cttgtgatc gccgaccacg aggaaaatca cgagccgacg 1320
 cccgacacct gggccaccgg ccatggcgag catgccgccg cccccacttc ccattga 1377

<210> 55
 <211> 458
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 55

Met Ala Thr Val Ser Val Ser Lys Lys Ala Cys Ala Val Asn Pro Leu
1 5 10 15

Lys Met Ser Gln Pro Val Gly Gly Ala Leu Ala Phe Met Gly Val Arg
20 25 30

Lys Ala Met Pro Leu Leu His Gly Ser Gln Gly Cys Thr Ser Phe Gly
35 40 45

Leu Val Leu Phe Val Arg His Phe Lys Glu Ala Ile Pro Met Gln Thr
50 55 60

Thr Ala Met Ser Glu Val Ala Thr Val Leu Gly Gly Leu Glu Asn Val
65 70 75 80

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

Gly Ile Cys Ser Thr Gly Val Thr Glu Thr Lys Gly Asp Asp Val Asp
100 105 110

Gly Tyr Ile Lys Leu Ile Arg Asp Lys Tyr Pro Gln Leu Ala Asp Phe
115 120 125

Pro Leu Val Tyr Val Ser Thr Pro Asp Phe Lys Asp Ala Phe Gln Asp
130 135 140

Gly Trp Glu Lys Thr Val Ala Lys Met Val Glu Ala Leu Val Lys Pro
145 150 155 160

Ala Ala Asp Lys Gln Lys Asp Lys Thr Arg Val Asn Val Leu Pro Gly
165 170 175

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

Asp Phe Gly Leu Thr Pro Tyr Phe Leu Pro Asp Leu Ala Gly Ser Leu
195 200 205

Asp Gly His Ile Pro Glu Asp Phe Ser Pro Thr Thr Ile Gly Gly Ile
210 215 220

Gly Ile Asp Glu Ile Ala Thr Met Gly Glu Ala Ala His Thr Ile Cys
225 230 235 240

Ile Gly Ala Gln Met Arg Arg Ala Gly Glu Ala Met Glu Lys Lys Thr
245 250 255

Gly Ile Pro Phe Lys Leu Phe Glu Arg Leu Cys Gly Leu Glu Ala Asn
260 265 270

Asp Ala Phe Ile Met His Leu Ser Gln Ile Ser Gly Arg Pro Val Pro
275 280 285

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

Gly His Phe His Leu Gly Gly Arg Lys Val Ala Met Gly Ala Glu Pro
305 310 315 320

Asp Leu Leu Tyr Asp Val Gly Ser Phe Leu His Glu Met Gly Ala His
325 330 335

Ile Leu Ser Ala Val Thr Thr Thr Gln Ser Pro Val Leu Ala Arg Leu
340 345 350

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

Ala Lys Ala Arg Gly Cys Asp Leu Leu Leu Thr His Ser His Gly Arg
370 375 380

Gln Ala Ala Glu Arg Leu His Ile Pro Phe Tyr Arg Ile Gly Ile Pro
385 390 395 400

Met Phe Asp Arg Leu Gly Ala Gly His Leu Leu Ser Val Gly Tyr Arg
405 410 415

Gly Thr Arg Asp Leu Ile Phe His Leu Ala Asn Leu Val Ile Ala Asp
420 425 430

His Glu Glu Asn His Glu Pro Thr Pro Asp Thr Trp Ala Thr Gly His
435 440 445

Gly Glu His Ala Ala Ala Pro Thr Ser His

450

455

<210> 56
 <211> 1560
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 56
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 cagcagatgc tggccaataa gaaaaagatg ttcgagaacc cccgcgatcc ggccgaagtc 120
 gagcgcgtgc gggaatgggc gaagactcct gaatacaagg agctgaactt cgcccgcgag 180
 gcgctcaccg tgaatccggc caaggcttgt cagccgctgg gcgcggtgtt cgtcgccgtc 240
 ggcttcgaga gcacgatccc ctctgtgcac ggctcgcagg gttgcgtcgc gtattaccgc 300
 tcgcacctct cccgccactt caaggagccg tcctcctgct tctcctcgtc catgaccgag 360
 gatgcggcgg tggtcggcgg cctcaacaac atgattgacg gcctcgcaa cacctacaac 420
 atgtacaagc cgaagatgat cgccgtctcc accacctgca tggcggaagt catcggcgac 480
 gatctgaacg cttcatcaa gaccgcgaag gaaaagggtc cggttccggc cgaatacgac 540
 gtgcccttcg cccacacccc ggcgttcgtc ggagccatg tcaccggcta cgacaatgag 600
 ctcaagggca tcctcgagca ctcttgggac ggcaaggccg gcaccgcgcc gaagctggag 660
 cgcgttccca acgagaagat caacttcacg ggcggcttcg acggctacac cgtcggcaac 720
 actcgcaag tgaagcgcat ctctgaggcg ttggcgccg attacacat cctcgccgac 780
 aattccgaag tggtcgacac cccgaccgac ggcgagttcc gcatgtatga cggcggcacg 840
 accctggagg acgcggcgaa cgcggtgcac gccaaaggcca ccatctccat gcaggaatac 900
 tgcacggaga agaccctgcc catgatcgcc ggtcatggcc aggacgtggt cgccctcaac 960
 caccctgtgg gcgtgggcgg caccgacaag ttctcatagg agatcgccc cctcaccggc 1020
 aaggagatcc ccgaggagct gaccgcgag cgcggccgtc tcgtggacgc tatcgcgac 1080
 tcttccgcgc acatccacgg caagaagttc gccatctacg gcgatccgga tctgtgcctg 1140
 ggcttcgccg cgttcctgct ggagctgggc gccgagccga ccatgtgct ggccaccaac 1200
 ggccaccaaga agtgggcca gaaggttcag gaactgttcg actcttcgcc gttcggcgcc 1260
 aactgcaagg tctatcccgg caaggacctg tggcacatgc gtcgctcct gttcgtggag 1320
 ccggtggatt tcatcatcgg caacacctac ggcaagtatc tcgagcgca cacgggcacc 1380
 ccgctgatcc gtatcggtt cccggtgttc gaccgtcacc accaccaccg ccgtccggtg 1440
 tggggctatc agggcgcat gaacgtcctg atcacgatcc tcgacaagat ctttgacgag 1500
 atcgaccgca acaccaacgt gccggccaag accgactact cgttcgacat cattcgttga 1560

<210> 57
 <211> 519
 <212> PRT
 <213> Unknown

<220>

<223> novel strain

<400> 57

Met Pro Gln Asn Ala Asp Asn Val Leu Asp His Phe Glu Leu Phe Arg
1 5 10 15

Gly Pro Glu Tyr Gln Gln Met Leu Ala Asn Lys Lys Lys Met Phe Glu
20 25 30

Asn Pro Arg Asp Pro Ala Glu Val Glu Arg Val Arg Glu Trp Ala Lys
35 40 45

Thr Pro Glu Tyr Lys Glu Leu Asn Phe Ala Arg Glu Ala Leu Thr Val
50 55 60

Asn Pro Ala Lys Ala Cys Gln Pro Leu Gly Ala Val Phe Val Ala Val
65 70 75 80

Gly Phe Glu Ser Thr Ile Pro Phe Val His Gly Ser Gln Gly Cys Val
85 90 95

Ala Tyr Tyr Arg Ser His Leu Ser Arg His Phe Lys Glu Pro Ser Ser
100 105 110

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

Asn Asn Met Ile Asp Gly Leu Ala Asn Thr Tyr Asn Met Tyr Lys Pro
130 135 140

Lys Met Ile Ala Val Ser Thr Thr Cys Met Ala Glu Val Ile Gly Asp
145 150 155 160

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

Ala Glu Tyr Asp Val Pro Phe Ala His Thr Pro Ala Phe Val Gly Ser
180 185 190

His Val Thr Gly Tyr Asp Asn Ala Leu Lys Gly Ile Leu Glu His Phe
195 200 205

Trp Asp Gly Lys Ala Gly Thr Ala Pro Lys Leu Glu Arg Val Pro Asn
210 215 220

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

Thr Arg Glu Val Lys Arg Ile Phe Glu Ala Phe Gly Ala Asp Tyr Thr
245 250 255

Ile Leu Ala Asp Asn Ser Glu Val Phe Asp Thr Pro Thr Asp Gly Glu
260 265 270

Phe Arg Met Tyr Asp Gly Gly Thr Thr Leu Glu Asp Ala Ala Asn Ala
275 280 285

Val His Ala Lys Ala Thr Ile Ser Met Gln Glu Tyr Cys Thr Glu Lys
290 295 300

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

His Pro Val Gly Val Gly Gly Thr Asp Lys Phe Leu Met Glu Ile Ala
325 330 335

Arg Leu Thr Gly Lys Glu Ile Pro Glu Glu Leu Thr Arg Glu Arg Gly
340 345 350

Arg Leu Val Asp Ala Ile Ala Asp Ser Ser Ala His Ile His Gly Lys
355 360 365

Lys Phe Ala Ile Tyr Gly Asp Pro Asp Leu Cys Leu Gly Leu Ala Ala
370 375 380

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

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

Pro Phe Gly Ala Asn Cys Lys Val Tyr Pro Gly Lys Asp Leu Trp His
420 425 430

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

Thr Tyr Gly Lys Tyr Leu Glu Arg Asp Thr Gly Thr Pro Leu Ile Arg
450 455 460

Ile Gly Phe Pro Val Phe Asp Arg His His His His Arg Arg Pro Val
465 470 475 480

Trp Gly Tyr Gln Gly Gly Met Asn Val Leu Ile Thr Ile Leu Asp Lys
485 490 495

Ile Phe Asp Glu Ile Asp Arg Asn Thr Asn Val Pro Ala Lys Thr Asp
500 505 510

Tyr Ser Phe Asp Ile Ile Arg
515

<210> 58
 <211> 621
 <212> DNA
 <213> Unknown

<220>
 <223> novel strain

<400> 58
 gtggagtcgc gtggctctga gccgggcgtg ggctgcgccg gccgcggcgt gatcacctcc 60
 atcaacttcc tggaggagaa cggcgcctac gaggacatcg actatgtgtc ctacgacgtg 120
 ctgggcgacg tgggtgtcgg cggcttcgcc atgcccattc gcgagaacaa ggcgagaggaa 180
 atctacatcg tgatgtccgg cgagatgatg gccatgtatg cggccaacaa catctccaag 240
 ggcatcctga agtatgcaa ttccggcggc gtgcgcctgg gcgggctggt ctgcaacgag 300
 cgccagaccg acaaggagct ggagctggcg gaggctctgg cgaagaagct cggcaccgag 360
 ctgatctact tcgtgccgcg cgacaacatc gtgcagcatg ccgagctgcg ccgcatgaca 420
 gtgatcgagt atgcgcccga ttccgcccag gcccgagcact accggaacct ggccgagaag 480
 gtgcacgcca acaagggcaa cggcatcatc ccgacccga tcaccatgga cgagctggaa 540
 gacatgctca tggagcacgg catcatgaag gccgtggacg agagccagat cggcaagacc 600
 gccgccgagc tcgccgtctg a 621

<210> 59
 <211> 206
 <212> PRT
 <213> Unknown

<220>
 <223> novel strain

<400> 59

Met Glu Ser Gly Gly Pro Glu Pro Gly Val Gly Cys Ala Gly Arg Gly
 1 5 10 15

Val Ile Thr Ser Ile Asn Phe Leu Glu Glu Asn Gly Ala Tyr Glu Asp
 20 25 30

Ile Asp Tyr Val Ser Tyr Asp Val Leu Gly Asp Val Val Cys Gly Gly
 35 40 45

Phe Ala Met Pro Ile Arg Glu Asn Lys Ala Gln Glu Ile Tyr Ile Val
 50 55 60

Met Ser Gly Glu Met Met Ala Met Tyr Ala Ala Asn Asn Ile Ser Lys
 65 70 75 80

Gly Ile Leu Lys Tyr Ala Asn Ser Gly Gly Val Arg Leu Gly Gly Leu
 85 90 95

Val Cys Asn Glu Arg Gln Thr Asp Lys Glu Leu Glu Leu Ala Glu Ala
 100 105 110

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

Asn Ile Val Gln His Ala Glu Leu Arg Arg Met Thr Val Ile Glu Tyr
130 135 140

Ala Pro Asp Ser Ala Gln Ala Gln His Tyr Arg Asn Leu Ala Glu Lys
145 150 155 160

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

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

Asp Glu Ser Gln Ile Gly Lys Thr Ala Ala Glu Leu Ala Val
195 200 205