

202663_ST25.txt
SEQUENCE LISTING

<110> Lonza AG

<120> A process for the identification and preparation of a (R)-specific omega-transaminase

<130> 202663

<160> 50

<170> PatentIn version 3.5

<210> 1

<211> 322

<212> PRT

<213> Mesorhizobium loti

<400> 1

Met Thr Leu Ala Thr Thr Asp Ala Thr Val Gly Val Pro Glu Val Glu
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Thr Thr His Lys Asp Thr Arg Arg Tyr Pro His Gly Val Ala Phe Met
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Asp Gly Gln Tyr Leu Pro Met Ser Glu Ala Lys Ile Ser Val Leu Asp
35 40 45

Trp Gly Phe Leu His Ser Asp Ala Thr Tyr Asp Thr Val His Val Trp
50 55 60

Glu Gly Arg Phe Phe Arg Leu Asp Leu His Leu Asp Arg Phe Phe Arg
65 70 75 80

Gly Met Asp Arg Leu Arg Met Lys Leu Pro Tyr His Arg Arg Glu Val
85 90 95

Glu Arg Val Leu Ser Asn Cys Val Ala Leu Ser Gly His Lys Ser Ala
100 105 110

Tyr Val Glu Met Ile Cys Thr Arg Gly Gly Ser Pro Thr Phe Ser Arg
115 120 125

Asp Pro Arg Glu Ala Glu Asn Arg Phe Ile Ala Phe Ala Val Pro Phe
130 135 140

Gly Ser Val Ala Asn Lys Glu Gln Leu Glu Arg Gly Leu His Val Gly
145 150 155 160

Val Ser Glu Thr Val Arg Ile Pro Pro Lys Ser Val Asp Pro Thr Ile
165 170 175

Lys Asn Tyr His Trp Leu Asp Leu Val Arg Gly Leu Tyr Asp Ala Tyr
180 185 190

Asp Val Gly Ala Glu Thr Ala Leu Ile Met Asp Thr Asn Gly Asn Ile
195 200 205

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

Lys Thr Pro Ala Phe Gly Val Leu Pro Gly Ile Thr Arg Gln Ser Val
225 230 235 240

Phe Asp Leu Cys Gly Glu Val Gly Leu Ala Val Thr Ala Ala Asp Leu
245 250 255

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

Ala Gly Gly Ile Met Pro Val Thr Arg Val Asp Gly Ser Ser Ile Gly
275 280 285

Ser Gly Lys Val Gly Val Val Thr Arg Gln Leu Met Asp Leu Tyr Trp
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Gln Lys His Ser Asp Asp Ala Trp Ser Thr Pro Val Lys Tyr Ala Ser
305 310 315 320

Gly Ser

<210> 2
<211> 969
<212> DNA
<213> Mesorhizobium loti

<400> 2
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gaagcaaaaa ttagcgttct ggattgggggt tttctgcatt ctgatgccac ctatgatacc 180
gttcatgttt gggaagggtcg tttttttcgt ctggatctgc atctggatcg cttttttcgt 240
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<210> 3
 <211> 328
 <212> PRT
 <213> Aspergillus terreus

<400> 3

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

Leu Asp Gln Gly Phe Met His Ser Asp Leu Thr Tyr Asp Val Pro Ser
 50 55 60

Val Trp Asp Gly Arg Phe Phe Arg Leu Asp Asp His Ile Thr Arg Leu
 65 70 75 80

Glu Ala Ser Cys Thr Lys Leu Arg Leu Arg Leu Pro Leu Pro Arg Asp
 85 90 95

Gln Val Lys Gln Ile Leu Val Glu Met Val Ala Lys Ser Gly Ile Arg
 100 105 110

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

Gly Thr Arg Pro Glu Asp Ile Val Asn Asn Leu Tyr Met Phe Val Gln
 130 135 140

Pro Tyr Val Trp Val Met Glu Pro Asp Met Gln Arg Val Gly Gly Ser
 145 150 155 160

Ala Val Val Ala Arg Thr Val Arg Arg Val Pro Pro Gly Ala Ile Asp
 165 170 175

Pro Thr Val Lys Asn Leu Gln Trp Gly Asp Leu Val Arg Gly Met Phe
 180 185 190

Glu Ala Ala Asp Arg Gly Ala Thr Tyr Pro Phe Leu Thr Asp Gly Asp
 195 200 205

202663_ST25.txt

Ala His Leu Thr Glu Gly Ser Gly Phe Asn Ile Val Leu Val Lys Asp
 210 215 220

Gly Val Leu Tyr Thr Pro Asp Arg Gly Val Leu Gln Gly Val Thr Arg
 225 230 235 240

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

Glu Phe Val Pro Val Glu Leu Ala Tyr Arg Cys Asp Glu Ile Phe Met
 260 265 270

Cys Thr Thr Ala Gly Gly Ile Met Pro Ile Thr Thr Leu Asp Gly Met
 275 280 285

Pro Val Asn Gly Gly Gln Ile Gly Pro Ile Thr Lys Lys Ile Trp Asp
 290 295 300

Gly Tyr Trp Ala Met His Tyr Asp Ala Ala Tyr Ser Phe Glu Ile Asp
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Tyr Asn Glu Arg Asn Ser Gly Ser
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<210> 4

<211> 987

<212> DNA

<213> Aspergillus terreus

<400> 4

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| accgaaacca ccaatccgtt tgcaaaaggt attgcatggg ttgaagggtga actggttccg | 120 |
| ctggcagaag cacgtattcc gctgctggat cagggtttta tgcatagcga tctgacctat | 180 |
| gatgttccga gcgtttggga tggctgtttt tttcgtctgg atgatcatat taccgctctg | 240 |
| gaagccagct gtaccaaact gcgtctgcgt ctgccgctgc ctcgtgatca ggttaaacia | 300 |
| attctggttg aaatggttgc caaaagcggg attcgtgatg catttgtgga actgattgtt | 360 |
| acccgtggtc tgaaagggtg tcgtggcacc cgtccggaag atatcgtgaa taatctgtat | 420 |
| atgtttgtgc agccgtatgt ttgggttatg gaaccggata tgcagcgtgt tgggtgtagc | 480 |
| gcagttgttg cacgtaccgt tcgtcgtgtt ccgcctgggt caattgatcc gaccgttaaa | 540 |
| aatctgcagt ggggtgatct ggttcgtggg atgtttgaag cagcagatcg tgggtgaacc | 600 |
| tatccgtttc tgaccgatgg tgatgcacat ctgaccgaag gtagcggttt taacattgtg | 660 |
| ctggtgaaag atggtgttct gtatacaccg gatcgtgggt ttctgcaggg tgttacacgt | 720 |
| aaaagcgtga ttaatgcagc agaagccttt ggtattgaag tgcgtgttga atttgttccg | 780 |
| gttgaaactgg catatcgctg tgatgaaatt tttatgtgta ccaccgcagg cgggtattatg | 840 |
| ccgattacca ccctggatgg tatgccgggt aatggtggtc agattggtcc gattacaaa | 900 |

aaaatttggg atggctattg ggcaatgcat tatgatgcag cctatagctt tgaaattgat 960
 tataatgaac gcaattcagg atcctga 987

<210> 5
 <211> 339
 <212> PRT
 <213> Mycobacterium aurum

<400> 5

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Pro Gly Ala Ile Arg Glu Asp Thr Pro Ala Gly Ser Val Ile Gln Tyr
 20 25 30

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

Trp Ile Glu Gly Glu Tyr Leu Pro Ala Glu Glu Ala Lys Ile Ser Ile
 50 55 60

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

Val Trp His Gly Asn Ile Phe Arg Leu Gly Asp His Leu Asp Arg Leu
 85 90 95

Leu Asp Gly Ala Ser Lys Leu Arg Leu Asp Ala Gly Tyr Ser Lys Asp
 100 105 110

Glu Leu Ala Glu Ile Thr Lys Lys Cys Val Ser Met Ser Gln Leu Arg
 115 120 125

Glu Ser Phe Val Asn Leu Thr Val Thr Arg Gly Tyr Gly Lys Arg Lys
 130 135 140

Gly Glu Lys Asp Leu Ser Lys Leu Thr His Gln Val Tyr Ile Tyr Ala
 145 150 155 160

Ile Pro Tyr Leu Trp Ala Phe Pro Pro Ala Glu Gln Ile Phe Gly Thr
 165 170 175

Thr Ala Ile Val Pro Arg His Val Arg Arg Ala Gly Arg Asn Thr Val
 180 185 190

Asp Pro Thr Ile Lys Asn Tyr Gln Trp Gly Asp Leu Thr Ala Ala Ser
 195 200 205

Phe Glu Ala Lys Asp Arg Gly Ala Arg Thr Ala Ile Leu Leu Asp Ser
 210 215 220

202663_ST25.txt

Asp Asn Cys Val Ala Glu Gly Pro Gly Phe Asn Val Cys Ile Val Lys
225 230 235 240

Asp Gly Lys Leu Ala Ser Pro Ser Arg Asn Ala Leu Pro Gly Ile Thr
245 250 255

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

Leu Arg Asp Val Thr Ser Arg Glu Leu Tyr Asp Ala Asp Glu Leu Met
275 280 285

Ala Val Thr Thr Ala Gly Gly Val Thr Pro Ile Asn Ser Leu Asp Gly
290 295 300

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

Asp Arg Phe Trp Ala Leu Met Asp Glu Pro Gly Pro Leu Ile Glu Thr
325 330 335

Ile Glu Tyr

<210> 6
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<212> DNA
<213> Mycobacterium aurum

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agcccgttcg ccggcgggcgt cgcttgatc gagggcgaat acctgccggc cgaagaagcg 180
aagatctcca tcttcgacac cggattcggc cattccgatc tgacctacac cgctcgcgcat 240
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tccaagctgc gcctggacgc cgggtacagc aaggacgaac tggccgagat caccaagaag 360
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atccccgtacc tgtgggacctt cccgccccgc gagcagatct tcggcaccac cgcgatcgtg 540
ccgcgccatg tccgccgcgc cggccgcaac accgtcgacc cgaccatcaa gaactaccag 600
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<211> 330
<212> PRT
<213> Arthrobacter

<400> 7

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Gly Leu Asp Tyr Ile Thr Tyr Ser Asp Tyr Glu Leu Asp Pro Ala Asn
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Pro Leu Ala Gly Gly Ala Ala Trp Ile Glu Gly Ala Phe Val Pro Pro
35 40 45

Ser Glu Ala Arg Ile Ser Ile Phe Asp Gln Gly Tyr Leu His Ser Asp
50 55 60

Val Thr Tyr Thr Val Phe His Val Trp Asn Gly Asn Ala Phe Arg Leu
65 70 75 80

Asp Asp His Ile Glu Arg Leu Phe Ser Asn Ala Glu Ser Met Arg Ile
85 90 95

Ile Pro Pro Leu Thr Gln Asp Glu Val Lys Glu Ile Ala Leu Glu Leu
100 105 110

Val Ala Lys Thr Glu Leu Arg Glu Ala Phe Val Ser Val Ser Ile Thr
115 120 125

Arg Gly Tyr Ser Ser Thr Pro Gly Glu Arg Asp Ile Thr Lys His Arg
130 135 140

Pro Gln Val Tyr Met Tyr Ala Val Pro Tyr Gln Trp Ile Val Pro Phe
145 150 155 160

Asp Arg Ile Arg Asp Gly Val His Ala Met Val Ala Gln Ser Val Arg
165 170 175

Arg Thr Pro Arg Ser Ser Ile Asp Pro Gln Val Lys Asn Phe Gln Trp
180 185 190

Gly Asp Leu Ile Arg Ala Val Gln Glu Thr His Asp Arg Gly Phe Glu
195 200 205

Ala Pro Leu Leu Leu Asp Gly Asp Gly Leu Leu Ala Glu Gly Ser Gly
210 215 220

202663_ST25.txt

Phe Asn Val Val Val Ile Lys Asp Gly Val Val Arg Ser Pro Gly Arg
225 230 235 240

Ala Ala Leu Pro Gly Ile Thr Arg Lys Thr Val Leu Glu Ile Ala Glu
245 250 255

Ser Leu Gly His Glu Ala Ile Leu Ala Asp Ile Thr Leu Ala Glu Leu
260 265 270

Leu Asp Ala Asp Glu Val Leu Gly Cys Thr Thr Ala Gly Gly Val Trp
275 280 285

Pro Phe Val Ser Val Asp Gly Asn Pro Ile Ser Asp Gly Val Pro Gly
290 295 300

Pro Ile Thr Gln Ser Ile Ile Arg Arg Tyr Trp Glu Leu Asn Val Glu
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Ser Ser Ser Leu Leu Thr Pro Val Gln Tyr
325 330

<210> 8
<211> 993
<212> DNA
<213> Arthrobacter sp.

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gagggctcgg ggttcaacgt cgtcgtgatc aaggacggcg tcgtgcgcag cccgggtcga 720
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 <212> PRT
 <213> Escherichia coli

<400> 9

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<210> 10
 <211> 8
 <212> PRT
 <213> Escherichia coli

<400> 10

Val Phe Glu Gly Ile Arg Cys Tyr
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<210> 11
 <211> 8
 <212> PRT
 <213> Escherichia coli

<400> 11

Asp Val Gly Met Gly Val Asn Pro
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<210> 12
 <211> 9
 <212> PRT
 <213> Escherichia coli

<400> 12

Pro Thr Ala Ala Lys Ala Gly Gly Asn
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<210> 13
 <211> 960
 <212> DNA
 <213> Penicillium chrysogenum

<400> 13
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 gaagcccgt tcccaatcct agaccaaggc ttcatgcaca gcgacttgac atacgatgtt 180
 ccctctgtct gggatggacg ctttttccgg ctcgatgacc acatcaccg gttggaagcc 240
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 ggattgaaag gtgtgcgagg ctctcgccct gaggatatcg tcaaccgtat ctatatgttt 420
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202663_ST25.txt

| | |
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| caatggggtg atctggttcg cggccttttc gaggttctg atcgtggcgc cgaatatccc | 600 |
| ttctgaccg atggtgacac caacctcacc gaaggttccg gcttcaacat tgttctcgtg | 660 |
| aaggacaata ttctgtacac tccagctcgc ggagtacttg aagggtgtgac acgcaagagt | 720 |
| gtgattgatg tcgctcgagc cagcggcttt gacattaagg tcgagttggt acctgtccaa | 780 |
| atggccttatg atgcggatga aatttttatg tgtaccactg ctggaggtat catgcccata | 840 |
| accagtcttg atggcaagcc cgtgaacgac ggaaagggtg ggtctgttac caagaagatc | 900 |
| tgggatgggt actgggctat ccactatgat cctgcctaca gcttcgagat tgcctattag | 960 |

<210> 14
 <211> 319
 <212> PRT
 <213> *Penicillium chrysogenum*
 <400> 14

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

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

Leu Thr Glu Gly Ser Gly Phe Asn Ile Val Leu Val Lys Asp Asn Ile
210 215 220

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

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

Val Pro Val Gln Met Ala Tyr Asp Ala Asp Glu Ile Phe Met Cys Thr
260 265 270

Thr Ala Gly Gly Ile Met Pro Ile Thr Ser Leu Asp Gly Lys Pro Val
275 280 285

Asn Asp Gly Lys Val Gly Ser Val Thr Lys Lys Ile Trp Asp Gly Tyr
290 295 300

Trp Ala Ile His Tyr Asp Pro Ala Tyr Ser Phe Glu Ile Ala Tyr
305 310 315

<210> 15
<211> 984
<212> DNA
<213> Aspergillus niger

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gtcattgatg ttgcacgagc ttgtggtatc caagttcatc tcgaagctgt gccggtggag 780
ttggtatatc agtgtgatga gatattcatg tgcacaacag cagggtggaat catgcccata 840

202663_ST25.txt

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 tgggacgggt attgggggtat gcattatgat ccagcctaca gcttcgcagt tagttatgat 960
 gacggatcaa aagcaaagct ctga 984

<210> 16
 <211> 327
 <212> PRT
 <213> Aspergillus niger

<400> 16

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

Gln Gly Phe Leu Arg Ser Asp Leu Thr Tyr Asp Val Ile Ser Val Trp
 50 55 60

Asp Gly Trp Phe Phe Arg Leu Asp Asp His Leu Ser Arg Leu Glu Leu
 65 70 75 80

Ala Cys Ala Lys Ser Arg Leu Lys Leu Pro Ile Ser Arg Asp Glu Val
 85 90 95

Lys Gln Ser Leu Val Arg Met Val Ala Gln Ser Gly Ile Arg Asp Ala
 100 105 110

Tyr Val Ala Leu Ile Val Thr Arg Gly Leu Gln Ser Val Arg Gly Ala
 115 120 125

Lys Pro Glu Asp Leu Val Asn Asn Leu Tyr Met Phe Val Gln Pro Tyr
 130 135 140

Val Trp Val Met Glu Pro Glu Val Gln Arg Val Gly Gly Ser Ala Val
 145 150 155 160

Val Thr Arg Thr Val Arg Arg Val Pro Pro Gly Ala Ile Tyr Pro Thr
 165 170 175

Val Lys Asn Leu Gln Trp Gly Asp Leu Thr Arg Gly Met Leu Glu Ala
 180 185 190

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

Leu Thr Glu Gly Ser Gly Tyr Asn Ile Val Leu Ile Lys Ala Gly Ala

210

215

Ile Tyr Thr Pro Asp Arg Gly Val Leu His Gly Val Thr Arg Thr Ser
225 230 235 240

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

Val Pro Val Glu Leu Val Tyr Gln Cys Asp Glu Ile Phe Met Cys Thr
260 265 270

Thr Ala Gly Gly Ile Met Pro Ile Thr Glu Leu Asp Gly Lys Pro Val
275 280 285

Asn Gly Gly Arg Ile Gly Pro Ile Thr Lys Lys Ile Trp Asp Gly Tyr
290 295 300

Trp Gly Met His Tyr Asp Pro Ala Tyr Ser Phe Ala Val Ser Tyr Asp
305 310 315 320

Asp Gly Ser Lys Ala Lys Leu
325

<210> 17
<211> 981
<212> DNA
<213> Aspergillus oryzae

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gacgcacgag tccactcct cgacgagggt ttcattgcata gcgacctcac gtacgatgtg 180
ccatcgggtct gggatgggcg ctttttccgc cttgatgatc atctcagtcg attggaagat 240
agttgtgaaa agatgcgact gaagatccca ctgtccaggg acgaagtcaa gcaaacccta 300
agggagatgg ttgctaagag tggaatcgaa gatgcctttg tggagctgat cgtcactcgt 360
ggcctgaaag ggggccgtgg caataagcca gaggatcttt tcgacaatca tctctatctg 420
atcgtcatgc cgtatgtctg ggtgatggag cccgccatcc aacataccgg aggtactgcg 480
atcattgccc gtacagtacg gcgcactccc cccggtgctt tcgatcctac catcaagaat 540
ctccagtggg gggacttgac acgggggtcta tttgaagcgg ctgaccgtgg cgcggattac 600
ccatttctct cagatggaga taccaatctc acagaaggat ccggtttcaa tatagtgttg 660
gttaaagatg gtattatcta cacgcccac cgtgggtgtt tggaaggcat tacacgtaag 720
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gaacatgcct atcacgccga tgagatattc atgtgtacta ctgctggtgg cattatgcct 840
atcacgaaac tcgatgggaa accgatccgg aatggagaag tcggtcccct tactacaaag 900
atatgggatg agtactgggc gatgcactat gaccgaaat atagctctgc tatcgattac 960

aggggccatg agggtaactg a

981

<210> 18
 <211> 326
 <212> PRT
 <213> Aspergillus oryzae

<400> 18

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

Glu Gly Phe Met His Ser Asp Leu Thr Tyr Asp Val Pro Ser Val Trp
 50 55 60

Asp Gly Arg Phe Phe Arg Leu Asp Asp His Leu Ser Arg Leu Glu Asp
 65 70 75 80

Ser Cys Glu Lys Met Arg Leu Lys Ile Pro Leu Ser Arg Asp Glu Val
 85 90 95

Lys Gln Thr Leu Arg Glu Met Val Ala Lys Ser Gly Ile Glu Asp Ala
 100 105 110

Phe Val Glu Leu Ile Val Thr Arg Gly Leu Lys Gly Val Arg Gly Asn
 115 120 125

Lys Pro Glu Asp Leu Phe Asp Asn His Leu Tyr Leu Ile Val Met Pro
 130 135 140

Tyr Val Trp Val Met Glu Pro Ala Ile Gln His Thr Gly Gly Thr Ala
 145 150 155 160

Ile Ile Ala Arg Thr Val Arg Arg Thr Pro Pro Gly Ala Phe Asp Pro
 165 170 175

Thr Ile Lys Asn Leu Gln Trp Gly Asp Leu Thr Arg Gly Leu Phe Glu
 180 185 190

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

Asn Leu Thr Glu Gly Ser Gly Phe Asn Ile Val Leu Val Lys Asp Gly
 210 215 220

Ile Ile Tyr Thr Pro Asp Arg Gly Val Leu Glu Gly Ile Thr Arg Lys

202663_ST25.txt

| | | | |
|---|-----|-----|-----|
| 225 | 230 | 235 | 240 |
| Ser Val Phe Asp Ile Ala Gln Val Lys Asn Ile Glu Val Arg Val Gln | 245 | 250 | 255 |
| Val Val Pro Leu Glu His Ala Tyr His Ala Asp Glu Ile Phe Met Cys | 260 | 265 | 270 |
| Thr Thr Ala Gly Gly Ile Met Pro Ile Thr Lys Leu Asp Gly Lys Pro | 275 | 280 | 285 |
| Ile Arg Asn Gly Glu Val Gly Pro Leu Thr Thr Lys Ile Trp Asp Glu | 290 | 295 | 300 |
| Tyr Trp Ala Met His Tyr Asp Pro Lys Tyr Ser Ser Ala Ile Asp Tyr | 305 | 310 | 315 |
| Arg Gly His Glu Gly Asn | 325 | | |

<210> 19
 <211> 972
 <212> DNA
 <213> Aspergillus fumigatus

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| <400> 19 | atggcctcta tggacaaagt cttttcggga tattatgcmc gccagaagct gcttgaacgg | 60 |
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| | gatgctagaa taccgctact cgacgaaggt ttcatgcaca gtgacctaac ctatgatgtt | 180 |
| | atatcggttt gggatggctg cttctttcga ttggacgatc atttgcaacg gatttttgaa | 240 |
| | agctgcgata agatgcggct caagttccca cttgcactga gctcagtga aaatattctg | 300 |
| | gctgagatgg tcgccaagag tggatccgg gatgcgtttg tggaaagtat tgtgacacgt | 360 |
| | ggtctgacag gtgtacgtgg ttcgaagcct gaggatctgt ataataaaa catatacctg | 420 |
| | cttgttcttc catacatttg ggttatggcg cctgagaacc agtccatgg tggcgaggct | 480 |
| | atcattacaa ggacagtgcg acgaacaccc ccaggtgcat ttgatcctac tatcaaaaat | 540 |
| | ctacagtggg gtgatttaac aaagggactt tttgaggcaa tggaccgtgg cgccacatac | 600 |
| | ccatttctca ctgatggaga caccaacctt actgaaggat ctggtttcaa cattgttttg | 660 |
| | gtgaagaacg gtattatcta taccctgat cgaggtgtct tgcgagggat cacacgtaaa | 720 |
| | agtgtgattg acgttgcccc agccaacagc atcgacatcc gccttgaggt cgtaccagtg | 780 |
| | gagcaggctt atcactctga tgagatcttc atgtgcacaa ctgccggcgg cattatgcct | 840 |
| | ataacattgc ttgatggta acctgttaat gacggccagg ttggccaat cacaagaag | 900 |
| | atatgggatg gctattggga gatgcactac aatccggcgt atagttttcc tgttgactat | 960 |
| | ggcagtggct aa | 972 |

202663_ST25.txt

<210> 20

<211> 323

<212> PRT

<213> Aspergillus fumigatus

<400> 20

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

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

Glu Gly Phe Met His Ser Asp Leu Thr Tyr Asp Val Ile Ser Val Trp
50 55 60

Asp Gly Arg Phe Phe Arg Leu Asp Asp His Leu Gln Arg Ile Leu Glu
65 70 75 80

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

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

Phe Val Glu Val Ile Val Thr Arg Gly Leu Thr Gly Val Arg Gly Ser
115 120 125

Lys Pro Glu Asp Leu Tyr Asn Asn Asn Ile Tyr Leu Leu Val Leu Pro
130 135 140

Tyr Ile Trp Val Met Ala Pro Glu Asn Gln Leu His Gly Gly Glu Ala
145 150 155 160

Ile Ile Thr Arg Thr Val Arg Arg Thr Pro Pro Gly Ala Phe Asp Pro
165 170 175

Thr Ile Lys Asn Leu Gln Trp Gly Asp Leu Thr Lys Gly Leu Phe Glu
180 185 190

Ala Met Asp Arg Gly Ala Thr Tyr Pro Phe Leu Thr Asp Gly Asp Thr
195 200 205

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

Ile Ile Tyr Thr Pro Asp Arg Gly Val Leu Arg Gly Ile Thr Arg Lys
225 230 235 240

Ser Val Ile Asp Val Ala Arg Ala Asn Ser Ile Asp Ile Arg Leu Glu

Val Val Pro Val Glu Gln Ala Tyr His Ser Asp Glu Ile Phe Met Cys
260 265 270

Thr Thr Ala Gly Gly Ile Met Pro Ile Thr Leu Leu Asp Gly Gln Pro
275 280 285

Val Asn Asp Gly Gln Val Gly Pro Ile Thr Lys Lys Ile Trp Asp Gly
290 295 300

Tyr Trp Glu Met His Tyr Asn Pro Ala Tyr Ser Phe Pro Val Asp Tyr
305 310 315 320

Gly Ser Gly

<210> 21
<211> 972
<212> DNA
<213> Neosartorya fischeri

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gacgccagaa taccgtact tgacgaaggc ttcatgcacg gtgacctaac ttatgatgtt 180
acaacggttt gggatggacg cttctttcga ttggatgatc atatgcaacg gatcctggaa 240
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gctgagatgg tcgccaagag tggatttcgg gatgcgtttg tggaagttat cgtgacacgt 360
ggctctgacag gtgtacgtgg ttcgaagccc gaggatctgt ataataacaa catatacctg 420
cttgttctcc catacgtttg gggtatggcg cctgagaacc agctccttgg tggcagtgc 480
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ggcagtggct aa 972

<210> 22
<211> 323
<212> PRT
<213> Neosartorya fischeri

<400> 22

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

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

Glu Gly Phe Met His Gly Asp Leu Thr Tyr Asp Val Thr Thr Val Trp
 50 55 60

Asp Gly Arg Phe Phe Arg Leu Asp Asp His Met Gln Arg Ile Leu Glu
 65 70 75 80

Ser Cys Asp Lys Met Arg Leu Lys Phe Pro Leu Ala Pro Ser Thr Val
 85 90 95

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

Phe Val Glu Val Ile Val Thr Arg Gly Leu Thr Gly Val Arg Gly Ser
 115 120 125

Lys Pro Glu Asp Leu Tyr Asn Asn Asn Ile Tyr Leu Leu Val Leu Pro
 130 135 140

Tyr Val Trp Val Met Ala Pro Glu Asn Gln Leu Leu Gly Gly Ser Ala
 145 150 155 160

Ile Ile Thr Arg Thr Val Arg Arg Thr Pro Pro Gly Ala Phe Asp Pro
 165 170 175

Thr Ile Lys Asn Leu Gln Trp Gly Asp Leu Thr Lys Gly Leu Phe Glu
 180 185 190

Ala Met Asp Arg Gly Ala Thr Tyr Pro Phe Leu Thr Asp Gly Asp Thr
 195 200 205

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

Ile Ile Tyr Thr Pro Asp Arg Gly Val Leu Arg Gly Ile Thr Arg Lys
 225 230 235 240

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

Val Val Pro Val Glu Gln Val Tyr His Ser Asp Glu Ile Phe Met Cys
 Page 18

Thr Thr Ala Gly Gly Ile Met Pro Ile Thr Leu Leu Asp Gly Gln Pro
275 280 285

Val Asn Asp Gly Gln Val Gly Pro Ile Thr Lys Lys Ile Trp Asp Gly
290 295 300

Tyr Trp Glu Met His Tyr Asn Pro Ala Tyr Ser Phe Pro Val Asp Tyr
305 310 315 320

Gly Ser Gly

<210> 23
<211> 978
<212> DNA
<213> Gibberella zeae

<400> 23
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gaagcccgc tccccctcat ggaccaaggt ttcattgcac gcgacttgac ctacgatgtc 180
cctgcagtct gggatggctg tttcttccgt cttgatgacc atctcgaccg tctcgaggca 240
agcgtcaaga agatgcgaat gcaattcccc attccccgcg atgagatcag aatgactctt 300
ctcgacatgc tcgccaagag tggaatcaag gatgcttttg ttgagctcat tgtcactcgt 360
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atcgtccaac cctacgtctg ggtcatgagc cccgaagctc agtacgtcgg cggtaatgcc 480
gttatcgac gaactgttcg tcgaatccct cctggatcca tggatccac catcaagaac 540
ctccaatgga gtgatttcac ccgcggcatg ttcgaagcat acgatcgtgg agcacaatac 600
cccttctca ccgacggcga cacaacatc accgaaggat ctggtttcaa cgttgtcttt 660
gtcaagaaca acgttattta caccggaac cgaggagttt tgcagggaat taccagaaag 720
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cagaaactga agctgtag 978

<210> 24
<211> 325
<212> PRT
<213> Gibberella zeae

<400> 24

Met Ser Thr Met Asp Lys Ile Phe Ala Gly His Ala Gln Arg Gln Ala

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

275

280

285

Val Lys Asp Gly Lys Val Gly Pro Val Thr Lys Ala Ile Trp Asp Arg
 290 295 300

Tyr Trp Ala Met His Trp Glu Asp Glu Phe Ser Phe Lys Ile Asp Tyr
 305 310 315 320

Gln Lys Leu Lys Leu
 325

<210> 25
 <211> 966
 <212> DNA
 <213> Hyphomonas neptunium

<400> 25
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 aaggcgcgga taccgatact tgatcagggc ttcctgcatt cggatctgac ctatgacgtc 180
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 ccctga 966

<210> 26
 <211> 321
 <212> PRT
 <213> Hyphonmonas neptunium

<400> 26

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Glu Asn Glu Phe Val Pro Ile Gly Lys Ala Arg Ile Pro Ile Leu Asp
35 40 45

Gln Gly Phe Leu His Ser Asp Leu Thr Tyr Asp Val Pro Ala Val Trp
50 55 60

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

Ser Cys Ala Lys Met Arg Leu Pro Leu Pro Ile Ala Arg Pro Glu Leu
85 90 95

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

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

Gln Ala Glu Asp Ile Ile Pro Asn Leu Tyr Leu Met Ala Val Pro Tyr
130 135 140

Val Trp Ile Leu Pro Leu Glu Tyr Gln Asn His Gly Ala Pro Ala Val
145 150 155 160

Val Thr Arg Thr Val Arg Arg Thr Pro Pro Gly Ala Leu Asp Pro Thr
165 170 175

Ile Lys Asn Leu Gln Trp Gly Asp Leu Val Arg Gly Leu Met Glu Ala
180 185 190

Gly Asp Arg Asp Ser Phe Phe Pro Ile Leu Pro Asp Gly Asp Gly Asn
195 200 205

Ala Thr Glu Gly Ala Gly Tyr Asn Ile Val Leu Val Arg Asn Gly Glu
210 215 220

Leu His Thr Pro Arg Arg Gly Val Leu Glu Gly Ile Thr Arg Arg Thr
225 230 235 240

Val Leu Glu Ile Ala Ala Ala Arg Gly Leu Lys Thr His Val Thr Glu
245 250 255

Ile Pro Ile Gln Ala Leu Tyr Glu Cys Asp Glu Leu Phe Met Cys Ser
260 265 270

Thr Ala Gly Gly Ile Met Pro Leu Val Leu Leu Asp Gly Asn Ile Val
275 280 285

Gly Asp Gly Thr Val Gly Pro Val Thr Arg Met Ile Trp Glu Ala Tyr

290

295

Trp Asp Leu His Asp Asp Pro Gln Leu Ser Glu Pro Val Thr Tyr Ala
305 310 315 320

Pro

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<211> 963
<212> DNA
<213> Mesorhizobium loti MAFF303099

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<210> 28
<211> 320
<212> PRT
<213> Mesorhizobium loti MAFF303099

<400> 28

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20 25 30

Leu Asp Gly Gln Tyr Leu Pro Met Ser Gln Ala Lys Val Ser Val Leu
Page 23

35

40

45

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

305

310

320

<210> 29
<211> 936
<212> DNA
<213> Roseobacter sp.

<400> 29
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ggtgacgggc atgacgccgc cagcggttga ggtcacgaac acttcatccg ccgccctcaa 180
ttcacttggg gccagatcat ccgtcgcgca ggtgatctgt aattcgtcac aaagatcaaa 240
gattgtttgg cgtgttattc ccatcagcac cccaaacttg ggcgaggaaa ttttgccgtt 300
tttcacggcg aagacgttga aaccggggccc ttccgctatg tttccggtgg cgtctaaaag 360
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caaaatctca gtcactcgg cagacaaaa cgggatcgac atgtgcaact tttccatccc 720
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aacatcgat gtcgcatctg agtggaggaa gccattatcc aacaccgaaa tctttgcctc 840
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agaatgacga tcagacagcg caggcaattt atacat 936

<210> 30
<211> 311
<212> PRT
<213> Roseobacter sp.

<400> 30

Met Tyr Lys Leu Pro Ala Leu Ser Asp Arg His Ser Asp Pro Ala Thr
1 5 10 15

Tyr Pro Pro Gly Ile Ala Phe Met Asp Gly Gln Tyr Leu Pro Ile Ser
20 25 30

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

Thr Tyr Asp Val Ala His Val Trp Lys Gly Ala Phe Phe Arg Leu Asp
50 55 60

Asp His Leu Asp Arg Phe Phe Ala Gly Met Glu Lys Leu His Met Ser
65 70 75 80

202663_ST25.txt

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

Ala Leu Ser Gly Leu Gln Asp Ala Tyr Val Glu Phe Ile Cys Thr Arg
100 105 110

Gly Thr Ser Pro Thr Phe Ser Arg Asp Pro Arg Asp Ala Val Asn Arg
115 120 125

Phe Ile Ala Phe Ala Ile Pro Phe Gly Ser Val Ala Asn Pro Glu Gln
130 135 140

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

Pro Ser Ser Val Asp Pro Thr Val Lys Asn Tyr His Trp Leu Asp Leu
165 170 175

Val Lys Gly Leu Tyr Ala Ala Tyr Ala Gln Gly Ala Glu Thr Ala Ile
180 185 190

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

Phe Ala Val Lys Asn Gly Lys Ile Ser Ser Pro Lys Phe Gly Val Leu
210 215 220

Met Gly Ile Thr Arg Gln Thr Ile Phe Asp Leu Cys Asp Glu Leu Gln
225 230 235 240

Ile Thr Cys Ala Thr Asp Asp Leu Ala Pro Ser Glu Leu Arg Ala Ala
245 250 255

Asp Glu Val Phe Val Thr Ser Thr Ala Gly Gly Val Met Pro Val Thr
260 265 270

Lys Ile Asp Glu Thr Ser Ile Gly Ser Gly Leu Val Gly Pro Ile Thr
275 280 285

Lys Glu Ile Thr Glu Ala Tyr Trp Arg Met His Glu Asp Asp Arg Phe
290 295 300

Arg Lys Ala Ile Arg Tyr Pro
305 310

<210> 31

<211> 945

<212> DNA

<213> Marinomonas sp.

<400> 31

ctatatTTTT gccgggggat aatgaatggg taggcaccaa tcagagTTTT tgtgcttttc

60

202663_ST25.txt

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acaaagatca aagacggttc ggcgagttat gcctggcaaa accccttttt ctggtgttgt 300
aattatcttt cccttaacac aaaaaacatt aaagccaggg ctttcggcga tattaccctc 360
tgaatccaac aggatggcgg tctcaccacc tttttcatag gcatcgtata acccggttac 420
caaatcaagc caatggtaat ttttgacctt tgaatcaacc gagtttggtg gaatacggac 480
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<210> 32
<211> 314
<212> PRT
<213> Marinomonas sp.

<400> 32

Met Ala Leu Leu Gln Leu Ser Asn Glu Tyr Lys Asp Pro His Asn Tyr
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Pro Lys Gly Val Ala Tyr Met Asp Gly Gln Tyr Leu Asp Met Ser Lys
20 25 30

Ala Lys Leu Ser Ile Leu Asp Tyr Gly Phe Leu His Ser Asp Ala Thr
35 40 45

Tyr Asp Val Val His Val Trp Gln Gly Ala Phe Phe Arg Leu Asp Leu
50 55 60

Tyr Leu Glu Arg Phe Phe Ser Gly Leu Glu Lys Ile His Met Thr Met
65 70 75 80

Pro Tyr Ser Lys Glu Glu Val Ala Glu Ile Leu His Asn Cys Val Ala
85 90 95

Leu Ser Gly His Lys Asn Ala Tyr Val Glu Met Ile Cys Thr Arg Gly
100 105 110

Asn Ser Pro Asp Phe Ser Arg Asp Pro Arg Asp Ser Ile Asn Arg Phe
Page 27

115

120

125

Met Ala Phe Ala Val Pro Phe Gly Ser Val Ala Asn Gln Asp Gln Met
 130 135 140

Lys Asn Gly Leu His Ala Ile Ile Ser Ser Ile Val Arg Ile Pro Pro
 145 150 155 160

Asn Ser Val Asp Ser Lys Val Lys Asn Tyr His Trp Leu Asp Leu Val
 165 170 175

Thr Gly Leu Tyr Asp Ala Tyr Glu Lys Gly Gly Glu Thr Ala Ile Leu
 180 185 190

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

Cys Val Lys Gly Lys Ile Ile Thr Thr Pro Glu Lys Gly Val Leu Pro
 210 215 220

Gly Ile Thr Arg Arg Thr Val Phe Asp Leu Cys Asp Glu Leu His Ile
 225 230 235 240

Ser Cys Cys Ala Thr Glu Val Thr Pro Thr Asp Leu Arg Asn Ala Asp
 245 250 255

Glu Val Phe Ile Thr Ser Thr Ala Gly Gly Ile Met Pro Ile Thr Lys
 260 265 270

Ile Asp His Asn Val Ile Gly Ser Gly Thr Thr Gly Pro Ile Phe Gln
 275 280 285

Leu Leu Lys Ser Ala Tyr Trp Glu Lys His Lys Asn Ser Asp Trp Cys
 290 295 300

Leu Pro Ile His Tyr Pro Pro Ala Lys Ile
 305 310

<210> 33

<211> 939

<212> DNA

<213> Rhizobium etli

<400> 33

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attataccaa tcgaagaggc gaaggtacca cttttagact ggggctttct gcgttcggac 120

gcgtgtcagg acacagtgtc ggtgtgggat ggcagctttt tccgtttgac tgaccacctg 180

gatcgatttg agcgatctgt ccagcgcctt cggatggata cagctcctgt tacaagaagc 240

gatatccacc ggatagtcca caaactcgtt gccgtgtgcg gtttccgtga tgcttacgtt 300

caaatcatca tgacccgcgg gcggcccccg atcggtagtc gggatcttcg tttatgctcg 360

202663_ST25.txt

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aacgttttcg cggtgatcga cggagtcttg aggaccctt ctttcggcat gctggatgga      660
atgaccagga ggacagttat ggaactgtgc aacgagctga atctcgatgt cacgcaagag      720
accatttctt tggagcggct tctaatcgcc tcggaaatct tccttacgac gaccgcaggc      780
gggattatcc cggtctcttc ggtgaacgga accggaatcg gtttcggatc agtgggtgaa      840
caaactcgcc gcattcaccg gtcatactgg gataagcgaa gcagcggatg gtatggcgag      900
cctgtcgcct acgcccacaaa agctctcttg gagccctag      939

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<210> 34
<211> 312
<212> PRT
<213> Rhizobium etli

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<400> 34
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Met Leu Asp Arg Gly Glu Glu Ser Ala Phe Gln Lys Gly Ser Ala Tyr
1          5          10          15
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Val Asp Gly Lys Ile Ile Pro Ile Glu Glu Ala Lys Val Pro Leu Leu
          20          25          30
```

```
Asp Trp Gly Phe Leu Arg Ser Asp Ala Cys Gln Asp Thr Val Ser Val
          35          40          45
```

```
Trp Asp Gly Ser Phe Phe Arg Leu Thr Asp His Leu Asp Arg Phe Glu
          50          55          60
```

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Arg Ser Val Gln Arg Leu Arg Met Asp Thr Ala Pro Val Thr Arg Ser
65          70          75          80
```

```
Asp Ile His Arg Ile Val His Lys Leu Val Ala Val Cys Gly Phe Arg
          85          90          95
```

```
Asp Ala Tyr Val Gln Ile Ile Met Thr Arg Gly Arg Pro Pro Ile Gly
          100          105          110
```

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Ser Arg Asp Leu Arg Leu Cys Ser Asn Ser Phe Gln Ala Phe Cys Val
          115          120          125
```

```
Pro Tyr Met Trp Ile Ala Asn Pro Glu Lys Gln Glu Ile Gly Met Ala
          130          135          140
```

```
Val His Val Ser Arg Arg Val Arg Ile Pro Pro Gln Ser Val Asp Pro
145          150          155          160
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202663_ST25.txt

Leu Val Lys His Tyr His Trp Leu Asp Phe Glu Met Gly Leu Phe Glu
165 170 175

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

Asn Ile Thr Glu Gly Pro Gly Phe Asn Val Phe Ala Val Ile Asp Gly
195 200 205

Val Leu Arg Thr Pro Ser Phe Gly Met Leu Asp Gly Met Thr Arg Arg
210 215 220

Thr Val Met Glu Leu Cys Asn Glu Leu Asn Leu Asp Val Thr Gln Glu
225 230 235 240

Thr Ile Ser Leu Glu Arg Leu Leu Ile Ala Ser Glu Ile Phe Leu Thr
245 250 255

Thr Thr Ala Gly Gly Ile Ile Pro Val Ser Ser Val Asn Gly Thr Gly
260 265 270

Ile Gly Phe Gly Ser Val Gly Glu Gln Thr Arg Arg Ile His Arg Ser
275 280 285

Tyr Trp Asp Lys Arg Ser Ser Gly Trp Tyr Gly Glu Pro Val Ala Tyr
290 295 300

Ala Gln Lys Ala Leu Leu Glu Pro
305 310

<210> 35
<211> 906
<212> DNA
<213> Rhodoferax ferrireducens

<400> 35
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ggtgaagcaa gcattccgat aactgactgg ggtttcctgc gctctgacgc cacctatgac 120
gtggtgacgg tgtgggatgg ttcctttttt cgcctggacg cccatctgga gcgcttcatg 180
cgagctgcc aacgctggcg gcttgacccg gggctgacgc ccgggcaa at caccggcgctg 240
ttgtcgcaat gcgtgcgcct gagcgggctt cgcgctctt atgtcgagat gatctgcacc 300
cggggccagc cgccttgggg atcgcgcgac ccacgcctgg ccgtcaatca gttctatgcc 360
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cactggaacg acttgacgat gggactgctg ggggcgctgg acgccggggc cgacagtgtt 540
gtgctggtcg actcagtcgg gaacgtggct gagggaccg ggttcaacgt gttttgtgtc 600
agccacggcg cgcttgtgac gccagcgag ggcattgctt aaggggtgtc gcgtcgacc 660

202663_ST25.txt

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|--|-----|
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| gagttgctg gagccgagga ggtgttcac tccacctcgg gcggtggtgt actgccctg | 780 |
| agccgggtgg acaaactcc ggttggtgat ggccgtccgg ggccgatcac gcagcgctg | 840 |
| gtacagacct actgggctg gcatgccgat ccggtgtaca gccagccgat agattattcg | 900 |
| ctttga | 906 |

<210> 36
 <211> 301
 <212> PRT
 <213> Rhodoferax ferrireducens

<400> 36

Met Pro Ala Pro Asp Leu Ser Lys Gly Val Ala Phe Val Arg Gly Gln
 1 5 10 15

Tyr Val Pro Ile Gly Glu Ala Ser Ile Pro Ile Thr Asp Trp Gly Phe
 20 25 30

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

Phe Phe Arg Leu Asp Ala His Leu Glu Arg Phe Met Arg Ser Cys Gln
 50 55 60

Arg Trp Arg Leu Asp Pro Gly Leu Thr Pro Gly Gln Ile Thr Gly Val
 65 70 75 80

Leu Ser Gln Cys Val Arg Leu Ser Gly Leu Arg Ala Ser Tyr Val Glu
 85 90 95

Met Ile Cys Thr Arg Gly Gln Pro Pro Trp Gly Ser Arg Asp Pro Arg
 100 105 110

Leu Ala Val Asn Gln Phe Tyr Ala Phe Ala Val Pro Tyr Val Trp Leu
 115 120 125

Ala Asn Ala Gln Gln Arg Glu Ala Gly Leu His Leu Met Ile Ser Asp
 130 135 140

Val Gln Arg Ile Pro Ala Thr Ser Val Asp Pro Ser Ala Lys Asn Tyr
 145 150 155 160

His Trp Asn Asp Leu Thr Met Gly Leu Leu Gly Ala Leu Asp Ala Gly
 165 170 175

Ala Asp Ser Val Val Leu Val Asp Ser Val Gly Asn Val Val Glu Gly
 180 185 190

Pro Gly Phe Asn Val Phe Cys Val Ser His Gly Ala Leu Val Thr Pro

195

200

205

Ser Glu Gly Met Leu Glu Gly Val Ser Arg Arg Thr Val Ile Glu Met
 210 215 220

Ala Arg Ala Leu Gly Leu Glu Thr Gln Leu Arg Ala Leu Pro Ala Asp
 225 230 235 240

Glu Leu Arg Gly Ala Glu Glu Val Phe Ile Ser Thr Ser Gly Gly Gly
 245 250 255

Val Leu Pro Val Ser Arg Val Asp Lys Arg Pro Val Gly Asp Gly Arg
 260 265 270

Pro Gly Pro Ile Thr Gln Arg Leu Val Gln Thr Tyr Trp Ala Trp His
 275 280 285

Ala Asp Pro Val Tyr Ser Gln Pro Ile Asp Tyr Ser Leu
 290 295 300

<210> 37
 <211> 900
 <212> DNA
 <213> Jannaschia sp.

<400> 37
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 caccgggatc acgccgccgc ccgaggacga caggaagacc tcatcggcct ccaggaattc 180
 gtccaggggc agcgggcgtg tttcgaccgt caggcccgcc tctgcggcca tttccagcac 240
 cgtgcggcgg gtgatgccat gcaacacacc gtggtccgac gtcacgatcc ggtcaccgaa 300
 cagggcgaag gcgttgaagc ccggcccttc ggtcacatgg cccgcgtggt ccagcagcaa 360
 gaccgtctca aacccttgt ctttcgcctc gaacaaccgc ccggtgaaat cgccccaatg 420
 gtagtttttc acggtgggat caacgctgtc ggcggggatg cggcgggtgc gtttggcgat 480
 ccagacggag gttccacgct cggcgatttc gggtttcacg atgtgcacgt acggcacgca 540
 ccaggcgtag aagtgggttg cacaatcgcg cgggtcccgc gatccgggca ccgggttgcg 600
 cccccgcgcg gcgacatgg cgacatagct gtcgcgcaat ccgcttgcgg ccaccatccg 660
 ggtcagggcc gttttcacgc cgtccccgtc gcgcccata tccatccgca gcgcgccgac 720
 ggaggccatg aaccgcgcca cgtaatcatc cagccggaag aagccgcccc gccagaccgg 780
 caccacgtca taggcgatgt cggaatgggt caggcccaa tcggtgacgg ggatcgcggc 840
 ctctgcgatg gggatgatgc ggctcccat ccaggccgcg ccgttgata aatcattcat 900

<210> 38
 <211> 299
 <212> PRT
 <213> Jannaschia sp.

<400> 38

Met Asn Asp Leu Ser Asn Gly Ala Ala Trp Met Gly Ser Arg Ile Ile
1 5 10 15

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

Ser Asp Ile Ala Tyr Asp Val Val Pro Val Trp Arg Gly Gly Phe Phe
35 40 45

Arg Leu Asp Asp Tyr Val Ala Arg Phe Met Ala Ser Val Gly Ala Leu
50 55 60

Arg Met Asp Ile Gly Arg Asp Gly Asp Gly Val Lys Thr Ala Leu Thr
65 70 75 80

Arg Met Val Ala Ala Ser Gly Leu Arg Asp Ser Tyr Val Ala Met Val
85 90 95

Ala Ala Arg Gly Arg Asn Pro Val Pro Gly Ser Arg Asp Pro Arg Asp
100 105 110

Cys Ala Asn His Phe Tyr Ala Trp Cys Val Pro Tyr Val His Ile Val
115 120 125

Lys Pro Glu Ile Ala Glu Arg Gly Thr Ser Val Trp Ile Ala Lys Arg
130 135 140

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

His Trp Gly Asp Phe Thr Gly Gly Leu Phe Glu Ala Lys Asp Lys Gly
165 170 175

Phe Glu Thr Val Leu Leu Leu Asp His Ala Gly His Val Thr Glu Gly
180 185 190

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

Asp His Gly Val Leu His Gly Ile Thr Arg Arg Thr Val Leu Glu Met
210 215 220

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

Glu Phe Leu Glu Ala Asp Glu Val Phe Leu Ser Ser Ser Gly Gly Gly
245 250 255

Val Ile Pro Val Ala Arg Val Asp Asn Arg Val Phe Ser Asn Asp Ala
Page 33

Ala Gly Pro Val Ala Leu Asp Leu Arg Arg Arg Tyr Phe Asp Trp Ile
275 280 285

Thr Arg Ala Glu His Arg Thr Asp Ile Ala Tyr
290 295

<210> 39
<211> 936
<212> DNA
<213> Labrenzia alexandrii

<400> 39
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ccgggtgacc ggtgcaacgc cgccaccgga cgtggatgatg aaaacttcgt cgctctcaaa 180
gaactcacta agcgccaagg cccgtatctc gatctcaagc ccctgttctg ccgcgatatc 240
cagcaccgtc tgacggctga tgccttccaa aacaccgctt tcagccgtca ccagcgttcg 300
gccctttaca gcaaacacat tgaagccggg cccttcggtc acgttgccat catcatcgag 360
caagatgaca gtctccgcgc cgtggtcctt ggcctcaaac agacccttgg tgaaatcacc 420
ccagtggtag tttttgacct tcggattgac actgccgggc gaaatccggt gcacggtctt 480
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cacgcaccat gcaaagaatt ggttcttgca gtcccgggga tcgcgcgaac ccggcacctg 600
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gaccggggacc acatcatagg taatgtccga atggatcagc cccaatctg taacaggcaa 840
tgcggcctcg gaaatcggca tgagcctgcc gccatccac gcggcaccgt tggacaaatc 900
tgagatggta acgcgaacat cgacggtgga ggacat 936

<210> 40
<211> 311
<212> PRT
<213> Labrenzia alexandrii

<400> 40

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

Gly Ala Ala Trp Met Gly Gly Arg Leu Met Pro Ile Ser Glu Ala Ala
20 25 30

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

202663_ST25.txt

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

202663_ST25.txt

<210> 41
<211> 981
<212> DNA
<213> Burkholderia sp.

<400> 41
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cgtatagagc tccccgttct tggcgaaaaa cacgttcgca ccggctgctt cggtgagggt 360
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ggcgttgcmc acgaggttgt ggagaatctc cttgacctgg tcgcmgttga acggttctc 720
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<210> 42
<211> 326
<212> PRT
<213> Burkholderia sp.

<400> 42

Met Ala Ile Ile Gln Val Gln Gln Ile Met His Glu Asn Pro Leu His
1 5 10 15

Ala Arg Ala Pro His Glu Pro Arg Tyr Glu Asp Gly Ser Ala Phe Cys
20 25 30

Asp Gly Asn Tyr Val Pro Ile Thr Glu Ala Thr Val Pro Leu Val Asp
35 40 45

Ala Gly Phe Leu His Ala Asp Ala Ala Tyr Asp Val Val Thr Val Ser
50 55 60

Arg Gly Asn Phe Phe Arg Leu Asp Asp His Leu Thr Arg Met Glu Glu
65 70 75 80

202663_ST25.txt

Ser Ser Ala Lys Phe Phe Leu Glu Asn Pro Phe Asn Arg Asp Gln Val
 85 90 95
 Lys Glu Ile Leu His Asn Leu Val Arg Asn Ala Gly Leu Lys Asp Ala
 100 105 110
 Tyr Val Trp Trp Cys Val Thr Arg Gly Pro Leu Ser Val Asp Arg Arg
 115 120 125
 Asp Arg Gly Ala Met Lys Asn Ala Met Phe Ala Phe Ala Val Pro Phe
 130 135 140
 Phe Phe Gln Ala Asp Asp Glu Val Arg Thr Arg Gly Ser Asn Leu Leu
 145 150 155 160
 Ile Ser Lys Leu Tyr Asn Arg Ile Ser Ala Lys Ala Val Asp Pro Thr
 165 170 175
 Ala Lys Asn Phe His Trp Met Asp Met Lys Leu Ala Leu Phe Glu Ala
 180 185 190
 Met Thr Gln Glu Lys Asp Trp Ala Val Leu Val Asp Glu Ser Asp Asn
 195 200 205
 Leu Thr Glu Ala Ala Gly Ala Asn Val Phe Phe Ala Lys Asn Gly Glu
 210 215 220
 Leu Tyr Thr Pro Ala Glu Gly Cys Leu Leu Gly Ile Thr Arg Gln Ser
 225 230 235 240
 Val Phe Asp Ile Ala Ala Glu Leu Gly Ile Lys Val Asn Ile Gly Lys
 245 250 255
 Tyr Thr Ala Thr Gln Leu Arg Glu Ala Asp Glu Ala Phe Thr Ser Ser
 260 265 270
 Ser Ala Gly Gly Ile Met Pro Val Ser Ala Ile Asp Asp Gln Pro Leu
 275 280 285
 Gly Asn Arg Asn Gly Pro Gly Pro Ile Ser Glu Lys Ile His Asn Leu
 290 295 300
 Tyr Trp Glu Lys Arg Trp Ala Gly Trp His Ala Gln Pro Ala Glu Tyr
 305 310 315 320
 Phe Ser Ser Val Pro Ala
 325

<210> 43
 <211> 954
 <212> DNA

<213> Burkholderia cenocepacia

<400> 43

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cagccgctg accggcatga tgccgccggc cgtcgacgtg atgaacactt cgtccgcgtc      180
gcgcaactgt gcatcgtcga tgcgcgcagc ctgggcgctg atgcccacatg ccgtcgccag     240
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cttcagcagg accgactccg cgcccgcgtc atagcccttc agcagcccgg cgacgaggtc     420
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<210> 44

<211> 317

<212> PRT

<213> Burkholderia cenocepacia

<400> 44

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

Ser Asp Val Thr Tyr Asp Thr Val His Val Trp Asn Gly Arg Phe Phe
          50          55          60

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

Arg Leu Asn Val Pro Leu Thr Asp Asp Ala Leu Arg Asp Ile Leu Val
          85          90          95

Glu Cys Val Arg Arg Ser Gly Leu Arg His Ala Tyr Val Glu Met Leu

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Cys Thr Arg Gly Val Ser Pro Thr Phe Ser Arg Asp Pro Arg Asp Ala
115 120 125
Val Asn Gln Phe Ile Ala Phe Ala Val Pro Tyr Gly Ser Val Ala Asn
130 135 140
Glu Arg Gln Leu Arg Glu Gly Leu His Leu His Val Ile Asp Asp Val
145 150 155 160
Arg Arg Ile Pro Pro Glu Ser Val Asp Pro Gln Ile Lys Asn Tyr His
165 170 175
Trp Leu Asp Leu Val Ala Gly Leu Leu Lys Gly Tyr Asp Ala Gly Ala
180 185 190
Glu Ser Val Leu Leu Lys Cys Thr Asp Gly Ser Ile Ala Glu Gly Pro
195 200 205
Gly Phe Asn Val Phe Val Val Arg Asp Gly Arg Leu Arg Thr Pro Glu
210 215 220
Arg Gly Val Leu His Gly Ile Thr Arg Gln Thr Val Phe Glu Leu Ala
225 230 235 240
Thr Ala Met Gly Ile Asp Ala Gln Ala Ala Arg Ile Asp Asp Ala Gln
245 250 255
Leu Arg Asp Ala Asp Glu Val Phe Ile Thr Ser Thr Ala Gly Gly Ile
260 265 270
Met Pro Val Thr Arg Leu Asn Asp Ala Thr Ile Gly Asp Gly Arg Pro
275 280 285
Gly Pro Met Thr Arg Arg Leu Phe Asp Ala Tyr Trp Ala Lys His Gly
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Asp Pro Ala Trp Ser Leu Ala Val Asp Tyr Ala Asp Gly
305 310 315

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<211> 864
<212> DNA
<213> alpha proteobacterium

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aacaggcatc acgcccccg cagtcgaggt tatgaagacc tcgtcagcgg ttttaagctt 180
gtcgacagta atgtcttgcg catgacatct aacttccaat tcttcgcaa tgtcaaaaat 240

202663_ST25.txt

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gtaattcttg acggtaggat caacagagct tgggtggaatg cgaacgacat ccgtgatcgc      480
cagatgcaaa ccacactcca actgttcttt gctggccact gaaccgaacg gaatggcaaa      540
agctatgaag cggttttctg catctcttgg atctcgactg aagttgggtg acgttcctct      600
tgtgcagatg aactcaacat atgcattttt gagcttggac aacgccacgc aattatgaag      660
aatttctatg atttgcgctt tgggtgaagg aattgacata tgcaaagcgt ccattccacg      720
ggaaaatcga tctaaatgat cacctaactt gaaaaatgct ccgccccata catgggcaac      780
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<210> 46
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 <212> PRT
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<400> 46

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Asp Tyr Gly Phe Leu His Ser Asp Ala Thr Tyr Asp Val Ala His Val
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Trp Gly Gly Ala Phe Phe Lys Leu Gly Asp His Leu Asp Arg Phe Ser
 35 40 45

Arg Gly Met Asp Ala Leu His Met Ser Ile Pro Tyr Thr Lys Ala Gln
 50 55 60

Ile Ile Glu Ile Leu His Asn Cys Val Ala Leu Ser Lys Leu Lys Asn
 65 70 75 80

Ala Tyr Val Glu Phe Ile Cys Thr Arg Gly Thr Ser Pro Asn Phe Ser
 85 90 95

Arg Asp Pro Arg Asp Ala Glu Asn Arg Phe Ile Ala Phe Ala Ile Pro
 100 105 110

Phe Gly Ser Val Ala Ser Lys Glu Gln Leu Glu Cys Gly Leu His Leu
 115 120 125

Ala Ile Thr Asp Val Val Arg Ile Pro Pro Ser Ser Val Asp Pro Thr
 130 135 140

Val Lys Asn Tyr His Trp Leu Asp Met Val Lys Gly Leu Tyr Ala Ala
 Page 40

145 150 160

Tyr Glu Arg Gly Ala Asp Thr Ala Thr Leu Ile Asp Leu Asn Gly Asn
165 170 175Val Ser Glu Gly Pro Gly Phe Asn Ile Phe Ser Ile Thr Asn Gly Val
180 185 190Val Ser Thr Pro Asp Val Ser Val Leu Leu Gly Ile Thr Arg Gln Thr
195 200 205Ile Phe Asp Ile Cys Glu Glu Leu Glu Val Arg Cys His Ala Gln Asp
210 215 220Ile Thr Val Asp Lys Leu Lys Thr Ala Asp Glu Val Phe Ile Thr Ser
225 230 235 240Thr Ala Gly Gly Val Met Pro Val Thr Arg Ile Asp Glu Arg Pro Ile
245 250 255Ala Ser Gly Asn Ile Gly Pro Leu Ser Lys Arg Ile Met His Ala Tyr
260 265 270Trp Gln Leu His Asn Glu Gly Lys His Arg Asp Pro Val Glu Tyr
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<210> 47

<211> 882

<212> DNA

<213> gamma proteobacterium

<400> 47

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| tggaagggca acatcttcaa gctcgacgcc catctcgatc ggttctttga ctcgattcag | 180 |
| gccgcgcgac tcaatcacga catgagtcga gacgcgtgga aggaagcgat catcgaaacc | 240 |
| acgcgtcgca atggactcga cgatgcctcg attcgcttta tcgtgacccg cggcgagccc | 300 |
| aaaggggtgg ttgctgatcc ccgggatttt aaaccgacgt gcatcgtctg ggtggcgcct | 360 |
| tatatcttcc tcgcggatga ggagaaacgc cgcaatggta ttcgcctgat gattagcgcg | 420 |
| acgcgggggtt tccctgctga caccctggac cctcgttaca aatgcctcga ccgcctgcat | 480 |
| tcacagctga ttcggcttga ggccctggag gcgggttatg acgatgcgct ttggctcgat | 540 |
| cattccgggtc acgtgtccga gtcagcagcg agcaacctgt ttatcgtcaa gaatggtgtg | 600 |
| ttgtacaccc cttcagcagg aattctgcgc ggcattacac gggacaccat tctcgagctc | 660 |
| gcgaccgagc tggacatccc ctggaaagag cgacagctca gtgcgttcga tgtctatatc | 720 |
| gccgatgagg tcttcacctg cagcacagcg ggtggcgcgc ttccggtcag ggaggtcgca | 780 |
| ggtcgaacga ttcgcggcac aacccccggc ccgattaccc aggcaatcga caacgcgtat | 840 |

tgggcatgc gtgaaacaga ccggtacgcg acgccgcttt aa

882

<210> 48
 <211> 293
 <212> PRT
 <213> gamma proteobacterium
 <400> 48

Met Ser Asp Glu Pro Ile Ile Tyr Ile Asn Gly Asp Tyr Leu Pro Leu
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 20 25 30

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

Asp Ala His Leu Asp Arg Phe Phe Asp Ser Ile Gln Ala Ala Arg Leu
 50 55 60

Asn His Asp Met Ser Arg Asp Ala Trp Lys Glu Ala Ile Ile Glu Thr
 65 70 75 80

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

Arg Gly Glu Pro Lys Gly Val Val Ala Asp Pro Arg Asp Phe Lys Pro
 100 105 110

Thr Cys Ile Val Trp Val Ala Pro Tyr Ile Phe Leu Ala Asp Glu Glu
 115 120 125

Lys Arg Arg Asn Gly Ile Arg Leu Met Ile Ser Ala Thr Arg Gly Phe
 130 135 140

Pro Ala Asp Thr Leu Asp Pro Arg Tyr Lys Cys Leu Asp Arg Leu His
 145 150 155 160

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

Leu Trp Leu Asp His Ser Gly His Val Ser Glu Ser Ala Ala Ser Asn
 180 185 190

Leu Phe Ile Val Lys Asn Gly Val Leu Tyr Thr Pro Ser Ala Gly Ile
 195 200 205

Leu Arg Gly Ile Thr Arg Asp Thr Ile Leu Glu Leu Ala Thr Glu Leu
 210 215 220

Asp Ile Pro Trp Lys Glu Arg Gln Leu Ser Ala Phe Asp Val Tyr Ile

225

230

240

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

Arg Glu Val Ala Gly Arg Thr Ile Arg Gly Thr Thr Pro Gly Pro Ile
260 265 270

Thr Gln Ala Ile Asp Asn Ala Tyr Trp Ala Met Arg Glu Thr Asp Arg
275 280 285

Tyr Ala Thr Pro Leu
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<210> 49

<211> 1014

<212> DNA

<213> Mycobacterium vanbaalenii

<400> 49

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tttgccggtg gtgttgcatg gattgaaggt gaatatctgc ctgcagaaga tgcaaaaatt 180
agcatttttg ataccggttt tggcatagc gatctgacct ataccgttgc acatgtttgg 240
catggcaata tttttcgtct gggcgatcat ctggatcgtc tgctggatgg tgcacgtaaa 300
ctgcgtcttg atagcggtta taccaaagat gaactggccg atattaccaa aaaatgtgtg 360
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cgtaaaggcg aaaaagatct gagcaaactg acccatcagg tgtatatatta tgccattccg 480
tatctgtggg catttcctcc ggcagagcag atttttggca ccaccgcagt tgttccgcgt 540
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gatctgaccg cagcaagctt tgaagcaaaa gatcgtggtg cacgtaccgc aattctgatg 660
gatgccgata attgtgttgc agaagggtccg ggttttaacg tgtgcattgt gaaagatggt 720
aaactggcaa gcccagaccg taatgcactg ccgggtatta cacgtaaaac cgtgtttgaa 780
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<210> 50

<211> 337

<212> PRT

<213> Mycobacterium vanbaalenii

<400> 50

Met Gly Ile Asp Thr Gly Thr Ser Asn Leu Val Ala Val Glu Pro Gly

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

275

280

285

Thr Thr Ala Gly Gly Val Thr Pro Ile Asn Thr Leu Asp Gly Val Pro
 290 295 300
 Ile Gly Asp Gly Glu Pro Gly Pro Val Thr Val Ala Ile Arg Asp Arg
 305 310 315 320
 Phe Trp Ala Leu Met Asp Glu Pro Gly Pro Leu Ile Glu Ala Ile Gln
 325 330 335
 Tyr