

BPS65845PC-2008050350
SEQUENCE LISTING

<110> BASF Plant Science GmbH
<120> Pathogen Control Genes and Methods of Use in plants
<130> 15209
<160> 162
<170> PatentIn version 3.4

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<212> DNA
<213> Escherichia coli

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<213> Escherichia coli

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35 40 45
Ala Pro Ile Thr Gln Gly Gly Asn Phe Ala Arg Tyr Ala Gly Phe Ser
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Val Pro Leu His Cys Glu Glu Gly Asp Val His Gly Val Val Leu Val
65 70 75 80
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Gly Leu Ala Ala Asp Glu Val Val Glu Glu Ala Leu Leu Arg Leu Gln
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 35 40 45

Arg Asn Asn Gln Phe Leu Asn Pro Asp Asn Ile Thr Tyr Ile Phe Thr
 50 55 60

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

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

Leu Arg Glu Trp Glu Tyr Gly Asp Tyr Glu Gly Met Leu Thr Arg Glu
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Ile Ile Glu Leu Arg Lys Ser Arg Gly Leu Asp Lys Glu Arg Pro Trp
 115 120 125

Asn Ile Trp Arg Asp Gly Cys Glu Asn Gly Glu Thr Thr Gln Gln Ile
 130 135 140

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

Gln Lys Lys Cys Glu Thr Ile Glu Glu Ile Gln Asn Val Lys Ser Tyr
 195 200 205

Asp Asp Asp Thr Val Pro Tyr Val Lys Leu Glu Ser Tyr Arg His Leu
 210 215 220

Val Asp Asn Pro Cys Phe Leu Leu Asp Ala Gly Gly Ile Gly Val Leu
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Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
 35 40 45

Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
 50 55 60

Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Lys Asn
 65 70 75 80

Pro Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Ile Gly
 85 90 95

Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile
 100 105 110

Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Met
 115 120 125

Ser His Gln Leu Gly Met Thr Pro Pro Pro Arg Ala Ile Leu Ser Leu
 130 135 140

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

Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Gly Val Leu
165 170 175

Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Asn Gly Ala Ala Leu
180 185 190

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

Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His
210 215 220

Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Glu Glu Tyr Gly
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Asp Met Ala Glu Gln Lys Cys Ser Lys Ile Leu Ala Phe Ala His Ile
245 250 255

Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser
260 265 270

Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu Gln Asn Ile Ser Ile
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Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Val Ile Ala Trp Met
290 295 300

Ala Pro Ile Ile Ala Ile Ile Ala Ile Thr Lys Ser Phe Leu Gly His
305 310 315 320

Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu
325 330 335

Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Arg Ile Thr
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Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro
355 360 365

Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met
370 375 380

Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met
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 <213> Escherichia coli

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 Thr Thr Ala₃₅ Gln Gln Met Pro Ser₄₀ Leu Ala Pro Met Leu₄₅ Glu Lys Val
 Met Pro₅₀ Ser Val Val Ser Ile₅₅ Asn Val Glu Gly Ser₆₀ Thr Thr Val Asn
 Thr₆₅ Pro Arg Met Pro Arg₇₀ Asn Phe Gln Gln Phe₇₅ Phe Gly Asp Asp Ser₈₀
 Pro Phe Cys Gln₈₅ Glu Gly Ser Pro Phe₉₀ Gln Ser Ser Pro Phe Cys₉₅ Gln
 Gly Gly Gln Gly₁₀₀ Gly Asn Gly Gly Gly₁₀₅ Gln Gln Gln Lys Phe₁₁₀ Met Ala
 Leu Gly Ser₁₁₅ Gly Val Ile Ile Asp₁₂₀ Ala Asp Lys Gly Tyr₁₂₅ Val Val Thr
 Asn Asn₁₃₀ His Val Val Asp Asn₁₃₅ Ala Thr Val Ile Lys₁₄₀ Val Gln Leu Ser
 Asp₁₄₅ Gly Arg Lys Phe Asp₁₅₀ Ala Lys Met Val Gly₁₅₅ Lys Asp Pro Arg Ser₁₆₀
 Asp Ile Ala Leu Ile₁₆₅ Gln Ile Gln Asn Pro₁₇₀ Lys Asn Leu Thr Ala₁₇₅ Ile
 Lys Met Ala Asp₁₈₀ Ser Asp Ala Leu Arg₁₈₅ Val Gly Asp Tyr Thr₁₉₀ Val Ala
 Ile Gly Asn₁₉₅ Pro Phe Gly Leu Gly₂₀₀ Glu Thr Val Thr Ser₂₀₅ Gly Ile Val
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 Val Asn Leu Asn Gly₂₄₅ Glu Leu Ile Gly Ile₂₅₀ Asn Thr Ala Ile Leu₂₅₅ Ala
 Pro Asp Gly Gly₂₆₀ Asn Ile Gly Ile Gly₂₆₅ Phe Ala Ile Pro Ser₂₇₀ Asn Met
 Val Lys Asn₂₇₅ Leu Thr Ser Gln Met₂₈₀ Val Glu Tyr Gly Gln₂₈₅ Val Lys Arg

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
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Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
 305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
 325 330 335

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

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
 355 360 365

Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
 370 375 380

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
 385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
 405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
 420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
 435 440 445

Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
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<211> 1479

<212> DNA

<213> *Saccharomyces cerevisiae*

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atcgacggtg gtaactcaca tttcccgac actaacagac gctacgaaga gctaacaag 360

caaggaattc tttttgtggg ctctggtgtc tcaggcgggtg aagatggtgc acgttttgg 420

ccatctttaa tgcctggtgg gtcagcagaa gcatggccgc acatcaagaa catctttcaa 480

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Ala Tyr Asn Arg Thr Gln Ser Lys Val Asp Arg Phe Leu Ala Asn Glu
 35 40 45

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

Ala Lys Leu Lys Lys Pro Arg Lys Ile Met Leu Leu Ile Lys Ala Gly
 65 70 75 80

Ala Pro Val Asp Thr Leu Ile Lys Glu Leu Val Pro His Leu Asp Lys
 85 90 95

Gly Asp Ile Ile Ile Asp Gly Gly Asn Ser His Phe Pro Asp Thr Asn
 100 105 110

Arg Arg Tyr Glu Glu Leu Thr Lys Gln Gly Ile Leu Phe Val Gly Ser
 115 120 125
 Gly Val Ser Gly Gly Glu Asp Gly Ala Arg Phe Gly Pro Ser Leu Met
 130 135 140
 Pro Gly Gly Ser Ala Glu Ala Trp Pro His Ile Lys Asn Ile Phe Gln
 145 150 155 160
 Ser Ile Ala Ala Lys Ser Asn Gly Glu Pro Cys Cys Glu Trp Val Gly
 165 170 175
 Pro Ala Gly Ser Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu
 180 185 190
 Tyr Gly Asp Met Gln Leu Ile Cys Glu Ala Tyr Asp Ile Met Lys Arg
 195 200 205
 Ile Gly Arg Phe Thr Asp Lys Glu Ile Ser Glu Val Phe Asp Lys Trp
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 Asn Thr Gly Val Leu Asp Ser Phe Leu Ile Glu Ile Thr Arg Asp Ile
 225 230 235 240
 Leu Lys Phe Asp Asp Val Asp Gly Lys Pro Leu Val Glu Lys Ile Met
 245 250 255
 Asp Thr Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ala Ile Asn Ala
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 Tyr Ala Gln Gly Phe Met Leu Ile Arg Glu Ala Ala Arg Ser Tyr Gly
 340 345 350
 Trp Lys Leu Asn Asn Pro Ala Ile Ala Leu Met Trp Arg Gly Gly Cys
 355 360 365
 Ile Ile Arg Ser Val Phe Leu Ala Glu Ile Thr Lys Ala Tyr Arg Asp
 370 375 380

Asp Pro Asp Leu Glu Asn Leu Leu Phe Asn Glu Phe Phe Ala Ser Ala
385 390 395 400

Val Thr Lys Ala Gln Ser Gly Trp Arg Arg Thr Ile Ala Leu Ala Ala
405 410 415

Thr Tyr Gly Ile Pro Thr Pro Ala Phe Ser Thr Ala Leu Ala Phe Tyr
420 425 430

Asp Gly Tyr Arg Ser Glu Arg Leu Pro Ala Asn Leu Leu Gln Ala Gln
435 440 445

Arg Asp Tyr Phe Gly Ala His Thr Phe Arg Ile Leu Pro Glu Cys Ala
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<212> DNA
<213> Escherichia coli

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<213> Escherichia coli

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35 40 45

Ala Pro Ile Thr Gln Gly Gly Asn Phe Ala Arg Tyr Ala Gly Phe Ser
50 55 60

Val Pro Leu His Cys Glu Glu Gly Asp Val His Gly Val Val Leu Val
65 70 75 80

Asn Gln Val Arg Met Met Asp Leu Arg Ala Arg Leu Ala Lys Arg Ile
85 90 95

Gly Leu Ala Ala Asp Glu Val Val Glu Glu Ala Leu Leu Arg Leu Gln
100 105 110

Ala Val Val Glu
115

<210> 13
<211> 351
<212> DNA
<213> Burkholderia vietnamiensis

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35 40 45

Ala Pro Ile Thr Gln Gly Gly Glu Cys Ala Arg Phe Ala Gly Phe Ala
50 55 60

Val Pro Leu Ser Gly Ser Gly Thr Glu Thr Gln Gly Val Ala Leu Val
65 70 75 80

Asn Met Val Arg Met Leu Asp Leu Asp Ala Arg Gly Ala Arg Lys Ile
85 90 95

Glu Arg Ala Pro Ala Glu Val Val Glu Asp Ala Leu Ala Arg Leu Gln
Seite 12

100

105

110

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<213> *Pseudomonas putida*

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caggtgcgca cagtcgacct tgaagcacga tttgccaagc gcatagagtc ggtgcctgaa 300
gctgtcatcc tggatgcact ggcgcgtgtg caaacctat tcgattaa 348

<210> 16
<211> 115
<212> PRT
<213> *Pseudomonas putida*

<400> 16

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

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

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

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

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

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

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

Leu Phe Asp
115

<210> 17
<211> 348
<212> DNA
<213> *Pseudomonas syringae*

<400> 17
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 ggccgtgaac aacagggcgga ttttcgtcca gcgttgattc tgacgcctgc ggcttataac 120
 gcatcggggc ttgtaattat tgtacccatc acgcagggcg gcgacttcgc tcggtatgcc 180
 ggtttcgcgg tgcctttaag cggttcaggt accgaaacgc aggggtgtcgt tctttgcaac 240
 cagattcgaa ccgttgacct tgaggctcgt ggcgcaaagc gtgttgagtc agttcccagag 300
 atgataatcg acgatgtgct ggctcgcgtt caagcccttt ttgaatag 348

<210> 18
 <211> 115
 <212> PRT
 <213> *Pseudomonas syringae*

<400> 18

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

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

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

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

Pro Leu Ser Gly Ser Gly Thr Glu Thr Gln Gly Val Val Leu Cys Asn
 65 70 75 80

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

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

Leu Phe Glu
 115

<210> 19
 <211> 336
 <212> DNA
 <213> *Mycobacterium celatum*

<400> 19
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 ccggtcgtgc tacctataac acgcggcggg aactttgccc gaacggcagg gttcgtctgc 180
 tcgctgaccg atgcgggtac tcgcaccgcc ggcgtaatac gctgcgatca gcctcgtctg 240
 attgatatcc gcgcccgtaa aggccgcaag gttgaacgtg tgccgtctgg gggtcttgac 300

gaagcgttgg ccaagctcgc cacgatcttg acttga

336

<210> 20
 <211> 111
 <212> PRT
 <213> Mycobacterium celatum

<400> 20

Met Thr Glu Arg Gly Asp Ile Tyr Ile Val Ser Leu Asp Pro Thr Ser
 1 5 10 15

Gly His Glu Gln Ser Gly Thr Arg Pro Val Leu Val Val Ser Pro Gly
 20 25 30

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

Gly Gly Asn Phe Ala Arg Thr Ala Gly Phe Ala Val Ser Leu Thr Asp
 50 55 60

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

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

Gly Val Leu Asp Glu Ala Leu Ala Lys Leu Ala Thr Ile Leu Thr
 100 105 110

<210> 21
 <211> 339
 <212> DNA
 <213> Synechococcus sp.

<400> 21

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cgtgagcagg ctggacgccg accggcagtg gtggtgtcgc catcggccta caacagcaag 120

gttggcctgg ctttgggtgtg tccaatcacc agcaaggtga agggataccc gtttgaagtg 180

gcactgccgg aacaaggaac ggtgcagggt gtgatcttgg cggatcaact acgcagcctg 240

gactggcgca gccaaagaagc cgagctgatc gccaaaggctc cgattcctgt ggtggaacgc 300

gttctgcagc tggttggcgc gctgttgagc agtccgtga 339

<210> 22
 <211> 112
 <212> PRT
 <213> Synechococcus sp.

<400> 22

Met Val Arg Ala Pro Glu Arg Gly Asp Leu Ile Trp Leu Ser Phe Thr
 1 5 10 15

Pro Gln Ser Gly Arg Glu Gln Ala Gly Arg Arg Pro Ala Val Val Val
 20 25 30

Ser Pro Ser Ala Tyr Asn Ser Lys Val Gly Leu Ala Leu Val Cys Pro
 35 40 45

Ile Thr Ser Lys Val Lys Gly Tyr Pro Phe Glu Val Ala Leu Pro Glu
 50 55 60

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

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

Val Val Glu Arg Val Leu Gln Leu Val Gly Ala Leu Leu Ser Ser Pro
 100 105 110

<210> 23
 <211> 402
 <212> DNA
 <213> Erwinia amylovora

<400> 23
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 gagcagcagg gaacgcggcc ggtactgatt gtcacgccgg ctgcctttta cgcggtgacc 180
 cgcctgcctg ttgtttgtgcc cgtgaccagc ggaggcaatt ttgcccgac tgctggcttt 240
 gcggtgtcgc ttgacggcgc cggcatatcgt accaccggcg ttgtgcgttg cgatcaaccc 300
 cggacgatcg atatgaaagc ccgcggcggc aaacgacttg aacgggtgcc tgagactatc 360
 atggatgacg ttcttggtcg tctggccacg attctgactt ga 402

<210> 24
 <211> 133
 <212> PRT
 <213> Erwinia amylovora

<400> 24
 Met Leu Lys Ser Gln Leu Lys Asn Glu Asn Gly Trp Met Arg Arg Arg
 1 5 10 15

Leu Val Arg Arg Lys Ser Asp Met Glu Arg Gly Glu Ile Trp Leu Val
 20 25 30

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

Leu Ile Val Thr Pro Ala Ala Phe Asn Arg Val Thr Arg Leu Pro Val
 50 55 60

Val Val Pro Val Thr Ser Gly Gly Asn Phe Ala Arg Thr Ala Gly Phe
 Seite 16


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<210> 25
<211> 360
<212> DNA
<213> Agrobacterium tumefaciens
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gtaggcagcg	aaatcaagga	cgaacatcgc	tgtgtcgtca	tcacgcccag	agaaattaac		120
gcggtcggac	tctgtctcgt	cgtcccgggtg	accaccggcg	gcatgtttac	gcgcaaggca		180
gggcttgccg	taaatatatc	cggccacaag	acaacggggcg	tcgctttgtg	caatcaggtg		240
agaagcatgg	atatcgtcgc	ccgggttgcc	cagaagaaag	cgaaatatat	cgaaaccctc		300
gatgatgcga	cgatcgatga	aatcgccggg	cgcgtcatca	gcatgatcga	tccagcttga		360

<210>	26
<211>	119
<212>	PRT
<213>	Agrobacterium tumefaciens

<400> 26

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

Leu Asn Pro Val Val Gly Ser Glu Ile Lys Asp Glu His Arg Cys Val
20 25 30

Val Ile Thr Pro Arg Glu Ile Asn Ala Val Gly Leu Cys Leu Val Val
35 40 45

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

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

Arg Ser Met Asp Ile Val Ala Arg Val Ala Gln Lys Lys Ala Lys Tyr
85 90 95

Ile Glu Thr Leu Asp Asp Ala Thr Ile Asp Glu Ile Ala Gly Arg Val
 100 105 110

Ile Ser Met Ile Asp Pro Ala
 115

<210> 27
 <211> 348
 <212> DNA
 <213> Neisseria meningitidis

<400> 27
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 gaaatcaagg gcgggcggtt tgcgctggct ctgtctccaa aagcattcaa ccgcgcaacg 120
 ggattggttt ttgcctgcc catttcacag gggaatgcag cggctgcacg aagcagcggc 180
 atgatttcaa ccttactcgg tgcaggaacg gaaacgcagg gcaatgtcca ctgccaccag 240
 ctcaaattctc tggactggca aatccgcaag gcttctttta aagaaactgt acccgattat 300
 gtattggacg atgtgctggc gcgcatcggc gccgtcttat tcgattaa 348

<210> 28
 <211> 115
 <212> PRT
 <213> Neisseria meningitidis

<400> 28

Met Tyr Ile Pro Asp Lys Gly Asp Ile Phe His Leu Asn Phe Asp Pro
 1 5 10 15

Ser Ser Gly Lys Glu Ile Lys Gly Gly Arg Phe Ala Leu Ala Leu Ser
 20 25 30

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

Ser Gln Gly Asn Ala Ala Ala Ala Arg Ser Ser Gly Met Ile Ser Thr
 50 55 60

Leu Leu Gly Ala Gly Thr Glu Thr Gln Gly Asn Val His Cys His Gln
 65 70 75 80

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

Val Pro Asp Tyr Val Leu Asp Asp Val Leu Ala Arg Ile Gly Ala Val
 100 105 110

Leu Phe Asp
 115

<210> 29
 <211> 360
 <212> DNA

<213> *Erwinia carotovora*

<400> 29

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ggtagagaga ttgctgggcc gcattacttc ctcgtaatat cggttgatac cgtgaacaaa    120
gaaaccggcg ttacagcctg tgccgcgata acatcaggcg cagggtcctt gcgcgaaaaa    180
aacatcgtcg tttatatcgg cggtggtgat acagagaaaag gcaaagtgac tggagtgatt    240
ctttgccacc aactgaactc tcttgatfff caggcaagaa gcgcgaaata tattgatacg    300
gtgtcacctc aggtcatggc tgatgtcgaa atcacactgg cgaacatatt gggcatatga    360

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<210> 30

<211> 119

<212> PRT

<213> *Erwinia carotovora*

<400> 30

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Met Met Ala Arg Met Pro Lys Arg Gly Glu Ile Trp Leu Val Asn Pro
1           5           10           15

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

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Ile Ser Val Asp Thr Val Asn Lys Glu Thr Gly Val Thr Ala Cys Ala
        35                40                45

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Ala Ile Thr Ser Gly Ala Gly Ser Leu Arg Glu Lys Asn Ile Val Val
        50                55                60

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Tyr Ile Gly Gly Gly Asp Thr Glu Lys Gly Lys Val Thr Gly Val Ile
65                70                75                80

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Leu Cys His Gln Leu Asn Ser Leu Asp Phe Gln Ala Arg Ser Ala Lys
                85                90                95

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Tyr Ile Asp Thr Val Ser Pro Gln Val Met Ala Asp Val Glu Ile Thr
                100                105                110

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Leu Ala Asn Ile Leu Gly Ile
                115

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<210> 31

<211> 363

<212> DNA

<213> *Synechocystis* sp.

<400> 31

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ctcaatccca cccaggggcg agaacaaatg ggagaggcgc ggccatgtct ggttttgagc    120
catactgcct ttaataaggc ccgcaatggc ttgatcattg tttccccaat tacgaatacc    180
attaagccag aaattcagac gttggttgtc cttcctgatg gttatcgggt acaaggatcg    240
gttattgctg agcaaaccg cactgtggat ttaagtttgc gttggtggcg ggatacggga    300

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gaagtccttc cccctagttt tgtggatcag gtcttggcgg ttctccagct aattattgga 360
tga 363

<210> 32
<211> 120
<212> PRT
<213> Synechocystis sp.

<400> 32

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

Ile Arg Leu Asn Leu Asn Pro Thr Gln Gly Arg Glu Gln Met Gly Glu
20 25 30

Ala Arg Pro Cys Leu Val Leu Ser His Thr Ala Phe Asn Lys Ala Arg
35 40 45

Asn Gly Leu Ile Ile Val Ser Pro Ile Thr Asn Thr Ile Lys Pro Glu
50 55 60

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

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

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

Ala Val Leu Gln Leu Ile Ile Gly
115 120

<210> 33
<211> 348
<212> DNA
<213> Crocosphaera watsonii

<400> 33

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caagcaggaa atcgtcctgt tttagtatta tccattaatt ctatcaatga cttaccttta 120
gttgtcacag tggttgtagg tactaagggt aaaaatattc gccaagatta tccgacaaat 180
gttagggttt ctctgatga aagtggactt tcgtagaaa caatatttct ctgttttcaa 240
attcgttcaa ttgataaaaa tcgtttttct tctgcaccag ttggtaaatt gtcagaggaa 300
aaaatgcaag aaattgaaac agctattcgt tattgttttag gtttatag 348

<210> 34
<211> 115
<212> PRT
<213> Crocosphaera watsonii

<400> 34

Met Lys Ile Glu Arg Gly Gln Ile Tyr Phe Val Asn Leu Asn Pro Ile
 1 5 10 15

Gln Gly Lys Glu Gln Ala Gly Asn Arg Pro Val Leu Val Leu Ser Ile
 20 25 30

Asn Ser Ile Asn Asp Leu Pro Leu Val Val Thr Val Val Val Gly Thr
 35 40 45

Lys Gly Lys Asn Ile Arg Gln Asp Tyr Pro Thr Asn Val Arg Val Ser
 50 55 60

Pro Asp Glu Ser Gly Leu Ser Leu Glu Thr Ile Phe Leu Cys Phe Gln
 65 70 75 80

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

Leu Ser Glu Glu Lys Met Gln Glu Ile Glu Thr Ala Ile Arg Tyr Cys
 100 105 110

Leu Gly Leu
 115

<210> 35

<211> 840

<212> DNA

<213> Candida glabrata

<400> 35
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 aagtcgggtc agtacaccgg ttgactgac ttgccattga ctgactatgg tgttggccaa 120
 atgctgagga ccggtgagtc tatcttctcc aacaaccgtt tcatcaacc tgaccacatc 180
 acatataatc tcacttctcc aagaaccagg gccaaagcaga ccattgagtt ggttttgaag 240
 ccattgagcg aggagcaaag gtctaagatc aagggttattg ttgacaatga cttgagagaa 300
 tgggagtacg gtgactatga agggctattg accaaggaga ttgtcgagct gcgtaagtcc 360
 cgtggtttgg acaaagctcg cccatggaat atctggagag atggctgtga gaacgggtgaa 420
 actactgaag aagtcggttt gagattgtct agagtcatcg cacgtatcca aaacctgcac 480
 aagaagcacc aggaacaagg cataccatct gatatcatgg tgtttgctca tggacatgct 540
 ttgcgttact ttgcggccat ctggctacgt ctaggtgaag agaaagagtg tatcactgct 600
 ttctctaagc agaaggttaa gtcctatgag gaggatgagt ctgtgggtccc atacgttgag 660
 attaccaagt tcagacactt ggtggacaac ccattcttct tacttgacgc tggtggtatc 720
 ggtgtattgt cttatgccca ccacagcatt gatgaacccg ccttggacct agctgggtgcg 780
 ttcatttccc caccagagga agagtcccaa cacgctccag ttccaaacaa gaattactga 840

<210> 36
 <211> 279
 <212> PRT
 <213> Candida glabrata

<400> 36

Met Gly His Ser Pro Thr Pro Arg Cys Ile Ile Val Arg His Gly Gln
 1 5 10 15

Thr Glu Trp Ser Lys Ser Gly Gln Tyr Thr Gly Leu Thr Asp Leu Pro
 20 25 30

Leu Thr Asp Tyr Gly Val Gly Gln Met Leu Arg Thr Gly Glu Ser Ile
 35 40 45

Phe Ser Asn Asn Arg Phe Ile Asn Pro Asp His Ile Thr Tyr Ile Phe
 50 55 60

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

Pro Leu Ser Glu Glu Gln Arg Ser Lys Ile Lys Val Ile Val Asp Asn
 85 90 95

Asp Leu Arg Glu Trp Glu Tyr Gly Asp Tyr Glu Gly Leu Leu Thr Lys
 100 105 110

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

Trp Asn Ile Trp Arg Asp Gly Cys Glu Asn Gly Glu Thr Thr Glu Glu
 130 135 140

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

Lys Lys His Gln Glu Gln Gly Ile Pro Ser Asp Ile Met Val Phe Ala
 165 170 175

His Gly His Ala Leu Arg Tyr Phe Ala Ala Ile Trp Leu Arg Leu Gly
 180 185 190

Glu Glu Lys Glu Cys Ile Thr Ala Phe Ser Lys Gln Lys Val Lys Ser
 195 200 205

Tyr Glu Glu Asp Glu Ser Val Val Pro Tyr Val Glu Ile Thr Lys Phe
 210 215 220

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

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

Leu Ala Gly Ala Phe Ile Ser Pro Pro Glu Glu Glu Ser Gln His Ala
 260 265 270

Pro Val Pro Asn Lys Asn Tyr
 275

<210> 37
 <211> 816
 <212> DNA
 <213> Kluyveromyces lactis

<400> 37
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 agaagaactg gtaaatgcgt ctttggtaac aagttcattg acccaaacca tatcacatac 180
 attttcactt ctctctgtca acgtgctaga aagactgttg atttaatttt ggaatccctt 240
 actgaagaac aacgttcaaa gatcagaatc gtagtcgata acgatctaag agaatgggaa 300
 tatgggtgatt acgaggtctt gttgacccat gaaattgtca aattgagaaa atcccgtggt 360
 ttggatcaag aaaggccttg gaacatctgg cgtgatgggt gtgaaaacgg tgaaagcacc 420
 aagcaaactg gttgtagact ttcccgtgtc atttccagaa ttcaaaacct acatcgccaa 480
 caacagaaaag acggagtacc aagtgatatc ttgggtgtttg cacatggcca tgcattacgt 540
 tatttcgcat ccttggtgat caaacatgga ttagaagaaa aatatgaacc atcattcgat 600
 ccacaaaac ctacttataa cgatgagact gttcctaattg taacaatgga aaagtacaga 660
 tacttggttg ataatccaaa cttcttggtg gatgctggtg gtatgggagt tctttcttat 720
 gcacaccata atattgacga acctgctcta gcgttggccg gaacatttat tgccccacca 780
 gaggaagaat ctcaacatga accggtagtt gaataa 816

<210> 38
 <211> 271
 <212> PRT
 <213> Kluyveromyces lactis

<400> 38

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 20 25 30

Thr Pro Tyr Gly Val Glu Gln Met Arg Arg Thr Gly Lys Cys Val Phe
 35 40 45

Gly Asn Lys Phe Ile Asp Pro Asn His Ile Thr Tyr Ile Phe Thr Ser
 50 55 60

Pro Arg Gln Arg Ala Arg Lys Thr Val Asp Leu Ile Leu Glu Ser Leu
 Seite 23

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

[illegible]

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 atcacgaaca tcagagctat ccacgaaaag gcgattcaag ataatgttcc ttgcgatgtc 540
 atagttgttg gacatggtca tatcttgaga tgttttgctg ctagatgggt gggtaaagac 600
 attaatgtca atccgcaagt cgtgttgat gctgggtggag ttggagtttt gagctatcaa 660
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 gaggaagggt ctgatata a 741

<210> 40
 <211> 246
 <212> PRT
 <213> Debaryomyces hansenii
 <400> 40

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

Leu Pro Leu Thr Asp Phe Gly Val Lys Gln Met Arg Asn Thr Gly Lys
35 40 45

His Leu Ile Gly Pro Ser Pro Phe Gln Leu Ile Lys Pro Glu Asn Leu
50 55 60

Lys Asn Val Phe Thr Ser Pro Arg Leu Arg Ala Lys Gln Thr Val Glu
65 70 75 80

Leu Leu Leu Glu Gly Leu Asn Asp Met Ala Lys Ala Lys Leu Leu Thr
85 90 95

Thr Glu Glu Asp Asn Leu Arg Glu Trp Glu Tyr Gly Asp Tyr Glu Gly
100 105 110

Leu Leu Thr Ser Gln Ile Ile Glu Leu Arg Asn Lys Arg Gly Leu Asp
115 120 125

Lys Asp Leu Pro Lys Gly Glu Glu Trp Asn Ile Trp Arg Asp Gly Cys
130 135 140

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

Ile Thr Asn Ile Arg Ala Ile His Glu Lys Ala Ile Gln Asp Asn Val
165 170 175

Pro Cys Asp Val Ile Val Val Gly His Gly His Ile Leu Arg Cys Phe
180 185 190

Ala Ala Arg Trp Val Gly Lys Asp Ile Asn Val Asn Pro Gln Val Val
 195 200 205

Leu Asp Ala Gly Gly Val Gly Val Leu Ser Tyr Gln His His Asn Ile
 210 215 220

His Glu Pro Ala Leu Cys Leu Ala Gly Ala Phe Val Val Pro Val Glu
 225 230 235 240

Glu Glu Gly Ser Asp Ile
 245

<210> 41
 <211> 723
 <212> DNA
 <213> Candida albicans

<400> 41
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 aagagtgggtc aatatacttc aagaaccgat ctcgacttga ctccatttgg tgtcaaacaa 120
 atgagaaata caggtaaagg tcttattggc cctggtaatt tacaaatgat caaaccggaa 180
 aatttaactc atatttttgt atctccaagg aagagagcac aacgtacctc acaattgcta 240
 ttagaagaag ttgatccaga aattaaggat aaaattccaa ttgaaataga tgaagatgtg 300
 agagaatggg agtatgggtga atacgaaggc ttaaaaacaa acgaatttat cgaattgaga 360
 aagcaaaaag gattagataa ggatctggag tggactatctt ggggttaaagg gcgtgaagga 420
 ggtgaacaac attatgaagt tgcagcaaga ttggatcggt ttattgagaa gatccaaaaa 480
 attcaccgtg aagctcttgc taaaggagtg gcattctgata taattgttgt tgcacatggt 540
 catatattaa gatgtcttgt tgcaagatgg gttaaactgt agttaagtac caatccccaa 600
 ttaatttttg atgctggtgg tgttggtggt ttgagctacc aacatcaciaa tgtcgacgaa 660
 ccagcaattt atttggctgg tgcgtttact gtccctgttg aagaagaagg tgcagatatt 720
 taa 723

<210> 42
 <211> 240
 <212> PRT
 <213> Candida albicans

<400> 42
 Met Thr Lys Ser Pro Cys Pro Arg Leu Ile Phe Val Arg His Gly Gln
 1 5 10 15

Thr Glu Trp Ser Lys Ser Gly Gln Tyr Thr Ser Arg Thr Asp Leu Asp
 20 25 30

Leu Thr Pro Phe Gly Val Lys Gln Met Arg Asn Thr Gly Lys Gly Leu
 35 40 45

Ile Gly Pro Gly Asn Leu Gln Met Ile Lys Pro Glu Asn Leu Thr His
 50 55 60

Ile Phe Val Ser Pro Arg Lys Arg Ala Gln Arg Thr Ser Gln Leu Leu
 65 70 75 80

Leu Glu Glu Val Asp Pro Glu Ile Lys Asp Lys Ile Pro Ile Glu Ile
 85 90 95

Asp Glu Asp Val Arg Glu Trp Glu Tyr Gly Glu Tyr Glu Gly Leu Lys
 100 105 110

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

Ser Glu Trp Thr Ile Trp Gly Lys Gly Arg Glu Gly Gly Glu Gln His
 130 135 140

Tyr Glu Val Ala Ala Arg Leu Asp Arg Phe Ile Glu Lys Ile Gln Lys
 145 150 155 160

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

Val Ala His Gly His Ile Leu Arg Cys Leu Val Ala Arg Trp Val Lys
 180 185 190

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

Gly Val Leu Ser Tyr Gln His His Asn Val Asp Glu Pro Ala Ile Tyr
 210 215 220

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

<210> 43
 <211> 726
 <212> DNA
 <213> Candida albicans

<400> 43
 atgtccaaaa ttccttatcc aagattgatt tttgttcgcc acggtcaaac tgaatggtct 60
 aaaagtgggtc aacacacttc aactaccgac attgacttga ctccatttgg ggtcgaacaa 120
 atgagaaata ctggtagagc acttatcggt ctagtaatt tacaaatgat caaaccagag 180
 aatttgactc gtatTTTTgt ttcaccaagg caaagagcac aacaaacttt acaattatta 240
 ttggaagatg ttgaccccgga atttaaggac aaaatcccag ttgaaataga tgaggatgtg 300
 agagaatggg attatggtga ttacgaagga ataacgagtg ctgaaatcaa cgaattaagg 360
 aaaaagaaaag gattagatga taaagatcac aaatgggtcca tatggagtga tggatgtgaa 420
 ggaggtgaac aacattatga tgtagcaaag aggttgata gatttattga aaaagtgaga 480

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gagtttcatc gtcaagcaat tgctaaaagg gaaccatgtg atatcctcgt cgttgctcat 540
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 caattgattt tggatgctgg tgggtgtagga actttgagtt atgaacacca taatatcgat 660
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 ctttag 726

<210> 44
 <211> 241
 <212> PRT
 <213> Candida albicans

<400> 44

Met Ser Lys Ile Pro Tyr Pro Arg Leu Ile Phe Val Arg His Gly Gln
 1 5 10 15

Thr Glu Trp Ser Lys Ser Gly Gln His Thr Ser Thr Thr Asp Ile Asp
 20 25 30

Leu Thr Pro Phe Gly Val Glu Gln Met Arg Asn Thr Gly Arg Ala Leu
 35 40 45

Ile Gly Pro Ser Asn Leu Gln Met Ile Lys Pro Glu Asn Leu Thr Arg
 50 55 60

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

Leu Glu Asp Val Asp Pro Glu Phe Lys Asp Lys Ile Pro Val Glu Ile
 85 90 95

Asp Glu Asp Val Arg Glu Trp Asp Tyr Gly Asp Tyr Glu Gly Ile Thr
 100 105 110

Ser Ala Glu Ile Asn Glu Leu Arg Lys Lys Lys Gly Leu Asp Asp Lys
 115 120 125

Asp His Lys Trp Ser Ile Trp Ser Asp Gly Cys Glu Gly Gly Glu Gln
 130 135 140

His Tyr Asp Val Ala Lys Arg Leu Asp Arg Phe Ile Glu Lys Val Arg
 145 150 155 160

Glu Phe His Arg Gln Ala Ile Ala Lys Arg Glu Pro Cys Asp Ile Leu
 165 170 175

Val Val Ala His Gly His Ile Leu Arg Cys Leu Gly Ala Arg Trp Val
 180 185 190

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

Val Gly Thr Leu Ser Tyr Glu His His Asn Ile Asp Glu Pro Ser Ile
 210 215 220

Phe Leu Ser Gly Ala Phe Thr Val Pro Val Ala Glu Gln Cys Ala Asp
 225 230 235 240

Leu

<210> 45
 <211> 726
 <212> DNA
 <213> Candida albicans

<400> 45
 atgtccaaaa ttccttatcc aagattgatt tttgttcgcc acggtcaaac tgaatggtct 60
 aaaagtgggtc aacatacttc aactaccgac attgacttga ctccatttgg ggtcgaacaa 120
 atgagaaata ctggtagagc acttatcggc cctagtaatt tacaaatgat caaaccagag 180
 aatttgactc gtatTTTTgt ttcaccaagg caaagagcac aacaaacttt acaattatta 240
 ttggaagatg ttgacccga atttaaggac aaaatcccag ttgaaataga tgaggatgtg 300
 agagaatggg attatggtga ttacgaagga ataacgagtg ctgaaatcaa cgaattaaga 360
 aaaaagaaag gattagatga taaagatcac aaatgggtcca tatggagtga tggatgtgaa 420
 ggaggtgagc aacattatga tgtagcaaag aggttgata gatttattga aaaagtaaga 480
 gagtttcatc gtcaagcaat tgctaaaaag gaaccatgtg atatcctcgt cgttgctcat 540
 ggtcatatat tgagatgtct aggagctaga tgggtccaac gtgaattgaa tgtcaatcca 600
 caattgattt tggatgctgg tgggttagga actttgagtt atgaacacca taatatcgat 660
 gaaccatcaa tctttttatc aggggcattc accgtaccgg ttgccgaaca atgtgctgat 720
 ctttag 726

<210> 46
 <211> 241
 <212> PRT
 <213> Candida albicans

<400> 46

Met Ser Lys Ile Pro Tyr Pro Arg Leu Ile Phe Val Arg His Gly Gln
 1 5 10 15

Thr Glu Trp Ser Lys Ser Gly Gln His Thr Ser Thr Thr Asp Ile Asp
 20 25 30

Leu Thr Pro Phe Gly Val Glu Gln Met Arg Asn Thr Gly Arg Ala Leu
 35 40 45

Ile Gly Pro Ser Asn Leu Gln Met Ile Lys Pro Glu Asn Leu Thr Arg
 50 55 60

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

Leu Glu Asp Val Asp Pro Glu Phe Lys Asp Lys Ile Pro Val Glu Ile
85 90 95

Asp Glu Asp Val Arg Glu Trp Asp Tyr Gly Asp Tyr Glu Gly Ile Thr
100 105 110

Ser Ala Glu Ile Asn Glu Leu Arg Lys Lys Lys Gly Leu Asp Asp Lys
115 120 125

Asp His Lys Trp Ser Ile Trp Ser Asp Gly Cys Glu Gly Gly Glu Gln
130 135 140

His Tyr Asp Val Ala Lys Arg Leu Asp Arg Phe Ile Glu Lys Val Arg
145 150 155 160

Glu Phe His Arg Gln Ala Ile Ala Lys Lys Glu Pro Cys Asp Ile Leu
165 170 175

Val Val Ala His Gly His Ile Leu Arg Cys Leu Gly Ala Arg Trp Val
180 185 190

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

Val Gly Thr Leu Ser Tyr Glu His His Asn Ile Asp Glu Pro Ser Ile
210 215 220

Phe Leu Ser Gly Ala Phe Thr Val Pro Val Ala Glu Gln Cys Ala Asp
225 230 235 240

Leu

<210> 47
<211> 741
<212> DNA
<213> Yarrowia lipolytica

<400> 47
atggcccctc gagttatctt tgtacgacac ggcgagaccg aatgggtcaaa gtccggccaa 60
cacacgtcgg tgactgatct gccattgact gagaacggag tcaagcgagt gcgagcgacg 120
ggacggggcgc tgggtgggccg aaaccggctg gtgaaccggc cgtacgtgga gcacattttt 180
gtttcgcccc gatctcgtgc ccagcagacg ctcaagctct tttttgagga cgagcccag 240
gctctcgcca agatccccca gaccgtgacc gaagacattc gagagtggga ctacggcaag 300
tacgagggcc gaaagtcagc cgaaatccgg gccgaccgaa ccgcgcgagg catcgacaag 360
gacggccaca agtgaacat ttggtccgac ggctgcgagg acggagagtc gcccacacag 420

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gtgcagaagc gactggacga gctcatcaag gagatccggg tgatccacaa gaaggcgctc 480
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tttgctctgc gatgggtcaa cggagacatc accatcaacc cggctctgat tctcgaggca 600
ggaggagtcg gtgtgctgtc ttacgagcat aacaacattg aggagccagc catttacctg 660
ggaggagcct tctttgtgcc cgacgaggat gtggagaaga acagcggagt cattgcgctg 720
gctgggggag agcagaacta g 741

<210> 48
<211> 246
<212> PRT
<213> Yarrowia lipolytica

<400> 48

Met Ala Pro Arg Val Ile Phe Val Arg His Gly Glu Thr Glu Trp Ser
1 5 10 15

Lys Ser Gly Gln His Thr Ser Val Thr Asp Leu Pro Leu Thr Glu Asn
20 25 30

Gly Val Lys Arg Val Arg Ala Thr Gly Arg Ala Leu Val Gly Arg Asn
35 40 45

Arg Leu Val Asn Pro Ala Tyr Val Glu His Ile Phe Val Ser Pro Arg
50 55 60

Ser Arg Ala Gln Gln Thr Leu Lys Leu Phe Phe Glu Asp Glu Pro Glu
65 70 75 80

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

Asp Tyr Gly Lys Tyr Glu Gly Arg Lys Ser Ala Glu Ile Arg Ala Asp
100 105 110

Arg Thr Ala Arg Gly Ile Asp Lys Asp Gly His Lys Trp Asn Ile Trp
115 120 125

Ser Asp Gly Cys Glu Asp Gly Glu Ser Pro Gln Gln Val Gln Lys Arg
130 135 140

Val Asp Glu Leu Ile Lys Glu Ile Arg Val Ile His Lys Lys Ala Leu
145 150 155 160

Asp Glu Gly Lys Glu His Cys Asp Val Met Val Phe Ala His Gly His
165 170 175

Ile Leu Arg Val Phe Ala Leu Arg Trp Val Asn Gly Asp Ile Thr Ile
180 185 190

Asn Pro Ala Leu Ile Leu Glu Ala Gly Gly Val Gly Val Leu Ser Tyr
Seite 31

195

Glu His Asn Asn Ile Glu Glu Pro Ala Ile Tyr Leu Gly Gly Ala Phe
210 215 220

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

Ala Gly Gly Glu Gln Asn
245

<210> 49
<211> 795
<212> DNA
<213> Magnaporthe grisea

<400> 49
atgcgacaag cgtcaccaaa gtcggggatg tcaacgcctc gtgtcttcat tgtccgccac 60
ggcgagaccg agtggtcctt cgacggccgc cacttggtt ccacggatat tcccctgacg 120
gccaatggcg agaagcgcgt gagggctacc ggccggggcca tggtcggaaa tgaccgcctg 180
atcgtgcca gaaagctcg acacatatac gtatctcctc gtaagcgcgc ccagcgcacc 240
tttgagctgc tcaaccttgg cctcaaggac cctctcccat gggaacctca tggcgacctg 300
gagaaggatc ctctgtactg cgacacggcc aagatcgagg tcaccgagga catccgcgag 360
tgggactatg gtgagtacga gggcatcacc agcccagaga tcaggagat ccgtaagaag 420
cagggcatag aggggaggtg ggatatctgg agggatggat gtcctgggtg agaaagccct 480
gaggacataa ccgcccggct tgatcgctc atagccgaca tccgtaacaa gttccacgcg 540
ccggtgatgg aaaagggagc aacggacccc aaggagcccc agccagccag cgacgtgctc 600
gtcgtggcgc atggatcatat cctccgggct ttcgcatgct gctgggcccg caagagtctc 660
caggatgggc cgactttcat cctggaggct ggcggtgtag gcagtcttag ctatgaacac 720
cacaacgtag ccgagcctgc catcctgctt ggcggtgcct ttgtgattga cgttcccga 780
gcgtccaagg actga 795

<210> 50
<211> 264
<212> PRT
<213> Magnaporthe grisea

<400> 50

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

Ile Val Arg His Gly Glu Thr Glu Trp Ser Leu Asp Gly Arg His Thr
20 25 30

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

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

Lys Leu Ala His Ile Tyr Val Ser Pro Arg Lys Arg Ala Gln Arg Thr
 65 70 75 80

Phe Glu Leu Leu Asn Leu Gly Leu Lys Asp Pro Leu Pro Trp Glu Pro
 85 90 95

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

Glu Val Thr Glu Asp Ile Arg Glu Trp Asp Tyr Gly Glu Tyr Glu Gly
 115 120 125

Ile Thr Ser Pro Glu Ile Arg Glu Ile Arg Lys Lys Gln Gly Ile Glu
 130 135 140

Gly Arg Trp Asp Ile Trp Arg Asp Gly Cys Pro Gly Gly Glu Ser Pro
 145 150 155 160

Glu Asp Ile Thr Ala Arg Leu Asp Arg Leu Ile Ala Asp Ile Arg Asn
 165 170 175

Lys Phe His Ala Pro Val Met Glu Lys Gly Ala Thr Asp Pro Lys Glu
 180 185 190

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

Arg Ala Phe Ala Met Arg Trp Ala Gly Lys Ser Leu Gln Asp Gly Pro
 210 215 220

Thr Phe Ile Leu Glu Ala Gly Gly Val Gly Ser Leu Ser Tyr Glu His
 225 230 235 240

His Asn Val Ala Glu Pro Ala Ile Leu Leu Gly Gly Ala Phe Val Ile
 245 250 255

Asp Val Pro Glu Ala Ser Lys Asp
 260

<210> 51
 <211> 720
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 51
 atggccccc gctgcttcat aatccgccac ggcgaaactg aatggtcgct gaacgggcg 60
 cacacgggaa tcacagacct gccactcacc gagaacggcg agaagcggat taaagcaact 120
 ggaaaggctc ttgtcggcaa cgacaggtta attgcgccga aaaagctagt ccatgtatat 180
 gtctctcctc gcacccgcgc gcagcggacg ctggaactgc ttgaaatcgg gtgtcgagag 240
 Seite 33

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cgcttccct ggacagagaa gcgcaaggcc gaatctgacg agccgatccg gacggaagcg 300
aaagtggaga ttacagaggc tatccgagaa tgggattacg gcgactacga gggtttgacg 360
agtaagcaga tccgagagcg aagggcgga caaggggagg ggagctggga tatttggcgg 420
gatgggtgtc ccgggggaga atcacctgaa gacgtcatga aacgactaga cgcgctgatt 480
gctgagattc gagaaaagca ccacaagccg tgtttcgagg gtaataagga gagcggcgac 540
gtgcttatcg ttgcgcacgg gcacatcctc cgtgcgtttg cgatgcgctg gacgggccga 600
ccgttaacgg agacggcgct gattctggag gctgggtggtg taggcacatt gagttacgag 660
caccataaca tcgaagagcc ggcgatcatc ctcggtggag gatttgtcgt ggagaattga 720

<210> 52
<211> 239
<212> PRT
<213> Aspergillus nidulans
<400> 52

Met Ala Pro Arg Cys Phe Ile Ile Arg His Gly Glu Thr Glu Trp Ser
1 5 10 15

Leu Asn Gly Arg His Thr Gly Ile Thr Asp Leu Pro Leu Thr Glu Asn
20 25 30

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

Arg Leu Ile Ala Pro Lys Lys Leu Val His Val Tyr Val Ser Pro Arg
50 55 60

Thr Arg Ala Gln Arg Thr Leu Glu Leu Leu Glu Ile Gly Cys Arg Glu
65 70 75 80

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

Arg Thr Glu Ala Lys Val Glu Ile Thr Glu Ala Ile Arg Glu Trp Asp
100 105 110

Tyr Gly Asp Tyr Glu Gly Leu Thr Ser Lys Gln Ile Arg Glu Arg Arg
115 120 125

Ala Glu Gln Gly Glu Gly Ser Trp Asp Ile Trp Arg Asp Gly Cys Pro
130 135 140

Gly Gly Glu Ser Pro Glu Asp Val Met Lys Arg Leu Asp Ala Leu Ile
145 150 155 160

Ala Glu Ile Arg Glu Lys His His Lys Pro Cys Phe Glu Gly Asn Lys
165 170 175

Glu Ser Gly Asp Val Leu Ile Val Ala His Gly His Ile Leu Arg Ala
 180 185 190

Phe Ala Met Arg Trp Thr Gly Arg Pro Leu Thr Glu Thr Ala Leu Ile
 195 200 205

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

Glu Glu Pro Ala Ile Ile Leu Gly Gly Gly Phe Val Val Glu Asn
 225 230 235

<210> 53
 <211> 732
 <212> DNA
 <213> Gibberella zeae

<400> 53
 atgtcaaccc cccgcgtttt cctcattcgc catggcgaga cggagtgggtc gcttgatggt 60
 cgtcactactg gtgtgactga cattcctctt actgccaatg gcgagaaacg tgtgaaggca 120
 acagggaagg ctcttgctcg cccagaccgt ctatttgctc ccaagaagat cgctcatatc 180
 tatgtctcac cccgaaagcg tgctcaacgc acatttgagc tgctcaacct tgggctgagc 240
 cgtccgctac cctggacacc acacggcgac acccctgatg ggactgggtct gcagtgtgag 300
 gccgagggtt aagtaacaga ctatatccga gaatgggact atggcgacta cgaaggcatt 360
 acatctccag agattcgcaa gatcagagcc gagcagggga tcaaggggtc ctgggacatt 420
 tggaaagatg gttgtccagg tggagagagc cctcatgatg tcagcaggag actcgatcaa 480
 ttgatagaag agattcgga taaatggcac aagccagtca tggaccaagg aagcgatcat 540
 tgtggcgacg tcttacttgt tgctcatgga cacattcttc gtgcttttgc catgagatgg 600
 gctgggttac ctttgcgaga aggtccaacc tttttactgg aagcaggcgg tgtcgggact 660
 ctgaggatcg aagaaccagc gctcttgctg ggcggcgcct ttgttgttga acttgacggc 720
 caagacaact ag 732

<210> 54
 <211> 243
 <212> PRT
 <213> Gibberella zeae

<400> 54

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

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

Asn Gly Glu Lys Arg Val Lys Ala Thr Gly Lys Ala Leu Val Gly Pro
 35 40 45

Asp Arg Leu Ile Ala Pro Lys Lys Ile Ala His Ile Tyr Val Ser Pro
 Seite 35

50

55

60

Arg Lys Arg Ala Gln Arg Thr Phe Glu Leu Leu Asn Leu Gly Leu Ser
65 70 75 80

Arg Pro Leu Pro Trp Thr Pro His Gly Asp Thr Pro Asp Gly Thr Gly
85 90 95

Leu Gln Cys Glu Ala Glu Val Glu Val Thr Asp Tyr Ile Arg Glu Trp
100 105 110

Asp Tyr Gly Asp Tyr Glu Gly Ile Thr Ser Pro Glu Ile Arg Lys Ile
115 120 125

Arg Ala Glu Gln Gly Ile Lys Gly Ser Trp Asp Ile Trp Lys Asp Gly
130 135 140

Cys Pro Gly Gly Glu Ser Pro His Asp Val Ser Arg Arg Leu Asp Gln
145 150 155 160

Leu Ile Glu Glu Ile Arg Asp Lys Trp His Lys Pro Val Met Asp Gln
165 170 175

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

Leu Arg Ala Phe Ala Met Arg Trp Ala Gly Tyr Ala Leu Arg Glu Gly
195 200 205

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

Glu Pro Ala Leu Leu Leu Gly Gly Ala Phe Val Val Glu Leu Asp Gly
225 230 235 240

Gln Asp Asn

<210> 55

<211> 582

<212> DNA

<213> Rhizobium leguminosarum

<400> 55

atgagcagtg cgtttcccga gatctacttg gtccgccacg gtgaaaccga atggagcctg 60

tccgggcgcc ataccggacg cagtgatatt cccttgacgt cgaatggcga agaggccgcc 120

cgcaaaatcg ccgaccggct ggcgggcctt agcttctccg ccgtctggtc gagcccctcc 180

gagcgagccc gcaagacctg cgcgctcgcc ggattcggat cgggcgcggt gatcaaggac 240

gatctcgccg aatgggacta tggcgcttac gaaggcatca ccaccaaggc gatccttgcc 300

gaccgccccg gctggcagct ctttcgcgac ggctgcccga agggcgaatt cgccgccgat 360

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atcttttcga gttcgcatTT cctgcgggtc ctcgccgcc gctggcttgg cctgccgccg 480
gaagacggcg cgcgtttcgt gctcgatacc gcgagcatca gcgtgctcgg ctatgagcac 540
gatctgaccg aaccggtcat ccgccgctgg aaccagagat ag 582

<210> 56
<211> 193
<212> PRT
<213> Rhizobium leguminosarum
<400> 56

Met Ser Ser Ala Phe Pro Glu Ile Tyr Leu Val Arg His Gly Glu Thr
1 5 10 15

Glu Trp Ser Leu Ser Gly Arg His Thr Gly Arg Ser Asp Ile Pro Leu
20 25 30

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

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

Lys Thr Cys Ala Leu Ala Gly Phe Gly Ser Gly Ala Val Ile Lys Asp
65 70 75 80

Asp Leu Ala Glu Trp Asp Tyr Gly Ala Tyr Glu Gly Ile Thr Thr Lys
85 90 95

Ala Ile Leu Ala Asp Arg Pro Gly Trp Gln Leu Phe Arg Asp Gly Cys
100 105 110

Pro Lys Gly Glu Phe Ala Ala Asp Val Gly Asp Arg Ala Asp Ala Val
115 120 125

Ile Gly Gly Leu Arg Gln Thr Ala Gly Thr Ile Leu Ile Phe Ser Ser
130 135 140

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

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

Gly Tyr Glu His Asp Leu Thr Glu Pro Val Ile Arg Arg Trp Asn Gln
180 185 190

Arg

<210> 57

<211> 1665
 <212> DNA
 <213> Ustilago maydis

<400> 57
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 cttgcgcca gcacgtcgg cgtcggcaac ggcaagttga ttgacccgac tagactcaat 180
 cacatctttg tcagtccacg caagcgatcg cagcgtacgc ttgagatcat gctacagcac 240
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 tgggactacg gtgcgtacga agggctcaag acggacgaga ttcgagccaa acatcccgga 360
 tgggatatct ggaccgaagg aacacccgat catcctgaca gacccgacga gctgccaggt 420
 gagtcggcac agcacatgag cgatcgtgtt gactcggta tcgctaaaat ccgcagtctg 480
 caatctgggc atgtcgacaa gcgcaatcag gggtcacgat tgggcagtaa gacgtgcat 540
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 gcgcatcaca gctttgctga acctaccgtc gccggtatct tctcgtccaa aactggcccc 720
 aagggtgaca aggaagggtc tcccggctcg tgtgggtcag cgaaacacga agaatcgag 780
 tacctcgagc tggttcaacg agttatctca acgggcgaat caagaccgga tcgaacgggc 840
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 gatctaggac ccgtctatgg tttccaatgg cgacactttg gtgctacgta caaagactgt 1140
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 aacaatccta ccgatcgtcg tatcttgctc agcgcatgga acccggcaga tctcgaactg 1260
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 tcgaagggtc aaggtaaaaa gcacctctcg tgccagatgt accagcgttc ctgcgacctt 1380
 gggttgggtg tacctttcaa cattgctagc tatgcgttgc taacctacat gatcgccaaa 1440
 gtgaccgatt gcgaacccaa ggaactcata ctggcaatgg gtgatgctca cgtttacaag 1500
 gaccatgtgc aaccgctcaa ggcgcagttg gagagagacc cgcttccctt ccctaagctc 1560
 aagatcga aa gggacgtcaa ggatattgac gactttacgt tcgatgattt cgtcgtgcaa 1620
 ggttacaaat gtcacggaaa gatcgatatg aagatgagcg ttttag 1665

<210> 58
 <211> 554
 <212> PRT
 <213> Ustilago maydis

<400> 58

Met Ala Met Pro Arg Val Phe Leu Ala Arg His Gly Glu Thr Glu Trp
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 Ser Ile Ser Gly Gln His Thr Gly Arg Ser Asp Ile Pro Leu Thr Pro
 20 25 30
 His Gly Glu Glu Val Met Arg Gln Leu Ala Pro Ser Ile Val Gly Val
 35 40 45
 Gly Asn Gly Lys Leu Ile Asp Pro Thr Arg Leu Asn His Ile Phe Val
 50 55 60
 Ser Pro Arg Lys Arg Ser Gln Arg Thr Leu Glu Ile Met Leu Gln His
 65 70 75 80
 Ile Pro Ala Ser Gln Arg Leu Gly Ile Pro Asp Val Glu Ile Val Gln
 85 90 95
 Asp Cys Arg Glu Trp Asp Tyr Gly Ala Tyr Glu Gly Leu Lys Thr Asp
 100 105 110
 Glu Ile Arg Ala Lys His Pro Gly Trp Asp Ile Trp Thr Glu Gly Thr
 115 120 125
 Pro Asp His Pro Asp Arg Pro Asp Glu Leu Pro Gly Glu Ser Ala Gln
 130 135 140
 His Met Ser Asp Arg Val Asp Ser Val Ile Ala Lys Ile Arg Ser Leu
 145 150 155 160
 Gln Ser Gly His Val Asp Lys Arg Asn Gln Gly His Asp Val Gly Ser
 165 170 175
 Lys Thr Cys Asp Val Leu Leu Val Cys His Gly His Phe Asn Arg Val
 180 185 190
 Phe Val Ala Arg Trp Leu Gly Leu Pro Leu Thr Asn Gly Arg Leu Phe
 195 200 205
 Glu Met Asp Ala Gly Gly Met Val Val Leu Gly Tyr Ala His His Ser
 210 215 220
 Phe Ala Glu Pro Thr Val Ala Gly Ile Phe Ser Ser Lys Thr Gly Pro
 225 230 235 240
 Lys Gly Asp Lys Glu Gly Ala Pro Gly Ser Cys Gly Ser Ala Lys His
 245 250 255
 Glu Glu Ser Gln Tyr Leu Glu Leu Val Gln Arg Val Ile Ser Thr Gly
 260 265 270
 Glu Ser Arg Pro Asp Arg Thr Gly Thr Gly Thr Leu Ala Leu Phe Ala
 Seite 39

275

280

285

Pro Gln Pro Ser Leu Arg Phe Asp Leu Thr Asn Gly Thr Leu Pro Leu
 290 295 300
 Leu Thr Thr Lys Arg Val Phe Phe Arg Gly Val Leu Glu Glu Leu Leu
 305 310 315 320
 Trp Phe Val Gly Gly Lys Thr Asp Ala Lys Leu Leu Thr Glu Lys Ser
 325 330 335
 Val His Ile Trp Asp Gly Asn Gly Ser Arg Ala Phe Leu Asp Ser Arg
 340 345 350
 Gly Leu Ser His Arg Arg Glu Gly Asp Leu Gly Pro Val Tyr Gly Phe
 355 360 365
 Gln Trp Arg His Phe Gly Ala Thr Tyr Lys Asp Cys Asp Thr Asp Tyr
 370 375 380
 Ala Gly Gln Gly Val Asp Gln Leu Ala Ser Val Ile Asp Lys Ile Arg
 385 390 395 400
 Asn Asn Pro Thr Asp Arg Arg Ile Leu Leu Ser Ala Trp Asn Pro Ala
 405 410 415
 Asp Leu Glu Leu Met Ala Leu Pro Pro Cys His Met Phe Ala Gln Phe
 420 425 430
 Phe Val Ser Asn Leu Asp Ala Tyr Ser Lys Gly Gln Gly Lys Lys His
 435 440 445
 Leu Ser Cys Gln Met Tyr Gln Arg Ser Cys Asp Leu Gly Leu Gly Val
 450 455 460
 Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr Tyr Met Ile Ala Lys
 465 470 475 480
 Val Thr Asp Cys Glu Pro Lys Glu Leu Ile Leu Ala Met Gly Asp Ala
 485 490 495
 His Val Tyr Lys Asp His Val Gln Pro Leu Lys Ala Gln Leu Glu Arg
 500 505 510
 Asp Pro Leu Pro Phe Pro Lys Leu Lys Ile Glu Arg Asp Val Lys Asp
 515 520 525
 Ile Asp Asp Phe Thr Phe Asp Asp Phe Val Val Gln Gly Tyr Lys Cys
 530 535 540
 His Gly Lys Ile Asp Met Lys Met Ser Val
 545 550

<210> 59
 <211> 1290
 <212> DNA
 <213> *Shigella flexneri*

<400> 59
 atggaaacga ctcaaaccag cacgattgcg tcgaaagact ctcgtagtgc ctggcgcaag 60
 acagacacca tgtggatgct gggcctttac ggcacggcaa tcggcgcggg cgtgctgttc 120
 ctgccaatca acgccggtgt tggcggtatg atcccgtga tcatcatggc tatccttgcg 180
 ttcccgatga cgttttttgc tcaccgcggc ctgactcgct tcgtactgtc tggtaaaaac 240
 ccggggaag acatcaccga ggtttagtaa gaacactttg gtattggcgc aggtaaactg 300
 attaccctgc tctacttctt cgctatctac ccgatcctgc tggtttatag cgtggcaatc 360
 accaataaccg ttgaaagctt catgtctcac cagctgggta tgacgccacc gccgcgtgcg 420
 attctgtcgc tgatcctgat cgtgggtatg atgaccatcg ttcgctttgg tgagcagatg 480
 atcgttaaag cgatgagtat tctgggtattc ccgtttgttg gcgtactgat gctgctggct 540
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 tctgcaaccg gaaacggtct gtggatgacc ctgtggctgg caattccggt aatggtgttc 660
 tcgttcaacc actctccgat catctcttct ttcgccgttg cgaatcgtga agagtacggc 720
 gatatggcag aacagaaatg ctccaagatc ctggcattcg cacacatcat gatggtgctg 780
 accgaaatga tcttcgtctt catctgcgta ctgagcctga ctccggcaga cctggctgcg 840
 gctaaagagc acaacatctc gattctgtct tacctggcta accactttta cgcaccggtt 900
 atcgcgtgga tggctccgat tatcgcgatt atcgctatca ccaaaccctt cctcggccac 960
 tacctgggcg cacgtgaagg cttcaacggt atggtgatta aatctctgcg tggtaaaggt 1020
 aagtctatcg aaatcaacaa gctgaaccgt atcactgcgc tgttcatgct ggtaacgacc 1080
 tggattgttg ccaccctgaa cccgagcatc ctgggtatga ttgaaaccct gggcggccca 1140
 atcatcgca tgatcctgtt cctgatgccg atgtacgcaa ttcagaaagt accggcaatg 1200
 cgtaagtaca gcggtcacat cagcaacgta ttcgttgtcg tgatgggtct gattgcaatc 1260
 tccgcaatct tctactctct gttcagctaa 1290

<210> 60
 <211> 429
 <212> PRT
 <213> *Shigella flexneri*

<400> 60

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

Ala Trp Arg Lys Thr Asp Thr Met Trp Met Leu Gly Leu Tyr Gly Thr
 20 25 30

Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
 Seite 41

Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
50 55 60

Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Lys Asn
65 70 75 80

Pro Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Ile Gly
85 90 95

Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile
100 105 110

Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Met
115 120 125

Ser His Gln Leu Gly Met Thr Pro Pro Pro Arg Ala Ile Leu Ser Leu
130 135 140

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

Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Gly Val Leu
165 170 175

Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Asn Gly Ala Ala Leu
180 185 190

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

Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His
210 215 220

Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Asn Arg Glu Glu Tyr Gly
225 230 235 240

Asp Met Ala Glu Gln Lys Cys Ser Lys Ile Leu Ala Phe Ala His Ile
245 250 255

Met Met Val Leu Thr Glu Met Ile Phe Val Phe Ile Cys Val Leu Ser
260 265 270

Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu His Asn Ile Ser Ile
275 280 285

Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Val Ile Ala Trp Met
290 295 300

Ala Pro Ile Ile Ala Ile Ile Ala Ile Thr Lys Ser Phe Leu Gly His
305 310 315 320

Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu
325 330 335

Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Arg Ile Thr
340 345 350

Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro
355 360 365

Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met
370 375 380

Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met
385 390 395 400

Arg Lys Tyr Ser Gly His Ile Ser Asn Val Phe Val Val Val Met Gly
405 410 415

Leu Ile Ala Ile Ser Ala Ile Phe Tyr Ser Leu Phe Ser
420 425

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<210> 61
<211> 1290
<212> DNA
<213> Salmonella typhimurium
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<400>	61						
atggaaacca	ctcagaccag	cactattgct	tcgattgact	ctcgaagcgc	atggcgcaaa		60
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ctgccgatca	acgcaggcgt	cggcggcatg	attccgctca	tcatcatggc	gattctcgct		180
ttcccgatga	cctttttcgc	acaccgtggt	ttaaccgcgt	tcgtgctgtc	cggtaaaaaat		240
ccgggtgaag	acatcactga	agtcgttgag	gaacacttcg	gtatcggcgc	aggtaaaactg		300
attaccctgc	tttacttctt	cgcgatttac	cccatcctgc	tggtttacag	cgtggcgatt		360
actaataccg	tggaaagctt	cctgaccac	cagttagcga	ttaatccgcc	gccgcgggcg		420
attctttccc	tgatcctgat	tgttggcatg	atgaccatcg	tgcgcttcgg	cgagcaaattg		480
atcgttaagg	cgatgagtat	cctggtattc	ccgttcgtcg	ctgcgctgat	gctgctggcc		540
ttgtacctga	tcccgcagtg	gaacggcgcg	gcgctggaaa	ctctgtcctt	tgattccgcc		600
gcgtctaccg	gtaacggtct	gtggatgacg	ctgtggctgg	cgattccggg	gatggttttc		660
tctttcaacc	actccccgat	catctctctc	ttcgcggttg	cgaagcgtga	agagtacggt		720
gaaggcgctg	agaagaaatg	ttctaaaatt	ctggccttcg	cccacatcat	gatggtgctg		780
accgtgatgt	tcttcgtctt	cagctgcgtg	ctgagcctga	cgccggcaga	tctggcagcg		840
gcaaaagagc	agaacatctc	tattctgtct	tacctggcga	accattttta	cgcgccgatc		900
atcgccctga	tggcgccgat	cattgcgatg	attgctatca	ccaaatcctt	cctcggccac		960
taccttggcg	cgcgtgaagg	ctttaacggg	atggtgatta	aatcgctgcg	tggttaaagg		1020

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aaatccatcg aaatcaacaa actgaataaa attaccgcgc tggtcatgct ggtcaccacc 1080
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 atcatcgca tgattctggt cctgatgccg atgtatgcca tccagaaagt accggcaatg 1200
 cgtaagtaca gcggtcatat cagcaacgta ttcgttgga ttatgggcct gattgccatc 1260
 tccgctatct tctactcact gttcagctaa 1290

<210> 62
 <211> 429
 <212> PRT
 <213> Salmonella typhimurium

<400> 62

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

Ala Trp Arg Lys Thr Asp Thr Met Trp Met Leu Gly Leu Tyr Gly Thr
20 25 30

Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
35 40 45

Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
50 55 60

Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Lys Asn
65 70 75 80

Pro Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Ile Gly
85 90 95

Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile
100 105 110

Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Leu
115 120 125

Thr His Gln Leu Ala Ile Asn Pro Pro Pro Arg Ala Ile Leu Ser Leu
130 135 140

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

Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Ala Ala Leu
165 170 175

Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Asn Gly Ala Ala Leu
180 185 190

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

Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His
 210 215 220

Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Glu Glu Tyr Gly
 225 230 235 240

Glu Gly Ala Glu Lys Lys Cys Ser Lys Ile Leu Ala Phe Ala His Ile
 245 250 255

Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser
 260 265 270

Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu Gln Asn Ile Ser Ile
 275 280 285

Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Ile Ile Ala Trp Met
 290 295 300

Ala Pro Ile Ile Ala Met Ile Ala Ile Thr Lys Ser Phe Leu Gly His
 305 310 315 320

Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu
 325 330 335

Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Lys Ile Thr
 340 345 350

Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro
 355 360 365

Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met
 370 375 380

Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met
 385 390 395 400

Arg Lys Tyr Ser Gly His Ile Ser Asn Val Phe Val Val Ile Met Gly
 405 410 415

Leu Ile Ala Ile Ser Ala Ile Phe Tyr Ser Leu Phe Ser
 420 425

<210> 63
 <211> 1290
 <212> DNA
 <213> *Salmonella enterica*

<400> 63
 atgaaaacca ctcagaccag cactgattgct tcgattgact ctggaagcgc atggcgcaaa 60
 acggatacca tgtggatgct gggcctttac ggcacggcaa tcggcgcggg cgttctgttc 120
 ctgccgatca acgcaggcgt cggcggcatg attccgctca tcatcatggc gattctcgct 180
 Seite 45

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attaccctgc tctacttctt cgcgatttac cccatcctgc tggtttacag cgtggcgatt 360
actaataccg tggaaagctt cctgaccac cagttagcga ttaatccgcc gccgcgggcg 420
attctttccc tgatcctgat tgttgcatg atgaccatcg tgcgcttcgg cgagcaaatg 480
atcgtaagg cgatgagtat cctggtattc ccgttcgtcg ctgcgtgat gctgctggcc 540
ttgtacctga tcccgcagtg gaacggcgcg gcgctggaaa ctctgtcctt tgattccgcc 600
gcgtctaccg gtaacggtct gtggatgacg ctgtggctgg cgattccggt gatgggttttc 660
tctttcaacc actccccgat catctcctcc ttgcgggttg cgaagcgtga agagtacggt 720
gaaggcgctg agaagaaatg ttctaaaatt ctggccttcg cccacatcat gatggtgctg 780
accgtgatgt tcttcgtctt cagctgcgtg ctgagcctga cgccggcaga tctggcagcg 840
gcaaaagagc agaacatctc tattctgtct tacctggcga accactttaa cgcgccgatc 900
atgcctgga tggcgccgat cattgcgatg attgctatca ccaaatcctt cctcgccac 960
tacctggcg cgcgtaagg cttaacggg atggtgatta aatcgctgcg tggtaaaggt 1020
aatccatcg aaatcaaaa actgaataaa attaccgcgc tgttcatgct ggtcaccacc 1080
tggtattgtg cgacgtgaa cccagcatc ctgggcatga ttgaaaccct gggcgcccg 1140
atcatcgca tgattctgtt cctgatgccg atgtatgcca tccagaaagt accggcaatg 1200
cgtaagtaca gcggtcatat cagcaacgta ttcgttgta ttatgggcct gattgccatc 1260
tccgctattt tctactcact gttcagctaa 1290

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<210> 64
 <211> 429
 <212> PRT
 <213> *Salmonella enterica*
 <400> 64

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

Ala Trp Arg Lys Thr Asp Thr Met Trp Met Leu Gly Leu Tyr Gly Thr
 20 25 30

Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
 35 40 45

Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
 50 55 60

Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Lys Asn
 65 70 75 80

Pro Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Ile Gly
 85 90 95

Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile
 100 105 110
 Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Leu
 115 120 125
 Thr His Gln Leu Ala Ile Asn Pro Pro Pro Arg Ala Ile Leu Ser Leu
 130 135 140
 Ile Leu Ile Val Gly Met Met Thr Ile Val Arg Phe Gly Glu Gln Met
 145 150 155 160
 Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Ala Ala Leu
 165 170 175
 Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Asn Gly Ala Ala Leu
 180 185 190
 Glu Thr Leu Ser Phe Asp Ser Ala Ala Ser Thr Gly Asn Gly Leu Trp
 195 200 205
 Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His
 210 215 220
 Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Glu Glu Tyr Gly
 225 230 235 240
 Glu Gly Ala Glu Lys Lys Cys Ser Lys Ile Leu Ala Phe Ala His Ile
 245 250 255
 Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser
 260 265 270
 Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu Gln Asn Ile Ser Ile
 275 280 285
 Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Ile Ile Ala Trp Met
 290 295 300
 Ala Pro Ile Ile Ala Met Ile Ala Ile Thr Lys Ser Phe Leu Gly His
 305 310 315 320
 Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu
 325 330 335
 Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Lys Ile Thr
 340 345 350
 Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro
 355 360 365

Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met
 370 375 380

Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met
 385 390 395 400

Arg Lys Tyr Ser Gly His Ile Ser Asn Val Phe Val Val Ile Met Gly
 405 410 415

Leu Ile Ala Ile Ser Ala Ile Phe Tyr Ser Leu Phe Ser
 420 425

<210> 65
 <211> 1302
 <212> DNA
 <213> Yersinia pseudotuberculosis

<400> 65
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 cgcaaaagtg acaccatgtg gatgttgggt ctgtacggta cagcgattgg cgcaggtgta 120
 ctctttttgc ccatcaacgc cggatttggg ggcctgctac cactgattgt tatggctatc 180
 attgctttcc caatgaccta ctacgctcac cgtggcctgt gccgattcgt gttatccggt 240
 aaaaatccag gtgaagatat tactgaggtg gttgaagaac atttcggtgt aggcgcaggt 300
 aaactgatta ccctgcttta cttcttcgct atctacccca ttctcttggg gtacagcgta 360
 gcaattacca ataccgtgga tagtttcatt acacatcaga tgcacctgcc atcaccacca 420
 cgcgccattt tgtccctgat tctgattgtg ggcctgatgg ctatcgtgcg ctttgggtgaa 480
 cagaccatcg tcaaagccat gagcatcttg gtattcccgt ttgttgccgt attgatgatg 540
 ttggcgatat acctgatccc aaactgggtca ggtgcaatat tcgaaaacgt atccatggac 600
 ggtaacggca caggtagcgg cctgtggatg acaatgtggc taatcattcc cgtcatgggtg 660
 ttctctttca accactcacc gatcatctca gcctttgctg tagcaaagcg cgaagagtac 720
 ggggtggatg cagagaaaaa atgttcacgc attttgagct ttgccacat catgatgggtt 780
 atcaccgtca tgttcttcgt cttcagttgc gtactgagcc tgtctcctgc ggatctgatg 840
 gatgcaaaaa accaaaacat ctccattttg tcttatctgg caaaccattt taatacgcca 900
 gtaattgcct atatggcacc gggtattgcc tttattgcca tcactaaatc attcctgggc 960
 cactatctgg gcgcccgtga aggttttaac ggtatgggtca ttaagtctct gcgtagtaga 1020
 ggcaaaacca ttgagcagaa caaactgaac cgcattactg cgttgttcat gttagtcacc 1080
 acctgggctg tcgcgacctt aaacccaagt atcttgggga tgatcgaaac attggggcggc 1140
 cctatcatcg cgatgctcct gttcctgatg ccgatgtatg ccattcataa agtcccggcc 1200
 atgcgtaaat acagcggcca gatcagtaac gtattcgtgg tactcatggg cttgatcgcc 1260
 atctctggga tcttattcaa cttagcaac ttgtttaatt ag 1302

<210> 66

<211> 433
 <212> PRT
 <213> *Yersinia pseudotuberculosis*

<400> 66

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

Ile Met Met Val Ile Thr Val Met Phe Phe Val Phe Ser Cys Val Leu
260 265 270

Ser Leu Ser Pro Ala Asp Leu Met Asp Ala Lys Asn Gln Asn Ile Ser
275 280 285

Ile Leu Ser Tyr Leu Ala Asn His Phe Asn Thr Pro Val Ile Ala Tyr
290 295 300

Met Ala Pro Val Ile Ala Phe Ile Ala Ile Thr Lys Ser Phe Leu Gly
305 310 315 320

His Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser
325 330 335

Leu Arg Ser Arg Gly Lys Thr Ile Glu Gln Asn Lys Leu Asn Arg Ile
340 345 350

Thr Ala Leu Phe Met Leu Val Thr Thr Trp Ala Val Ala Thr Leu Asn
355 360 365

Pro Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala
370 375 380

Met Leu Leu Phe Leu Met Pro Met Tyr Ala Ile His Lys Val Pro Ala
385 390 395 400

Met Arg Lys Tyr Ser Gly Gln Ile Ser Asn Val Phe Val Val Leu Met
405 410 415

Gly Leu Ile Ala Ile Ser Gly Ile Leu Phe Asn Leu Ser Asn Leu Phe
420 425 430

Asn

<210> 67
<211> 1302
<212> DNA
<213> Yersinia pestis

<400> 67
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cgcaaaagtg acaccatgtg gatgttgggt ctgtacggta cagcgattgg cgcaggtgta 120
ctctttttgc ccatcaacgc cggatttgggt ggcctgctac cactgattgt tatggctatc 180
attgctttcc caatgaccta ctacgctcac cgtggcctgt gccgattcgt gttatccggt 240
aaaaatccag gtgaagatat tactgaggtg gttgaagaac atttcggtgt aggcgcaggt 300
aaactgatta ccctgcttta cttcttcgct atctacccca ttctcttggt gtacagcgta 360
gcaattacca ataccgtgga tagtttcatt acacatcaga tacacctgcc atcaccacca 420

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 ttggcgatat acctgatccc aaactgggtca ggtgcaatat tcgaaaacgt atccatggac 600
 ggtaacggca caggtagcgg cctgtggatg acaatgtggc taatcattcc cgtcatggtg 660
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 ggggtggatg cagagaaaaa atgttcacgc attttgagct ttgccacat catgatggtt 780
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 gtaattgcct atatggcacc gggtattgcc tttattgcc a tcaactaaatc attcctgggc 960
 cactatctgg gcgcccgtga aggttttaac ggtatggtca ttaagtctct gcgtagtaga 1020
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<210> 68
 <211> 433
 <212> PRT
 <213> Yersinia pestis

<400> 68

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

Ser Ser Thr Trp Arg Lys Ser Asp Thr Met Trp Met Leu Gly Leu Tyr
20 25 30

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

Ile Gly Gly Leu Leu Pro Leu Ile Val Met Ala Ile Ile Ala Phe Pro
50 55 60

Met Thr Tyr Tyr Ala His Arg Gly Leu Cys Arg Phe Val Leu Ser Gly
65 70 75 80

Lys Asn Pro Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly
85 90 95

Val Gly Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr
100 105 110

Pro Ile Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Asp Ser
115 120 125

Phe Ile Thr His Gln Ile His Leu Pro Ser Pro Pro Arg Ala Ile Leu
 130 135 140
 Ser Leu Ile Leu Ile Val Gly Leu Met Ala Ile Val Arg Phe Gly Glu
 145 150 155 160
 Gln Thr Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Ala
 165 170 175
 Val Leu Met Met Leu Ala Ile Tyr Leu Ile Pro Asn Trp Ser Gly Ala
 180 185 190
 Ile Phe Glu Asn Val Ser Met Asp Gly Asn Gly Thr Gly Ser Gly Leu
 195 200 205
 Trp Met Thr Met Trp Leu Ile Ile Pro Val Met Val Phe Ser Phe Asn
 210 215 220
 His Ser Pro Ile Ile Ser Ala Phe Ala Val Ala Lys Arg Glu Glu Tyr
 225 230 235 240
 Gly Val Asp Ala Glu Lys Lys Cys Ser Arg Ile Leu Ser Phe Ala His
 245 250 255
 Ile Met Met Val Ile Thr Val Met Phe Phe Val Phe Ser Cys Val Leu
 260 265 270
 Ser Leu Ser Pro Ala Asp Leu Met Asp Ala Lys Asn Gln Asn Ile Ser
 275 280 285
 Ile Leu Ser Tyr Leu Ala Asn His Phe Asn Thr Pro Val Ile Ala Tyr
 290 295 300
 Met Ala Pro Val Ile Ala Phe Ile Ala Ile Thr Lys Ser Phe Leu Gly
 305 310 315 320
 His Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser
 325 330 335
 Leu Arg Ser Arg Gly Lys Thr Ile Glu Gln Asn Lys Leu Asn Arg Ile
 340 345 350
 Thr Ala Leu Phe Met Leu Val Thr Thr Trp Ala Val Ala Thr Leu Asn
 355 360 365
 Pro Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala
 370 375 380
 Met Leu Leu Phe Leu Met Pro Met Tyr Ala Ile His Lys Val Pro Ala
 385 390 395 400

Met Arg Lys Tyr Ser Gly Gln Ile Ser Asn Val Phe Val Val Leu Met
 405 410 415

Gly Leu Ile Ala Ile Ser Gly Ile Leu Phe Asn Leu Ser Asn Leu Phe
 420 425 430

Asn

<210> 69
 <211> 1323
 <212> DNA
 <213> Yersinia pestis

<400> 69
 gtgttcacaa tggagatttt catggacact acgcaaacaa gcactcttgc ctcggcaaga 60
 aaaatctcat caagtacatg gcgcaaaagt gacaccatgt ggatgttggg tctgtacggt 120
 acagcgattg gcgcaggtgt actctttttg cccatcaacg ccggtattgg tggcctgcta 180
 ccactgattg ttatggctat cattgctttc ccaatgacct actacgctca ccgtggcctg 240
 tgccgattcg tgttatccgg taaaaatcca ggtgaagata ttactgaggt gggtgaagaa 300
 catttcggtg taggcgcagg taaactgatt accctgcttt acttcttcgc tatctacccc 360
 attctcttgg tgtacagcgt agcaattacc aataccgtgg atagtttcat tacacatcag 420
 atacacctgc catcaccacc acgcgccatt ttgtccctga ttctgattgt gggcctgatg 480
 gctatcgtgc gctttggtga acagaccatc gtcaaagcca tgagcatctt ggtattcccg 540
 tttgttgccg tattgatgat gttggcgata tacctgatcc caaactggtc aggtgcaata 600
 ttcgaaaacg tatccatgga cggtaacggc acaggtagcg gcctgtggat gacaatgtgg 660
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 atcactaaat cattcctggg ccactatctg ggcgcccgtg aaggttttta cggtatggtc 1020
 attaatgtctc tgcgtagtag aggcaaaacc attgagcaga acaaactgaa ccgcattact 1080
 gcgttggtca tgtagtcac cacctgggct gtcgcgacct taaaccaag tatcttgggg 1140
 atgatcgaac cattgggcgg ccctatcatc gcgatgctcc tgttcctgat gccgatgtat 1200
 gccattcata aagtcccgcc catgcgtaaa tacagcggcc agatcagtaa cgtattcgtg 1260
 gtactcatgg gcttgatcgc catctctggg atcttattca acttaagcaa cttgtttaat 1320
 tag 1323

<210> 70
 <211> 440
 <212> PRT
 <213> Yersinia pestis

<400> 70

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

Phe Val Phe Ser Cys Val Leu Ser Leu Ser Pro Ala Asp Leu Met Asp
 275 280 285

Ala Lys Asn Gln Asn Ile Ser Ile Leu Ser Tyr Leu Ala Asn His Phe
 290 295 300

Asn Thr Pro Val Ile Ala Tyr Met Ala Pro Val Ile Ala Phe Ile Ala
 305 310 315 320

Ile Thr Lys Ser Phe Leu Gly His Tyr Leu Gly Ala Arg Glu Gly Phe
 325 330 335

Asn Gly Met Val Ile Lys Ser Leu Arg Ser Arg Gly Lys Thr Ile Glu
 340 345 350

Gln Asn Lys Leu Asn Arg Ile Thr Ala Leu Phe Met Leu Val Thr Thr
 355 360 365

Trp Ala Val Ala Thr Leu Asn Pro Ser Ile Leu Gly Met Ile Glu Thr
 370 375 380

Leu Gly Gly Pro Ile Ile Ala Met Leu Leu Phe Leu Met Pro Met Tyr
 385 390 395 400

Ala Ile His Lys Val Pro Ala Met Arg Lys Tyr Ser Gly Gln Ile Ser
 405 410 415

Asn Val Phe Val Val Leu Met Gly Leu Ile Ala Ile Ser Gly Ile Leu
 420 425 430

Phe Asn Leu Ser Asn Leu Phe Asn
 435 440

<210> 71
 <211> 1290
 <212> DNA
 <213> *Erwinia carotovora*

<400> 71
 atgagcacia ttcaagatag cagccacgtg ttagaacagg cttcaggatg gcgtaaaagc 60
 gacaccgtct ggatgctcgg cctctatggc acggccatcg gtgcgggCGT gttattctta 120
 cccatcaatg ctggcattgg tggtttaatt cCGTTAatta tcatggcact gattgccttt 180
 ccgatgacgt attattctca cCGTgcatta tgccgctttg tattatccgg caagaaaggt 240
 ggCGaagata ttaccgaagt cgttgaagaa catttcggcg ttggtgcggg taaattaatc 300
 actttgcttt attttttcgc ttttatccg atcctattag tttatagcgt cgctatcacc 360
 aatacggtag atagctttat tactaccaaa ttgcatttac cttctccgcc gcgtgctgcg 420
 ctgtcattaa tattgatcct cgggttgatg tttattgtcc gtttcggtga agcgatgatc 480
 gttaaagcaa tgagtgttct ggtttaccct tttgttgccg tactgatgtt gctggcgctt 540
 Seite 55

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 aaccactcgc caatcatctc ctctttcgcc gttgccaaac gcaaagaata tggatgatgat 720
 gcagagaaga aatgctcacg cattctgtct tacagccaca ttatgatggg gttgacgggtg 780
 atgttcttcg ttttcagctg cgtactgagc ctttctccaa ccgagctgat ggaagcaaaa 840
 acacaaaaca tttctattct gtcctatctg gcgaaccatt ttaatagccc ggtaatcggc 900
 tatctggccc cagtaattgc aaccatcgcg atctctaaat ccttcctggg ccactatctg 960
 ggcgcgggtg aaggctttaa cggcatgatc gtgaaatccc tgcgcagcag agggaaaaacc 1020
 atctccagca ccaaactgaa ccgtatcact tcgctgttca tgttgatcac cacctggatt 1080
 gtcgcgacgc tgaacccaag cattctgggt atgatcgaaa ccttgggagg cccgattatc 1140
 gcgtgcctgc tgttcctgat gccgatgtac gccatccaga aagtcccagc gatgaaaaaa 1200
 tacagcggcc acattagcaa cgtctttgtc accctcatgg gactgatcgc tatttcggcc 1260
 attgtttaca gcctgcgcga tctgctgtaa 1290

<210> 72
 <211> 429
 <212> PRT
 <213> Erwinia carotovora

<400> 72

Met Ser Thr Ile Gln Asp Ser Ser His Val Leu Glu Gln Ala Ser Gly
 1 5 10 15

Trp Arg Lys Ser Asp Thr Val Trp Met Leu Gly Leu Tyr Gly Thr Ala
 20 25 30

Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Ile Gly Gly
 35 40 45

Leu Ile Pro Leu Ile Ile Met Ala Leu Ile Ala Phe Pro Met Thr Tyr
 50 55 60

Tyr Ser His Arg Ala Leu Cys Arg Phe Val Leu Ser Gly Lys Lys Gly
 65 70 75 80

Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Val Gly Ala
 85 90 95

Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile Leu
 100 105 110

Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Asp Ser Phe Ile Thr
 115 120 125

His Gln Leu His Leu Pro Ser Pro Pro Arg Ala Ala Leu Ser Leu Ile
 130 135 140

Leu Ile Leu Gly Leu Met Phe Ile Val Arg Phe Gly Glu Ala Met Ile
 145 150 155 160
 Val Lys Ala Met Ser Val Leu Val Tyr Pro Phe Val Ala Val Leu Met
 165 170 175
 Leu Leu Ala Leu Tyr Leu Ile Pro Asn Trp Asn Thr Ser Val Phe Glu
 180 185 190
 Asn Ile Ser Leu Ser Ser Ser Val Thr Gly Asn Gly Leu Leu Ala Thr
 195 200 205
 Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His Ser Pro
 210 215 220
 Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Lys Glu Tyr Gly Asp Asp
 225 230 235 240
 Ala Glu Lys Lys Cys Ser Arg Ile Leu Ser Tyr Ser His Ile Met Met
 245 250 255
 Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser Leu Ser
 260 265 270
 Pro Thr Glu Leu Met Glu Ala Lys Thr Gln Asn Ile Ser Ile Leu Ser
 275 280 285
 Tyr Leu Ala Asn His Phe Asn Ser Pro Val Ile Gly Tyr Leu Ala Pro
 290 295 300
 Val Ile Ala Thr Ile Ala Ile Ser Lys Ser Phe Leu Gly His Tyr Leu
 305 310 315 320
 Gly Ala Gly Glu Gly Phe Asn Gly Met Ile Val Lys Ser Leu Arg Ser
 325 330 335
 Arg Gly Lys Thr Ile Ser Ser Thr Lys Leu Asn Arg Ile Thr Ser Leu
 340 345 350
 Phe Met Leu Ile Thr Thr Trp Ile Val Ala Thr Leu Asn Pro Ser Ile
 355 360 365
 Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Cys Leu Leu
 370 375 380
 Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met Lys Lys
 385 390 395 400
 Tyr Ser Gly His Ile Ser Asn Val Phe Val Thr Leu Met Gly Leu Ile
 405 410 415

Ala Ile Ser Ala Ile Val Tyr Ser Leu Arg Asp Leu Leu
 420 425

<210> 73
 <211> 1299
 <212> DNA
 <213> Photorhabdus luminescens

<400> 73
 atggatatga ctcaaacagg tacgatcgca tcgcaggcga ccagcccaag cgattataaa 60
 acctggcgta aatcagatac agtatggatg cttggcttat acggtactgc gattgggtgcc 120
 ggtgtattat tcttaccat caatgctggg attgggtggcc tactacctct tttggtaatg 180
 gcgctactgg ctttcccaat gactttcttc gccaccgcg ggatgtgtcg tttcgttcta 240
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 gcaggtaaac ttattactct gctctacttc ttcgctatct acccgattct cttagtttac 360
 agcgttgcta ttaccaacac cgtagacagc tttattgttc accaattaca cctgccatca 420
 cctcctcgtg ctctgctggc tctgatccta attactgggtg taatgaccat catccgtttt 480
 ggtgaacagg ctattgttaa ggcaatgagc gtgctgggtat tcccatttgt tgccgttttg 540
 atgctactgg cgttttatct gatccctaac tggaataccg caatcttcga aaacatcagc 600
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 atggtgttct cttcaacca ctgcgaatt atctcggcat ttgcggtggc aaaacgtgga 720
 gaatatggtg agcatgctga gaaaaaatgc tcccgcattc tagcttacgc ccatatcatg 780
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 ctggcagaag ccaaagcaca aaatatttct attctgtctt acctggctaa ccactttaat 900
 acaccagtgg ttgcctacat cgctccgttt attgcattca tagcaattac caaatctttc 960
 cttggccatt atctgggtgc acgtgaaggt tttaatggta ttgtgggttaa gacattgcgt 1020
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 ggtggtccta ttatcgcaat gttgttggtc attatgcaa tgtatgcaat cagcaaagtt 1200
 cctgcaatgc gcaaatatag cggcaagctg agtaatctgt ttgtcgtctt tatgggatta 1260
 gttgctatct ctgctgtcct ctactcactg tttgcataa 1299

<210> 74
 <211> 432
 <212> PRT
 <213> Photorhabdus luminescens

<400> 74
 Met Asp Met Thr Gln Thr Gly Thr Ile Ala Ser Gln Ala Thr Ser Pro
 1 5 10 15

Ser Asp Tyr Lys Thr Trp Arg Lys Ser Asp Thr Val Trp Met Leu Gly
 20 25 30

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

Ala Tyr Ile Ala Pro Phe Ile Ala Phe Ile Ala Ile Thr Lys Ser Phe
305 310 315 320

Leu Gly His Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Ile Val Val
325 330 335

Lys Thr Leu Arg Asp Gln Gly Lys Thr Ile Glu Pro Lys Lys Leu Asn
340 345 350

Arg Ile Thr Thr Ile Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr
355 360 365

Leu Asn Pro Ser Ile Leu Glu Met Ile Glu Arg Leu Gly Gly Pro Ile
370 375 380

Ile Ala Met Leu Leu Phe Ile Met Pro Met Tyr Ala Ile Ser Lys Val
385 390 395 400

Pro Ala Met Arg Lys Tyr Ser Gly Lys Leu Ser Asn Leu Phe Val Val
405 410 415

Phe Met Gly Leu Val Ala Ile Ser Ala Val Leu Tyr Ser Leu Phe Ala
420 425 430

<210> 75
<211> 1299
<212> DNA
<213> Chromobacterium violaceum

<400> 75
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gacaccacct ggatgctcgg cctgtacggc accgccatcg gcgccggcgt cctgttcctc 120
ccgatcaacg ccggcatcgg cggcctgtgg ccgctgatgc tgatggccat cctggccctg 180
ccgctgacct tcttcgcca ccgcggcctg acccgcttcg tgctgtccgg cagcaaggaa 240
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accctgctgt acttcttcgc catctacccg atcctgctga tgtacagcgt ggccatcacc 360
aacacgggtg tgctcttcct gaacaaccag ctgcacatcg aagtgggcac cggcatcgcc 420
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ggccagatga tcgtcaaggc gatgagcatc ctggtgtacc cgttcgtggt ggtgctgatg 540
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ctgggcgacg cgctgtccag cggcgcttc tacaagacgc tgtggctggc catcccggtg 660
atggtgttct cgttcaacca ctcgccgatc atctcgtcct tctccgtcga ccagcgcaag 720
cttcacggcg atgacgccga gccggcctcc agccgcgtgc tgattcgcgc ccacaccatg 780
atggtgctga ccgtgatgtt cttcgtgttc agctgcgtgt tcagcctgag cccggccgac 840
ctggccgccg ccaaggccca gaacatctcc atcctgtcct acctggccaa ccacttccaa 900

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ctggggccact acctgggagc caaggaaggc ttcaacggcc tggatgatcaa gcagctgcgc 1020
cagaacggca agagcatcga atcgccaag ctggaccgct acaccgccat cttcatgatc 1080
gtcacctgct ggatcatcgc caccatcaac ccgtccatcc tgggcatgat cgaaaccctg 1140
ggcggccccg tgatcgcgat gctgctgttc ctgatgccga tgtacgcgat ccagaaagtg 1200
ccggcgatga agaagtactc cggcgccgcc agcaacatct tcgtgacgct gatcggcctg 1260
atcgccatct ccgccatctt ctacgatctg atcgccctga 1299

<210> 76

<211> 432

<212> PRT

<213> *Chromobacterium violaceum*

<400> 76

Met Ser Gln Ala Ile Ala Ser Thr Ala Ser Arg Ser Gly Ser Ser Gly
1 5 10 15

Trp Ser Lys His Asp Thr Thr Trp Met Leu Gly Leu Tyr Gly Thr Ala
20 25 30

Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Ile Gly Gly
35 40 45

Leu Trp Pro Leu Met Leu Met Ala Ile Leu Ala Leu Pro Leu Thr Phe
50 55 60

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

Gly Ala Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Leu Gly Ala
85 90 95

Gly Lys Ile Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile Leu
100 105 110

Leu Met Tyr Ser Val Ala Ile Thr Asn Thr Val Leu Ser Phe Leu Asn
115 120 125

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

Phe Ser Leu Ala Leu Ile Leu Gly Leu Met Ser Ile Val Arg Leu Gly
145 150 155 160

Gly Gln Met Ile Val Lys Ala Met Ser Ile Leu Val Tyr Pro Phe Val
165 170 175

Val Val Leu Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Ser Asp
180 185 190

Thr Ala Ile Arg His Ala Gly Ser Leu Gly Asp Ala Leu Ser Ser Gly
 195 200 205

Ala Phe Tyr Lys Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser
 210 215 220

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

Leu His Gly Asp Asp Ala Glu Pro Ala Ser Ser Arg Val Leu Ile Arg
 245 250 255

Ala His Thr Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys
 260 265 270

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

Ile Ser Ile Leu Ser Tyr Leu Ala Asn His Phe Gln Asn Pro Val Met
 290 295 300

Glu Trp Val Ala Pro Ile Ile Ala Met Val Ala Ile Ser Lys Ser Phe
 305 310 315 320

Leu Gly His Tyr Leu Gly Ala Lys Glu Gly Phe Asn Gly Leu Val Ile
 325 330 335

Lys Gln Leu Arg Gln Asn Gly Lys Ser Ile Glu Ser Ser Lys Leu Asp
 340 345 350

Arg Tyr Thr Ala Ile Phe Met Ile Val Thr Cys Trp Ile Ile Ala Thr
 355 360 365

Ile Asn Pro Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Val
 370 375 380

Ile Ala Met Leu Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val
 385 390 395 400

Pro Ala Met Lys Lys Tyr Ser Gly Ala Ala Ser Asn Ile Phe Val Thr
 405 410 415

Leu Ile Gly Leu Ile Ala Ile Ser Ala Ile Phe Tyr Asp Leu Ile Ala
 420 425 430

<210> 77
 <211> 1290
 <212> DNA
 <213> Photobacterium sp.

<400> 77
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agcaaaagtg atacattatg gatgcttggg ctatacggta cagccgtagg cgcaggtact 120
 ctatTTTTTtac caattaatgc ggggggttggg ggtttaattc cactacttgt aatggccggt 180
 ctcgcttttc caatgacatt ctttgcccac cgtgcaatga cacgttttgt attatcaagt 240
 tcgaatcctg gcgctgatat tacagaagtt gttgaagagc actttggtta gggcatgggt 300
 aaagtgatca cactacttta tttctttgct atctacccta tcctattagt ttacagtgtt 360
 gcactaacia atactgttga aagctttatg cttaaccagt taggtatcga accaccagca 420
 cgtgcaattt tagcgttagt attgatcctt ggtttaatgg caattgttcg tttaggtgag 480
 caattaattg ttaaagcgat gagtatcttg gtattcccat tcgttgctgt attattaatt 540
 cttgcactat ttcttgtacc gtactggaat gactctatct tccacaacgt tatgccagca 600
 gacggtggct taaactcagt gatgcttgca gtatggctaa ttttaccggt aatggttttc 660
 tcgtttaacc actcacctgt tatctcatca tttgctgttg ctaagcaaaa agaatacggc 720
 gtaaaccgag agcgtcaaag ttcacgtatt ctagcgcgtg ctcacattat gatggtatta 780
 accgtaatgt tcttcgtttt cagctgtgta ttaagcttat cacctgaaaa cttagcagaa 840
 gctaaagcga ataacgtatc tattctgact tacttagcga accacttcga tacaccgatc 900
 attgcttatg ttgcaccgat tgtagcgatt attgcaatta ctaagtcttt ccttggccac 960
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 aagaaatact caggcgcaat cagtaatgta tttgtgacgg ttatcggact tgtttctatc 1260
 tctgcaatct tctactcatt atttatgtaa 1290

<210> 78
 <211> 429
 <212> PRT
 <213> Photobacterium sp.

<400> 78

Met Gly Thr Glu Gln Asn Leu Thr Ala Thr Ala Ser Ala Gln Ser Lys
1 5 10 15

Lys Leu Gly Trp Ser Lys Ser Asp Thr Leu Trp Met Leu Gly Leu Tyr
20 25 30

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

Val Gly Gly Leu Ile Pro Leu Leu Val Met Ala Val Leu Ala Phe Pro
50 55 60

Met Thr Phe Phe Ala His Arg Ala Met Thr Arg Phe Val Leu Ser Ser
65 70 75 80

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Ser Asn Pro Gly Ala Asp Ile Thr Glu Val Val Glu Glu His Phe Gly
 85 90 95
 Lys Gly Met Gly Lys Val Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr
 100 105 110
 Pro Ile Leu Leu Val Tyr Ser Val Ala Leu Thr Asn Thr Val Glu Ser
 115 120 125
 Phe Met Leu Asn Gln Leu Gly Ile Glu Pro Pro Ala Arg Ala Ile Leu
 130 135 140
 Ala Leu Val Leu Ile Leu Gly Leu Met Ala Ile Val Arg Leu Gly Glu
 145 150 155 160
 Gln Leu Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Ala
 165 170 175
 Val Leu Leu Ile Leu Ala Leu Phe Leu Val Pro Tyr Trp Asn Asp Ser
 180 185 190
 Ile Phe His Asn Val Met Pro Ala Asp Gly Gly Leu Asn Ser Val Met
 195 200 205
 Leu Ala Val Trp Leu Ile Leu Pro Val Met Val Phe Ser Phe Asn His
 210 215 220
 Ser Pro Val Ile Ser Ser Phe Ala Val Ala Lys Gln Lys Glu Tyr Gly
 225 230 235 240
 Val Asn Ala Glu Arg Gln Ser Ser Arg Ile Leu Ala Arg Ala His Ile
 245 250 255
 Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser
 260 265 270
 Leu Ser Pro Glu Asn Leu Ala Glu Ala Lys Ala Asn Asn Val Ser Ile
 275 280 285
 Leu Thr Tyr Leu Ala Asn His Phe Asp Thr Pro Ile Ile Ala Tyr Val
 290 295 300
 Ala Pro Ile Val Ala Ile Ile Ala Ile Thr Lys Ser Phe Leu Gly His
 305 310 315 320
 Tyr Leu Gly Ala Ser Glu Gly Leu Asn Gly Leu Val Ile Lys Val Thr
 325 330 335
 Arg Asp Lys Asn Lys Glu Ile Ser Ser Lys Ala Leu Asn Arg Phe Thr
 340 345 350

Ala Ile Phe Met Leu Val Thr Thr Trp Ala Val Ala Thr Leu Asn Pro
 355 360 365

Ser Ile Leu Gly Met Ile Glu Ser Leu Gly Gly Pro Ile Ile Ala Met
 370 375 380

Leu Leu Phe Ile Met Pro Met Tyr Ala Ile Lys Lys Val Pro Ala Met
 385 390 395 400

Lys Lys Tyr Ser Gly Ala Ile Ser Asn Val Phe Val Thr Val Ile Gly
 405 410 415

Leu Val Ser Ile Ser Ala Ile Phe Tyr Ser Leu Phe Met
 420 425

<210> 79

<211> 1302

<212> DNA

<213> Pseudomonas fluorescens

<400> 79

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 accgccattg gcgccggcac cctgttcctg ccgatcaacg ccggtgtcgg cggcttctgg 180
 ccgttgctga tcctggcggt gctggctttc ccgatgacct tcttcgcgca ccgtggcctc 240
 acccgcttcg tgctctcggg ccgctccggt gacatcaccc aagtgggtgga ggaacacttc 300
 ggcatcggcg ccggcaaact gattacgctg ctgtatttct tcgcaatctt cccgatcctg 360
 ctggtgtaca gcgtggcgct gaccaacact ctcggcagct tcctcgaaca ccagttgcac 420
 atgccccgc caccgcgcgc ggtgctgtcg ctggcgctga tcctcgggtct gatggccatc 480
 gtccgttgcg gtcagaacgt gatcgtcaaa gccatgagtg tgctgggtgta tccgttcgtc 540
 gccgcgttgc tgttgctcgg catcagcctg attccgaact ggaacggcgc attcttcgcc 600
 agcgtcaag aaccgatgga aatgtcggtg ttcctcaaga ccctgtggct ggcgatcccg 660
 gtgatgggtg tctcgttcaa ccattcacc atcatctctg cgttcgccgt cgagcagaaa 720
 cagcgctacg gcgagcaggc cgaacgcaag agcagcggca tcctcgccat ggcccacggc 780
 atgatggtcg tcacggtgat gttcttctgc ttcagctgcg tgctggcgct gtcgccgacg 840
 gatctggcag cggccaaggc gcagaacatc tcgatcctgt cgtatctggc caaccacttc 900
 cagaccccg tcatcgctta cgccgcgcca ttgattgcgc tgggtggcgat caccaaatcc 960
 ttcctcggcc actacatcgg cgccagcgaa ggcttcagg gcatgatcgt caaaagcctg 1020
 cgcagccgtg gccgggtgat gtcggcgagc tggctgaacc gtgcgaccgc gctgttcatg 1080
 atcctcagct gctgggccgt ggcgacctc aaccgagca tcctcggcat gatcgaaacc 1140
 ctcggcgggc cggtgattgc ctgcctgctg ttcctgatgc cgatgtacgc gatccgccgc 1200
 gtgccagcct tgcgccagta ttcgggccag gtgtcgaacg tgttcgtggt gctgatcggc 1260
 ctgattgcac tgcagcgat catctactcg gttctgcct ga 1302

<210> 80
 <211> 433
 <212> PRT
 <213> Pseudomonas fluorescens

<400> 80

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

Gln Arg Tyr Gly Glu Gln Ala Glu Arg Lys Ser Ser Gly Ile Leu Ala
 245 250 255

Met Ala His Gly Met Met Val Val Thr Val Met Phe Phe Cys Phe Ser
 260 265 270

Cys Val Leu Ala Leu Ser Pro Thr Asp Leu Ala Ala Ala Lys Ala Gln
 275 280 285

Asn Ile Ser Ile Leu Ser Tyr Leu Ala Asn His Phe Gln Thr Pro Val
 290 295 300

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

Phe Leu Gly His Tyr Ile Gly Ala Ser Glu Gly Phe Gln Gly Met Ile
 325 330 335

Val Lys Ser Leu Arg Ser Arg Gly Arg Val Met Ser Ala Ser Trp Leu
 340 345 350

Asn Arg Ala Thr Ala Leu Phe Met Ile Leu Ser Cys Trp Ala Val Ala
 355 360 365

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

Val Ile Ala Cys Leu Leu Phe Leu Met Pro Met Tyr Ala Ile Arg Arg
 385 390 395 400

Val Pro Ala Leu Arg Gln Tyr Ser Gly Gln Val Ser Asn Val Phe Val
 405 410 415

Val Leu Ile Gly Leu Ile Ala Leu Ser Ala Ile Ile Tyr Ser Val Leu
 420 425 430

Pro

<210> 81

<211> 1257

<212> DNA

<213> *Vibrio parahaemolyticus*

<400> 81

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aaacatgaca cacattgggt acttagccta ttcgggaccg ccgttggtgc cggatatttg 120

tttctgcaa tcaacttggg cattggtgga ttttgccac tagtcgcaat ggcgttttg 180

gcatttcaa tgacttacct cgcccatcgc ggtttagcgc gctttgtatt gtcttctaag 240

atcaaaaatg ccgactttac cgatgtgggt gaagaacact ttggcgcaaa agcgggacgt 300

tcaatctctc tgctttattt cctatcgatt tttcctatcc tgtaattta cggcgtgggc 360

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atcaccaata ctgtagacag ctttatggtg aaccaagcgg gaatggaagc cttaccacgc 420
gagctacttt cgggcgtatt agtggttcgct ttgattgccca ttatgatggc gggcgaaaaa 480
gtgatgctgc gcgcgtttgc cgttatggtg taccacttg ttgcgattct agctttcctc 540
tcattctact taatgccgaa ctggacaatg cccgtgcttg atacaccgga catgggtgcg 600
tttgcgagca caatgtgggt agccgttcct gttgtgattt tctcgtttag ccatgcagca 660
gcgatctcta gctttgccaa tgttcagcgc cgacactacg gcgatgatgc cgatgcaaaa 720
gccgaactga ttttacgttg cacgagcatc atgcttatcg cattcgtact attgtttggtt 780
ttctcgtcgc tattagcact ttgccagag caacttgcac aggcaaaagc gcaaaacgta 840
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agcttgaacg gcttaatcac aaagcactca aatttgtctg aaacacgtgt tgatcgtatt 1020
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ttggcggtagc ataagattga gtcgatgaag cagtatcgtg gaaagctctc tacctatatt 1200
gttctgatca caggtattgt tgcggtaagt gctttggttt ttagcttact cagctaa 1257

<210> 82
<211> 418
<212> PRT
<213> *Vibrio parahaemolyticus*

<400> 82

Met Lys Glu Ser Arg Asn Thr Leu Asn Ser Ser Glu Leu Asn Thr Thr
1 5 10 15

Thr Ser Trp Ser Lys His Asp Thr His Trp Val Leu Ser Leu Phe Gly
20 25 30

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

Gly Gly Phe Trp Pro Leu Val Ala Met Ala Phe Leu Ala Phe Pro Met
50 55 60

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

Ile Lys Asn Ala Asp Phe Thr Asp Val Val Glu Glu His Phe Gly Ala
85 90 95

Lys Ala Gly Arg Ser Ile Ser Leu Leu Tyr Phe Leu Ser Ile Phe Pro
100 105 110

Ile Leu Leu Ile Tyr Gly Val Gly Ile Thr Asn Thr Val Asp Ser Phe
115 120 125

Met Val Asn Gln Ala Gly Met Glu Ala Leu Pro Arg Glu Leu Leu Ser
 130 135 140
 Gly Val Leu Val Phe Ala Leu Ile Ala Ile Met Met Ala Gly Glu Lys
 145 150 155 160
 Val Met Leu Arg Ala Phe Ala Val Met Val Tyr Pro Leu Val Ala Ile
 165 170 175
 Leu Ala Phe Leu Ser Phe Tyr Leu Met Pro Asn Trp Thr Met Pro Val
 180 185 190
 Leu Asp Thr Pro Asp Met Gly Ala Phe Ala Ser Thr Met Trp Leu Ala
 195 200 205
 Val Pro Val Val Ile Phe Ser Phe Ser His Ala Ala Ala Ile Ser Ser
 210 215 220
 Phe Ala Asn Val Gln Arg Arg His Tyr Gly Asp Asp Ala Asp Ala Lys
 225 230 235 240
 Ala Glu Leu Ile Leu Arg Cys Thr Ser Ile Met Leu Ile Ala Phe Val
 245 250 255
 Leu Leu Phe Val Phe Ser Cys Val Leu Ala Leu Ser Pro Glu Gln Leu
 260 265 270
 Ala Gln Ala Lys Ala Gln Asn Val Ser Val Leu Ser Tyr Leu Ala Asn
 275 280 285
 Ala Thr Asp Asn Pro Phe Ile Ala Thr Leu Gly Pro Leu Val Ala Phe
 290 295 300
 Val Ala Ile Thr Ser Ser Phe Leu Gly His Phe Leu Gly Ala Arg Glu
 305 310 315 320
 Ser Leu Asn Gly Leu Ile Thr Lys His Ser Asn Leu Ser Glu Thr Arg
 325 330 335
 Val Asp Arg Ile Ser Val Val Val Leu Phe Leu Ser Ile Trp Ala Ala
 340 345 350
 Ala Ile Met Asn Pro Ser Ile Leu Gly Met Met Glu Ala Leu Ser Gly
 355 360 365
 Pro Val Ile Ala Met Ile Leu Phe Ile Met Pro Met Leu Ala Val His
 370 375 380
 Lys Ile Glu Ser Met Lys Gln Tyr Arg Gly Lys Leu Ser Thr Tyr Phe
 385 390 395 400

Val Leu Ile Thr Gly Ile Val Ala Val Ser Ala Leu Val Phe Ser Leu
 405 410 415

Leu Ser

<210> 83
 <211> 1425
 <212> DNA
 <213> *Shigella flexneri*

<400> 83
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 ccgctctctg caacggcggc tgagacttct tcagcaacga cagcccagca gatgccaagc 120
 cttgcaccga tgctcgaaaa ggtgatgcct tcagtgggtca gcattaacgt agaaggtagc 180
 acaaccgtta atacgccgcg tatgccgcgt aatttccagc agttcttcgg tgatgattct 240
 ccgttctgcc aggaagggtc tccgttccag agctctccgt tctgccaggg gggccagggc 300
 ggtaatggcg gcggccagca acagaaattc atggcgctgg gttccggcgt catcattgat 360
 gccgataaag gctatgtcgt caccaacaac cacgttggtg ataacgcgac ggtgattaaa 420
 gtccagctga gcgatggtcg taagtctgac gcgaagatgg ttggcaaaga tccgcgctct 480
 gatatcgcgc tgatccaaat ccagaacccg aaaaaactga ccgcaattaa gatggcggat 540
 tctgatgcac tgcgcgtggg tgattacacc gtagcgattg gtaaccggtt tgggtctgggc 600
 gagacggtaa cttccgggat tgtctctgcg ctggggcgta gcggcctgaa tgctgaaaac 660
 tacgaaaact tcatccagac cgatgcagcg atcaaccgtg gtaactccgg tgggtgcgctg 720
 gttaacctga acggcgaact gatcggtatc aacaccgcga tcctcgcacc ggacggcggc 780
 aacatcggtg tcggttttgc tatcccagat aacatggtga aaaacctgac ctcgcagatg 840
 gtggaatacg gccagggtgaa acgcggtgag ctgggtatta tggggactga gctgaattcc 900
 gaactggcga aagcgatgaa agttgacgcc cagcgcggtg ctttcgtaag ccaggttctg 960
 cctaattcct ccgctgcaaa agcggggcatt aaagcgggtg atgtgatcac ctactgaac 1020
 ggtaagccga tcagcagctt tgccgcactg cgtgctcagg tgggtactat gccggtgggc 1080
 agcaaaactga ccctgggctt actgcgcgac ggtaagcagg ttaacgtgaa cctggaactg 1140
 cagcagagca gccagaatca ggttgattcc agctccatct tcaacggcat tgaaggcgct 1200
 gagatgagca acaaaggcaa agatcagggc gtggtagtga acaacgtgaa gacgggcact 1260
 ccggctgcgc agatcggcct gaagaaagggt gatgtgatta ttggtgcgaa ccagcaggca 1320
 gtgaaaaaca tcgctgaact gcgtaaagtt ctcgacagca aaccgtctgt gctggcactg 1380
 aacattcagc gcggcgacag caccatctac ctgttaatgc agtaa 1425

<210> 84
 <211> 474
 <212> PRT
 <213> *Shigella flexneri*

<400> 84

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

Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
 275 280 285

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
 290 295 300

Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
 305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
 325 330 335

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

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
 355 360 365

Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
 370 375 380

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
 385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
 405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
 420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
 435 440 445

Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
 450 455 460

Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
 465 470

<210> 85
 <211> 1425
 <212> DNA
 <213> Escherichia coli

<400> 85
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 ccgctctctg caacggcggc tgagacttct tcagcaacga cagcccagca gatgccaagc 120
 cttgcaccga tgctcgaaaa ggtgatgcct tcagtgggtca gcattaacgt agaaggtagc 180
 acaaccgtta atacgccgcg tatgccgcgt aatttccagc agttcttcgg tgatgattct 240
 ccgttctgcc aggagggttc tccgttccag agctctccgt tctgccaggg gggcctgggc 300

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ggtaatggcg gcggccagca acagaaattc atggcgctgg gttccggcgt tatcattgat 360
 gccgataaag gctatgtcgt caccaacaac cacgttggtg ataacgcgac ggtgattaaa 420
 gtccaactga gcgatggtcg taagttcgac gcgaagatgg ttggcaaaga tccgcgctct 480
 gatatcgcgc tgatccagat ccagaacccg aaaaacctga ccgcaattaa gatggcggat 540
 tctgatgcgc tgcgcgtggg tgattacacc gtagcaattg gtaaccggtt cggcctgggc 600
 gagacagtaa cttccgggat tgtctctgcg ctgggacgta gcggcctgaa cgctgaaaac 660
 tacgaaaact tcatccagac cgatgcagcg atcaaccggg gtaactcagg tgggtgcgttg 720
 gttaacctga acggcgaact gatcggtatc aacaccgcga tcctcgcacc ggacggcgga 780
 aacatcggtg tcggttttgc tatcccagac aacatgggtg aaaacctgac ctcgcagatg 840
 gtggaatacg gccaggtgaa acgtggtgag ttgggtatta tgggcactga gctgaactcc 900
 gatctggcga aagcgatgaa agttgacgcc cagcgcggtg ctttcgtaag ccaggttctg 960
 ccgaattctt ccgccgcgaa agcgggcatt aaagcgggtg atgtgatcac ctcactgaac 1020
 ggtaagccaa tcagcagctt tgccgcactg cgtgctcagg tgggcactat gccggtaggt 1080
 agcaaaactga ccctgggctt actgcgcgac gggaagcagg ttaacgtgaa cctggaactt 1140
 cagcagagca gccagaatca ggttgattcc agcaccatct tcaacggcat tgaaggcgct 1200
 gagatgagca acaaaggtaa agatcagggc gtggtggtga acaacgtgaa aacgggcact 1260
 ccggctgcg cagatcggcct gaagaaaggt gatgtgatta ttggcgcgaa ccagcaggca 1320
 gtgaaaaaca tcgctgaact gcgtaaagtt ctcgacagca aaccgtctgt gctggcactg 1380
 aacattcagc gcggcgacag caccatctac ctgttaatgc agtaa 1425

<210> 86
 <211> 474
 <212> PRT
 <213> Escherichia coli
 <400> 86

Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
 1 5 10 15

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
 20 25 30

Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
 35 40 45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
 50 55 60

Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
 65 70 75 80

Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
 85 90 95

Gly Gly Leu Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
 100 105 110
 Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
 115 120 125
 Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser
 130 135 140
 Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
 145 150 155 160
 Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
 165 170 175
 Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
 180 185 190
 Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
 195 200 205
 Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
 210 215 220
 Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu
 225 230 235 240
 Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
 245 250 255
 Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
 260 265 270
 Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
 275 280 285
 Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Asp Leu Ala Lys
 290 295 300
 Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
 305 310 315 320
 Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
 325 330 335
 Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
 340 345 350
 Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
 355 360 365

Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
 370 375 380

Gln Asn Gln Val Asp Ser Ser Thr Ile Phe Asn Gly Ile Glu Gly Ala
 385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
 405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
 420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
 435 440 445

Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
 450 455 460

Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
 465 470

<210> 87
 <211> 1476
 <212> DNA
 <213> Shigella sonnei

<400> 87
 atgaaaaaaa ccacattagc actgagtcga ctggctctga gtttaggttt ggcgttatct 60
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 cttgcaccga tgctcgaaaa ggtgatgcct tcagtgggtca gcattaacgt agaaggtagc 180
 acaaccgtta atacgccgcg tatgccgctg aatttccagc agttcttcgg tgatgattct 240
 ccgttctgcc aggaagggtc accgtttcag agctctccgt tctgccaggg gggccagggc 300
 ggtaatggcg gcggccagca acagaaattc atggcgctgg gttccggcgt catcattgat 360
 gccgataaag gctatgtcgt caccaacaac catgttggtg ataacgagc ggtgattaaa 420
 gtccagctga gcgatggccg taagtctgac gcgaagatgg ttggcaaaga tccgcgctct 480
 gatatcgcg tgatccaaat ccagaacctg aaaaacctga ccgcaattaa gatggcggat 540
 tctgatgcac tgcgctgggg tgattacacc gtagcgattg gtaacctgtt tgggtctgggc 600
 gagacggtaa cttccgggat tgtctctgcg ctggggcgta gcggcctgaa tgccgaaaac 660
 tacgaaaact tcatccagac cgatgcagcg atcaaccgtg gtaactccgg tgggtgcgctg 720
 gttaacctga acggcgaact gatcggatat aacaccgca tcctcgacc ggacggcggc 780
 aacatcggtg tcggttttgc tatcccagat aacatgggtg taaacctgac ctcgcagatg 840
 gtggaatacg gccaggtgaa acgcggtgag ctggggatta tggggactga gctgatctcc 900
 gaactggcca aagcgatgaa agttgacgcc cagcgcggtg ctttcgtaag ccaggttctg 960
 cctaattcct ctgctgcaaa agcgggcatt aaagcgggtg atgtgatcac ctactgaac 1020
 ggtaagccga tcagcagctt tgccgcactg cgtgctcagg tgggtactat gccggtgggc 1080

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cagcagagca gccagaatca ggttgattcc agctccatct tcaacggcat tgaaggcgct 1200
gagatgatca acaaaggcag agatcagggc gtggtagtga acaacgtgaa aacgggcact 1260
ccgcgtgcmc agatcggcct gaagaaaggt gatgtgatta ttggcgcgaa ccagcaggca 1320
gtgaaaaaca tcgctgaact gcgtaaagtg ctcgacagca aaccgtctgt gctggcactc 1380
aacattcagc gcggcgaccg ccattctacct gttaatgcag taatctccct caacccttc 1440
ctgaaaacgg gaaggggttc tccttacaat ctgtga 1476

<210> 88
<211> 491
<212> PRT
<213> Shigella sonnei
<400> 88

Met Lys Lys Thr Thr Leu Ala Leu Ser Arg Leu Ala Leu Ser Leu Gly
1 5 10 15

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
20 25 30

Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
35 40 45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
50 55 60

Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
65 70 75 80

Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
85 90 95

Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
100 105 110

Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
115 120 125

Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser
130 135 140

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

Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
165 170 175

Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
180 185 190

Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
 195 200 205
 Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
 210 215 220
 Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu
 225 230 235 240
 Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
 245 250 255
 Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
 260 265 270
 Val Ile Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
 275 280 285
 Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Ile Ser Glu Leu Ala Lys
 290 295 300
 Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
 305 310 315 320
 Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
 325 330 335
 Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
 340 345 350
 Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
 355 360 365
 Arg Asp Gly Lys Gln Val Asn Val Asn Leu Glu Leu Gln Gln Ser Ser
 370 375 380
 Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
 385 390 395 400
 Glu Met Ile Asn Lys Gly Arg Asp Gln Gly Val Val Val Asn Asn Val
 405 410 415
 Lys Thr Gly Thr Pro Arg Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
 420 425 430
 Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
 435 440 445
 Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
 450 455 460

Gly Asp Arg His Leu Pro Val Asn Ala Val Ile Ser Leu Asn Pro Phe
 465 470 475 480

Leu Lys Thr Gly Arg Gly Ser Pro Tyr Asn Leu
 485 490

<210> 89
 <211> 1428
 <212> DNA
 <213> *Salmonella typhimurium*

<400> 89
 atgaaaaaaa ccacattagc aatgagtgc ctggctctga gtttaggttt ggcattgtcg 60
 cctctgtctg ccacggcggc tgaaacgtcc tcttcagcaa tgactgcca gcagatgcca 120
 agcctggcac cgatgctcga aaaagtgatg ccatcggtagg tcagtattaa tgttgaaggc 180
 agcaccacgg tgaatacgcc gcgtatgccg cgtaatttcc agcagttctt tggcgatgac 240
 tccccgttct gccaggacgg ttctccgttc cagaattctc cgttctgcca gggcggcggc 300
 aacggcggca acggcggcga acaacagaaa ttcattggcg tgggctccgg cgtaattatt 360
 gacgccgca agggctacgt cgtcaccaac aaccacgtgg ttgataacgc cagcgtgatt 420
 aaagtacagc ttagcgatgg gcgtaaattc gatgctaaag tgggtgggca agatccgcgt 480
 tctgatatcg cgctgattca aattcagaat ccgaagaacc tgacggcgat taagctggcg 540
 gactccgacg cgctgcgcgt gggggattat accgtcgcta ttggtaacct gtttggctctg 600
 ggcgaaacgg tgacgtcagg tatcgtttcg gcgctggggc gtagcggcct gaacgtagaa 660
 aattacgaga actttattca gaccgacgcc gcgattaacc gtggtaactc cggcggcgcg 720
 ctggtgaacc tgaacggtga gctgatcggc attaacaccg cgattctggc gccggacggc 780
 ggcaacatcg gtatcggcct cgctatcccc agtaacatgg tgaacaaacct gacgtcgtag 840
 atggtggaat acggccaggc gaaacgcggc gaactgggga tcatggggac tgagctgaat 900
 tccgaattgg cgaaagcgat gaaagtcgac gccagcggc gcgcgttcgt cagccaggcg 960
 atgccgaatt cgtccgcgcc gaaagcgggt atcaaagccg gggatgtcat tacctcgctg 1020
 aacggtaaac cgatcagcag ctttgcggcg ctgcgcgctc aggtcggcac tatgccggtc 1080
 ggcagcaaaa tcagcctcgg tctgctgcgt gaaggtaaag cgattacggc gaatctggaa 1140
 ctgcagcaga gcagccagag tcaggttgat tccagcacca tcttcagcgg gattgaaggc 1200
 gctgaaatga gcaataaagg ccaggataaa ggcgttgtgg tgagcagcgt gaaagcgaac 1260
 tcacccgccg cgcaaattgg cctcaaaaaa ggcgatgtga ttatcggcgc taaccagcag 1320
 ccggtgaaaa atatcgccga gctgcgtaag attctcgaca gcaagccgct gggtctggcg 1380
 ctgaatattc agcgtggtga tagttctatt tatttgctga tgcagtaa 1428

<210> 90
 <211> 475
 <212> PRT
 <213> *Salmonella typhimurium*

<400> 90

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

Met Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys
 275 280 285

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

Lys Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val
 305 310 315 320

Met Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val
 325 330 335

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

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

Leu Arg Glu Gly Lys Ala Ile Thr Val Asn Leu Glu Leu Gln Gln Ser
 370 375 380

Ser Gln Ser Gln Val Asp Ser Ser Thr Ile Phe Ser Gly Ile Glu Gly
 385 390 395 400

Ala Glu Met Ser Asn Lys Gly Gln Asp Lys Gly Val Val Val Ser Ser
 405 410 415

Val Lys Ala Asn Ser Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp
 420 425 430

Val Ile Ile Gly Ala Asn Gln Gln Pro Val Lys Asn Ile Ala Glu Leu
 435 440 445

Arg Lys Ile Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln
 450 455 460

Arg Gly Asp Ser Ser Ile Tyr Leu Leu Met Gln
 465 470 475

<210> 91
 <211> 1428
 <212> DNA
 <213> Salmonella enterica

<400> 91
 atgaaaaaaa ccacattagc aatgagtgca ctggctctga gtttaggttt ggcattgtcg 60
 cctctgtctg ccacggcggc tgaacgtcc tcttcagcaa tgactgccca gcagatgcc 120
 agcctggcac cgatgctcga aaaagtgatg ccatcggtgg tcagtattaa tgtagaagg 180
 agcaccacgg tgaatacgcc gcgtatgccg cgtaatttcc agcaattctt tggcgatgac 240
 tccccgttct gccaggacgg ttctccgttc cagaattctc cgttctgcca gggcggcgg 300

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aacggcggca acggcgggtca acaacagaaa ttcatggcgc tgggctccgg cgtaattatt 360
 gacgccgcga agggctacgt cgtcaccaac aaccacgtgg ttgataacgc cagcgtgatt 420
 aaagtacagc ttagcgatgg gcgtaaattc gatgctaaag tgggtgggcaa agatccgcgt 480
 tctgatatcg cgctgattca aattcagaat ccgaagaacc tgacggcgat taagctggcg 540
 gactccgacg cgctgcgcgt gggggattat accgtcgcta ttggtaaccc gtttgggtctg 600
 ggcgaaacgg tgacgtcagg tatcgtttcg gcgctggggc gtagcggcct gaacgtagaa 660
 aattacgaga actttattca gaccgacgcc gcgattaacc gcggtaactc cggcggcgcg 720
 ctggtgaacc tgaacggtga gctgatcggg attaacaccg cgattctggc gccggacggc 780
 ggcaacatcg gtatcggcctt cgctatcccc agtaacatgg tgaaaaacct gacgtcgcag 840
 atggtggaat acggccaggt gaaacgcggc gaactgggga tcatggggac tgagctgagc 900
 tctgagctgg cgaaagcgat gaaagtcgac gccagcgtg gcgcgttcgt cagccaggtg 960
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 aacggtaaac cgatcagcag ctttgcggcg ctgcgcgctc aggtcggcac tatgccggtc 1080
 ggagcaaaa tcagcctcgg tctgctgcgt gaaggtaaag cgattacggt taatctggaa 1140
 ctgcagcaga gcagccagag tcaggttgat tccagcacca tcttcagcgg gattgagggc 1200
 gctgaaatga gtaataaagg ccagataaaa ggcgttgttg tgagcagcgt gaaagcgaac 1260
 tcacccgccg cgcaaattgg cctcaaaaaa ggcgatgtga ttatcggcgc taaccagcag 1320
 ccggtgaaaa atatcgccga gctgcgtaag attctcgaca gcaagccgtc ggtgctggcg 1380
 ctgaatattc agcgtggtga tagttctatt tatttgctga tgcagtaa 1428

<210> 92
 <211> 475
 <212> PRT
 <213> *Salmonella enterica*

<400> 92

Met Lys Lys Thr Thr Leu Ala Met Ser Ala Leu Ala Leu Ser Leu Gly
1 5 10 15

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ser
20 25 30

Ala Met Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys
35 40 45

Val Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val
50 55 60

Asn Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp
65 70 75 80

Ser Pro Phe Cys Gln Asp Gly Ser Pro Phe Gln Asn Ser Pro Phe Cys
85 90 95

Gln Gly Gly Gly Asn Gly Gly Asn Gly Gly Gln Gln Gln Lys Phe Met
 100 105 110
 Ala Leu Gly Ser Gly Val Ile Ile Asp Ala Ala Lys Gly Tyr Val Val
 115 120 125
 Thr Asn Asn His Val Val Asp Asn Ala Ser Val Ile Lys Val Gln Leu
 130 135 140
 Ser Asp Gly Arg Lys Phe Asp Ala Lys Val Val Gly Lys Asp Pro Arg
 145 150 155 160
 Ser Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala
 165 170 175
 Ile Lys Leu Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val
 180 185 190
 Ala Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile
 195 200 205
 Val Ser Ala Leu Gly Arg Ser Gly Leu Asn Val Glu Asn Tyr Glu Asn
 210 215 220
 Phe Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Ala
 225 230 235 240
 Leu Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu
 245 250 255
 Ala Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn
 260 265 270
 Met Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys
 275 280 285
 Arg Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Ser Ser Glu Leu Ala
 290 295 300
 Lys Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val
 305 310 315 320
 Met Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val
 325 330 335
 Ile Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg
 340 345 350
 Ala Gln Val Gly Thr Met Pro Val Gly Ser Lys Ile Ser Leu Gly Leu
 355 360 365

Leu Arg Glu Gly Lys Ala Ile Thr Val Asn Leu Glu Leu Gln Gln Ser
 370 375 380

Ser Gln Ser Gln Val Asp Ser Ser Thr Ile Phe Ser Gly Ile Glu Gly
 385 390 395 400

Ala Glu Met Ser Asn Lys Gly Gln Asp Lys Gly Val Val Val Ser Ser
 405 410 415

Val Lys Ala Asn Ser Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp
 420 425 430

Val Ile Ile Gly Ala Asn Gln Gln Pro Val Lys Asn Ile Ala Glu Leu
 435 440 445

Arg Lys Ile Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln
 450 455 460

Arg Gly Asp Ser Ser Ile Tyr Leu Leu Met Gln
 465 470 475

<210> 93
 <211> 1434
 <212> DNA
 <213> *Klebsiella pneumoniae*

<400> 93
 atgaaaaaaa ccacgtagc aatgagtgc ctggctctga gtttaggtct ggcgttgctc 60
 ccgctctctg cgagcgcggc agaaacggca tcttcggcca ctaatgcaca gcagatgcc 120
 agcctggccc cgatgctgga gaaggtgatg ccgtcggtag tgagcattaa cgttgaaggt 180
 agcaccaccg ttaatacccc acggatgcc cgttaacttc agcagttctt tggcgataat 240
 tcgccgttct gccaggatgg ttctcctttc cagagttcgc cgttttgcc gggcggcgga 300
 cagggcggtc agcctgacgg cggccagcaa cagaaattta tggcgctggg ctccggcgctc 360
 atcattgatg ccgccaaagg gtatgtggtg accaacaacc acgtcgttga caacgccacc 420
 acgattaagg ttcagctgag cgatggccgt aggtttgatg ccaaagtcgt cggcaaagat 480
 ccgcgctctg atatcgcgct gattcagatt caggatccaa aaaacctgac ggcgattaag 540
 cttgccgact ccgatgcgct gcggtcgggt gattacaccg tggctatcgg caaccgttc 600
 ggtctgggcg aaaccgtgac ctccgggatt gtctccgcgc tgggccgtag cggcctcaac 660
 gtggaaaact acgaaaactt tatccagacc gatgcggcga ttaaccgcgg gaactccggc 720
 ggtgcgctgg tgaacctcaa cggcgagctg atcggatatc acaccgccat tctggcgccg 780
 gacggcggca acatcggtat cggttttgct atcccagca acatggtgaa aaacctgacc 840
 gagcagatgg tgaatatgg ccaggtgaaa cgcggtgagc tcggcattat gggcaccgaa 900
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 caggtaatgc caggttcggc ggccgcgaaa gcgggcatta aagccggcga tgtcatcacg 1020
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 gaaggggcag aaatgagcaa taagggtcag gataagggcg tgggtggtcaa taatgtgaaa 1260
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 cagcagccgg tgaaaaacat cgccgatctg tggaaaatct tcgacgcaa accgtccgta 1380
 ctggcgctga acattcagcg cggcgacgcc tctatctatc tgctgttgca gtaa 1434

<210> 94
 <211> 477
 <212> PRT
 <213> Klebsiella pneumoniae

<400> 94

Met Lys Lys Thr Thr Leu Ala Met Ser Ala Leu Ala Leu Ser Leu Gly
 1 5 10 15

Leu Ala Leu Ser Pro Leu Ser Ala Ser Ala Ala Glu Thr Ala Ser Ser
 20 25 30

Ala Thr Asn Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys
 35 40 45

Val Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val
 50 55 60

Asn Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asn
 65 70 75 80

Ser Pro Phe Cys Gln Asp Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys
 85 90 95

Gln Gly Gly Gly Gln Gly Gly Gln Pro Asp Gly Gly Gln Gln Gln Lys
 100 105 110

Phe Met Ala Leu Gly Ser Gly Val Ile Ile Asp Ala Ala Lys Gly Tyr
 115 120 125

Val Val Thr Asn Asn His Val Val Asp Asn Ala Thr Thr Ile Lys Val
 130 135 140

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

Pro Arg Ser Asp Ile Ala Leu Ile Gln Ile Gln Asp Pro Lys Asn Leu
 165 170 175

Thr Ala Ile Lys Leu Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr
 180 185 190

Thr Val Ala Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser
 195 200 205
 Gly Ile Val Ser Ala Leu Gly Arg Ser Gly Leu Asn Val Glu Asn Tyr
 210 215 220
 Glu Asn Phe Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly
 225 230 235 240
 Gly Ala Leu Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala
 245 250 255
 Ile Leu Ala Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro
 260 265 270
 Ser Asn Met Val Lys Asn Leu Thr Glu Gln Met Val Lys Tyr Gly Gln
 275 280 285
 Val Lys Arg Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu
 290 295 300
 Leu Ala Lys Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser
 305 310 315 320
 Gln Val Met Pro Gly Ser Ala Ala Ala Lys Ala Gly Ile Lys Ala Gly
 325 330 335
 Asp Val Ile Thr Ser Leu Asn Gly Lys Ala Ile Ser Ser Phe Ala Ala
 340 345 350
 Leu Arg Ala Gln Val Gly Thr Met Pro Ile Gly Ser Lys Val Glu Leu
 355 360 365
 Gly Leu Leu Arg Asp Gly Lys Pro Val Thr Val Thr Val Glu Leu Gln
 370 375 380
 Gln Ser Asn Gln Thr Gln Val Asp Ser Ser Thr Ile Phe Asn Gly Ile
 385 390 395 400
 Glu Gly Ala Glu Met Ser Asn Lys Gly Gln Asp Lys Gly Val Val Val
 405 410 415
 Asn Asn Val Lys Ala Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys
 420 425 430
 Gly Asp Val Ile Ile Gly Ala Asn Gln Gln Pro Val Lys Asn Ile Ala
 435 440 445
 Asp Leu Trp Lys Ile Phe Asp Ala Lys Pro Ser Val Leu Ala Leu Asn
 450 455 460
 Ile Gln Arg Gly Asp Ala Ser Ile Tyr Leu Leu Leu Gln

465

470

475

<210> 95
 <211> 1416
 <212> DNA
 <213> Edwardsiella tarda

<400> 95
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 ccgatgtcgg ccagcgcggc agagacctct tccgccacca cagcccaggc gctgccgagc 120
 ctggcaccaa tgctggagaa agtgatgccg tccgtggtca gcatcaacgt cgagggcagc 180
 gcgaccgtca ataacagccg cgtgccgccc cagttccagc agtttttttg cgaagactcc 240
 ccgctgtgcc agccgggttc gccgttcggg gattcgccga tgtgccaggg cggcggcaat 300
 gcgccgtcca aagagcgctt taaggcgctg ggctccgggg tcattatcga cgcgggtaaa 360
 ggctatgtcg tgaccaacaa ccacgtggtg gccaacgccg acagcattaa agtgcagctg 420
 agcgacggtc gccgcttcga cgccaagggt atcggcaccg atccgcgtac cgatatcgcg 480
 ctgatccagc tgaaggatgc caagaacctg accgccatta aaatggcgga ctctgacaat 540
 ttgcgcgtgg gcgactatgc ggtggcgatc ggcaaccctt acgggctggg tgagaccgtc 600
 acctccggga tcgtttccgc gctgggccgc agcggcctga acgtggaaaa ctacgaaaac 660
 ttatttcaga ctgacgcggc gattaaccgc ggtaactccg gcggtgcgct ggtgaacctg 720
 aacggcgatc tcatcgggat caacaccgcc attctggcgc cggacggcgg caacatcggc 780
 atcggcttcg ccattccgag caacatggtg aaaaacttga ccggtcagat ggtggagtac 840
 ggccagggtg aacgcggtga gctggggatc atggggaccg agctgaactc cgagctggcg 900
 aaggcgatga agatcgacgc ccagcgcggc gcctttatca gccagggtgct gccgaagtca 960
 gccgccgcga aggccgggct gaaacggcta gatgtcatcg tctccctgaa cgggaagaac 1020
 atctccagct tcgcttcctt ccgcgctgaa atcggcacca tgccggtcgg cagcaagctg 1080
 gcgctgggga tcatccgcga cggtaaagcc atgaacgtgg aggtaacctt ggagcagagc 1140
 gcgcagagcc aggtggcctc tgacaacatc ttcagcggtg tcgaaggggc cgagctgagc 1200
 aatgcggccg gtggcaaggg cgtgaagggt gacaacgtga agaaaggctc caccgccgcg 1260
 cgtatcggtc tgcaagaagg cgacgtgatc ctgggcgtga accagcacgc gatcgctaac 1320
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 cgtggcgaca acacctgta tctgctgatg cagtaa 1416

<210> 96
 <211> 471
 <212> PRT
 <213> Edwardsiella tarda

<400> 96

Met Lys Lys Thr Thr Leu Val Leu Ser Ala Val Ala Leu Ser Leu Gly
 1 5 10 15

Met Ala Leu Ser₂₀ Pro Met Ser Ala Ser₂₅ Ala Ala Glu Thr Ser₃₀ Ser Ala
 Thr Thr Ala₃₅ Gln Ala Leu Pro Ser₄₀ Leu Ala Pro Met Leu₄₅ Glu Lys Val
 Met Pro₅₀ Ser Val Val Ser Ile₅₅ Asn Val Glu Gly Ser₆₀ Ala Thr Val Asn
 Asn Ser Arg Val Pro₇₀ Gln Phe Gln Gln Phe₇₅ Phe Gly Glu Asp Ser₈₀
 Pro Leu Cys Gln₈₅ Pro Gly Ser Pro Phe Gly₉₀ Asp Ser Pro Met Cys₉₅ Gln
 Gly Gly Gly Asn₁₀₀ Ala Pro Ser Lys Glu₁₀₅ Arg Phe Lys Ala Leu Gly Ser
 Gly Val Ile₁₁₅ Ile Asp Ala Gly Lys₁₂₀ Gly Tyr Val Val Thr₁₂₅ Asn Asn His
 Val Val₁₃₀ Ala Asn Ala Asp Ser₁₃₅ Ile Lys Val Gln Leu₁₄₀ Ser Asp Gly Arg
 Arg Phe Asp Ala Lys Val₁₅₀ Ile Gly Thr Asp Pro₁₅₅ Arg Thr Asp Ile Ala₁₆₀
 Leu Ile Gln Leu Lys₁₆₅ Asp Ala Lys Asn Leu₁₇₀ Thr Ala Ile Lys Met₁₇₅ Ala
 Asp Ser Asp Asn₁₈₀ Leu Arg Val Gly Asp₁₈₅ Tyr Ala Val Ala Ile₁₉₀ Gly Asn
 Pro Tyr Gly₁₉₅ Leu Gly Glu Thr Val₂₀₀ Thr Ser Gly Ile Val₂₀₅ Ser Ala Leu
 Gly Arg₂₁₀ Ser Gly Leu Asn Val₂₁₅ Glu Asn Tyr Glu Asn₂₂₀ Phe Ile Gln Thr
 Asp Ala Ala Ile Asn Arg₂₃₀ Gly Asn Ser Gly Gly₂₃₅ Ala Leu Val Asn Leu₂₄₀
 Asn Gly Asp Leu Ile₂₄₅ Gly Ile Asn Thr Ala₂₅₀ Ile Leu Ala Pro Asp₂₅₅ Gly
 Gly Asn Ile Gly₂₆₀ Ile Gly Phe Ala Ile₂₆₅ Pro Ser Asn Met Val₂₇₀ Lys Asn
 Leu Thr Gly₂₇₅ Gln Met Val Glu Tyr₂₈₀ Gly Gln Val Lys Arg₂₈₅ Gly Glu Leu
 Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys Ala Met Lys

290

295

300

Ile Asp Ala Gln Arg Gly Ala Phe Ile Ser Gln Val Leu Pro Lys Ser
 305 310 315 320

Ala Ala Ala Lys Ala Gly Leu Lys Arg Leu Asp Val Ile Val Ser Leu
 325 330 335

Asn Gly Lys Asn Ile Ser Ser Phe Ala Ser Phe Arg Ala Glu Ile Gly
 340 345 350

Thr Met Pro Val Gly Ser Lys Leu Ala Leu Gly Ile Ile Arg Asp Gly
 355 360 365

Lys Pro Met Asn Val Glu Val Thr Leu Glu Gln Ser Ala Gln Ser Gln
 370 375 380

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

Asn Ala Ala Gly Gly Lys Gly Val Lys Val Asp Asn Val Lys Lys Gly
 405 410 415

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

Val Asn Gln His Ala Ile Ala Asn Ile Gly Glu Leu Arg Lys Ile Leu
 435 440 445

Asp Ala Lys Pro Pro Val Leu Ala Leu Asn Ile Gln Arg Gly Asp Asn
 450 455 460

Thr Leu Tyr Leu Leu Met Gln
 465 470

<210> 97

<211> 1437

<212> DNA

<213> Yersinia enterocolitica

<400> 97

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ctggcgccaa tgctagagaa ggtaatgcct tcggttgatga gtatcaatgt ggagggaagt 180

gctcaggtaa gtaatgccgg cggcatacca ccacagttcc agcaattctt tggatgatgat 240

tcgccattct gccaggacgg ttctccgttc caagggtcac caatgtgtca gggggggcct 300

ggtagcaggg ggggagcacc cagcaagcag gatttccgtg cgctgggttc tggcgtaatt 360

attgatgctg ctaaaggtta tgtcgtcact aataaccacg tagtagataa tgcaacaaaa 420

atcaatgta agctcagtga tggccgtagt tatgaagcaa aagtgattgg taaagatccg 480

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ctgggtgaaa ccgtcacttc cggtatcgtg tcggcgttgg gccgcagtgg tttgaatgtg 660
gaaaactacg aaaactttat ccagactgac gcggcaatta accgtggtaa ctccggtggt 720
gcattgatca atctgaacgg tgaactgatc gggatcaaca cggctattct ggcacctgat 780
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<210> 98
<211> 478
<212> PRT
<213> Yersinia enterocolitica
<400> 98

Met Lys Lys Thr Thr Leu Val Leu Ser Ala Leu Ala Leu Ser Ile Gly
1 5 10 15

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

Ser Ser Ser Gln Gln Leu Pro Ser Leu Ala Pro Met Leu Glu Lys Val
35 40 45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Ala Gln Val Ser
50 55 60

Asn Ala Gly Gly Ile Pro Pro Gln Phe Gln Gln Phe Phe Gly Asp Asp
65 70 75 80

Ser Pro Phe Cys Gln Asp Gly Ser Pro Phe Gln Gly Ser Pro Met Cys
85 90 95

Gln Gly Gly Pro Gly Ser Arg Gly Gly Ala Pro Ser Lys Gln Asp Phe
100 105 110

Arg Ala Leu Gly Ser Gly Val Ile Ile Asp Ala Ala Lys Gly Tyr Val
Seite 89

Val Thr Asn Asn His Val Val Asp Asn Ala Thr Lys Ile Asn Val Lys
130 135 140

Leu Ser Asp Gly Arg Ser Tyr Glu Ala Lys Val Ile Gly Lys Asp Pro
145 150 155 160

Arg Thr Asp Ile Ala Leu Leu Gln Leu Lys Asp Ala Lys Asn Leu Thr
165 170 175

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

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

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

Asn Phe Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly
225 230 235 240

Ala Leu Ile Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile
245 250 255

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

Asn Met Val Lys Asn Leu Thr Ser Gln Met Val Glu Phe Gly Gln Val
275 280 285

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

Ala Lys Ala Met Lys Val Asp Ala Gln Lys Gly Ala Phe Ile Ser Gln
305 310 315 320

Val Leu Pro Lys Ser Ala Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp
325 330 335

Val Ile Val Ser Met Asn Gly Lys Ala Ile Asn Ser Phe Ala Gly Phe
340 345 350

Arg Ala Glu Ile Gly Thr Leu Pro Val Gly Ser Lys Met Thr Leu Gly
355 360 365

Leu Leu Arg Asp Gly Lys Pro Val Asn Val Glu Val Thr Leu Glu Gln
370 375 380

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

Gly Ala Glu Leu Ser Asn Ser Asp Val Asn Gly Lys Lys Gly Val Lys
405 410 415

Val Asp Ser Val Lys Pro Gly Thr Ala Ala Ala Arg Ile Gly Leu Lys
420 425 430

Lys Gly Asp Val Ile Met Gly Val Asn Gln Gln Pro Val Gln Asn Leu
435 440 445

Gly Glu Leu Arg Lys Ile Leu Asp Thr Lys Pro Ser Val Leu Ala Leu
450 455 460

Ser Ile Gln Arg Gly Asp Thr Ser Leu Tyr Leu Leu Met Gln
465 470 475

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<210> 99
<211> 1446
<212> DNA
<213> Yersinia pseudotuberculosis
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ctggcgccaa	tgctagagaa	agtaatgcct	tcagtgggtca	gtatcaacgt	tgaaggtagt		180
gcgctgtaa	gcagtgtctg	tgacgcggt	atgccaccac	aattccagca	gttttttgggt		240
gataactcgc	cattctgtca	ggacggttca	ccgttccaag	gctcgccaat	gtgtcaaggg		300
gatctggg	gactagggca	gggaatgcc	agtaagcggg	aattccgttc	gcttggttca		360
ggtgtcatta	ttgatgcggg	caaggggtat	gtcgttacca	ataaccacgt	ggtcgataat		420
gcgaacaaga	tcagcgtaaa	actgagcgat	ggccgcagtt	ttgatgccaa	ggtgatcgggt		480
aaagatccac	gtaccgatat	cgcactgtta	caactgaaag	acgctaaaaa	tctgactgcg		540
attaagattg	ccaattcgga	tcaactgcgt	gtcgggtgatt	ataccgtcgc	tatcgggaac		600
ccgtatggct	tgggtgaaac	cgtgacatcc	ggtattgtct	ctgctttagg	gcgcagtgggt		660
ttgaatgtag	aaaactatga	aaactttatc	cagactgatg	cggcgattaa	ccgcggtaat		720
tccggcggg	cattaatcaa	cctgaacggt	gagttgattg	gtattaacac	cgctattctg		780
gcaccggatg	gcggtaacat	tggtattggc	tttgctatcc	caagcaacat	ggtgaagaac		840
ctgacatcac	agatggttga	gtttgggtcag	gtaaaacgcg	gtgaactggg	cattatgggg		900
accgagctaa	actctgaact	ggcaaaagcc	atgaaggttg	atgcgcagaa	aggtgccttt		960
atcagccagg	tcgtgcctaa	atctgctgcg	gcaaaagcgg	gtatcaaagc	gggcgatatc		1020
attgtcagta	tgaatgggaa	agccatcaat	agttttgcag	ggttccgcgc	cgagatcggc		1080
acgttacctg	ttggcagcaa	aatgaccttg	ggtctgctgc	gtgatggcaa	accgatcaat		1140
gtgaatgtcg	tcctggagca	gagcagccac	agtcagggtg	aatccggtaa	tctctacacc		1200
ggtattgagg	gggctgaact	gagtaacagc	aacgttagcg	gcaagaaagg	ggtgaaagtt		1260

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atgggggatta accagcaacc agtccagaac ctaggtgagc tgcggaaaat cctcgatgct 1380
aaaccaccgg tattggcggtt gaattattcaa cgtggtgata cttcactcta tttattgatg 1440
cagtaa 1446

<210> 100
<211> 481
<212> PRT
<213> *Yersinia pseudotuberculosis*
<400> 100

Met Lys Lys Thr Thr Leu Val Leu Ser Ala Leu Ala Leu Ser Ile Gly
1 5 10 15

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

Ser Ser Ser Gln Gln Leu Pro Ser Leu Ala Pro Met Leu Glu Lys Val
35 40 45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Ala Pro Val Ser
50 55 60

Ser Ala Gly Ala Arg Gly Met Pro Pro Gln Phe Gln Gln Phe Phe Gly
65 70 75 80

Asp Asn Ser Pro Phe Cys Gln Asp Gly Ser Pro Phe Gln Gly Ser Pro
85 90 95

Met Cys Gln Gly Asp Leu Gly Gly Leu Gly Gln Gly Met Pro Ser Lys
100 105 110

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

Gly Tyr Val Val Thr Asn Asn His Val Val Asp Asn Ala Asn Lys Ile
130 135 140

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

Lys Asp Pro Arg Thr Asp Ile Ala Leu Leu Gln Leu Lys Asp Ala Lys
165 170 175

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

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

Thr Ser Gly Ile Val Ser Ala Leu Gly Arg Ser Gly Leu Asn Val Glu
 210 215 220
 Asn Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn
 225 230 235 240
 Ser Gly Gly Ala Leu Ile Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn
 245 250 255
 Thr Ala Ile Leu Ala Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala
 260 265 270
 Ile Pro Ser Asn Met Val Lys Asn Leu Thr Ser Gln Met Val Glu Phe
 275 280 285
 Gly Gln Val Lys Arg Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn
 290 295 300
 Ser Glu Leu Ala Lys Ala Met Lys Val Asp Ala Gln Lys Gly Ala Phe
 305 310 315 320
 Ile Ser Gln Val Val Pro Lys Ser Ala Ala Ala Lys Ala Gly Ile Lys
 325 330 335
 Ala Gly Asp Ile Ile Val Ser Met Asn Gly Lys Ala Ile Asn Ser Phe
 340 345 350
 Ala Gly Phe Arg Ala Glu Ile Gly Thr Leu Pro Val Gly Ser Lys Met
 355 360 365
 Thr Leu Gly Leu Leu Arg Asp Gly Lys Pro Ile Asn Val Asn Val Val
 370 375 380
 Leu Glu Gln Ser Ser His Ser Gln Val Glu Ser Gly Asn Leu Tyr Thr
 385 390 395 400
 Gly Ile Glu Gly Ala Glu Leu Ser Asn Ser Asn Val Ser Gly Lys Lys
 405 410 415
 Gly Val Lys Val Asp Ser Val Lys Pro Gly Thr Ala Ala Ala Arg Ile
 420 425 430
 Gly Leu Lys Lys Gly Asp Ile Ile Met Gly Ile Asn Gln Gln Pro Val
 435 440 445
 Gln Asn Leu Gly Glu Leu Arg Lys Ile Leu Asp Ala Lys Pro Pro Val
 450 455 460
 Leu Ala Leu Asn Ile Gln Arg Gly Asp Thr Ser Leu Tyr Leu Leu Met
 465 470 475 480

Gln

<210> 101
 <211> 1446
 <212> DNA
 <213> *Yersinia pestis*

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ctggcgccaa tgctagagaa agtaatgcct tcagtgggtca gtatcaacgt tgaaggtagt      180
gcgcctgtaa gcagtgtctg tgcacgcggt atgccaccac aattccagca gttttttggt      240
gataactcgc cattctgtca ggacggttca ccgttccaag gctcgccaat gtgtcaaggg      300
gatctgggcg gactagggca gggaatgcca agtaagcggg aattccgttc gcttggttca      360
ggtgtcatta ttgatgcggg caaggggtat gtcgttacca ataaccacgt ggtcgataat      420
gcgaacaaga tcagcgtaaa actgagcgat ggccgcagtt ttgatgccaa ggtgatcggg      480
aaagatccac gtaccgatat cgcactgtta caactgaaag acgctaaaaa tctgactgcg      540
attaagattg ccaattcgga tcaactgcgt gtcggtgatt ataccgtcgc tatcggaac      600
ccgtatggct tgggtgaaac cgtgacatcc ggtattgtct ctgctttagg gcgcagtggt      660
ttgaatgtag aaaactatga aaactttatc cagactgatg cggcgattaa ccgtggtaat      720
tccggcggcg cattaatcaa cctgaacggg gagttgattg gtattaacac cgctattctg      780
gcaccggatg gcggtaacat tgggtattggc tttgctatcc caagcaacat ggtgaagaac      840
ctgacatcac agatggttga gtttggtcag gtaaaacgcg gtgaactggg cattatgggg      900
accgagctaa actctgaact ggcaaaagcc atgaaggttg atgcgcagaa aggtgccttt      960
atcagccagg tcgtgcctaa atctgctgcg gcaaaagcgg gtatcaaagc gggcgatatc     1020
attgtcagta tgaatgggaa agccatcaat agttttgcag ggttccgcgc cgagatcggc     1080
acgttacctg ttggcagcaa aatgaccttg ggtctgctgc gtgatggcaa accgatcaat     1140
gtggatgtcg tcctggagca gagcagccac agtcagggtg aatccggcaa tctctacacc     1200
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gatagcgtaa aaccaggcac tgctcggcg cgatatcgcc tgaaaaaagg tgatatcatc     1320
atgggggatta accagcaacc agtcagaac ctaggtgagc tgcggaaaat cctcgatgct     1380
aaaccaccgg tattggcggt gaatattcaa cgtggtgata cttcactcta tttattgatg     1440
cagtaa                                             1446
  
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<210> 102
 <211> 481
 <212> PRT
 <213> *Yersinia pestis*

```

<400> 102
Met Lys Lys Thr Thr Leu Val Leu Ser Ala Leu Ala Leu Ser Ile Gly
1          5          10          15
  
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 Ser Ser Ser₃₅ Gln Gln Leu Pro Ser₄₀ Leu Ala Pro Met₄₅ Leu Glu Lys Val
 Met Pro₅₀ Ser Val Val Ser Ile₅₅ Asn Val Glu Gly Ser₆₀ Ala Pro Val Ser
 Ser Ala Gly Ala Arg Gly₇₀ Met Pro Pro Gln Phe₇₅ Gln Gln Phe Phe Gly₈₀
 Asp Asn Ser Pro Phe₈₅ Cys Gln Asp Gly Ser₉₀ Pro Phe Gln Gly Ser₉₅ Pro
 Met Cys Gln Gly₁₀₀ Asp Leu Gly Gly Leu₁₀₅ Gly Gln Gly Met₁₁₀ Pro Ser Lys
 Arg Glu Phe₁₁₅ Arg Ser Leu Gly Ser₁₂₀ Gly Val Ile Ile Asp₁₂₅ Ala Gly Lys
 Gly Tyr Val Val Thr Asn Asn₁₃₅ His Val Val Asp Asn₁₄₀ Ala Asn Lys Ile
 Ser Val Lys Leu Ser Asp₁₅₀ Gly Arg Ser Phe Asp₁₅₅ Ala Lys Val Ile Gly₁₆₀
 Lys Asp Pro Arg Thr₁₆₅ Asp Ile Ala Leu Leu₁₇₀ Gln Leu Lys Asp Ala₁₇₅ Lys
 Asn Leu Thr Ala₁₈₀ Ile Lys Ile Ala Asn₁₈₅ Ser Asp Gln Leu Arg Val Gly
 Asp Tyr Thr₁₉₅ Val Ala Ile Gly Asn₂₀₀ Pro Tyr Gly Leu Gly₂₀₅ Glu Thr Val
 Thr Ser Gly Ile Val Ser Ala₂₁₅ Leu Gly Arg Ser Gly₂₂₀ Leu Asn Val Glu
 Asn Tyr Glu Asn Phe Ile₂₃₀ Gln Thr Asp Ala Ala₂₃₅ Ile Asn Arg Gly Asn₂₄₀
 Ser Gly Gly Ala Leu₂₄₅ Ile Asn Leu Asn Gly₂₅₀ Glu Leu Ile Gly Ile Asn₂₅₅
 Thr Ala Ile Leu₂₆₀ Ala Pro Asp Gly Gly₂₆₅ Asn Ile Gly Ile Gly₂₇₀ Phe Ala
 Ile Pro Ser₂₇₅ Asn Met Val Lys Asn₂₈₀ Leu Thr Ser Gln Met₂₈₅ Val Glu Phe

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

Ser Glu Leu Ala Lys Ala Met Lys Val Asp Ala Gln Lys Gly Ala Phe
305 310 315 320

Ile Ser Gln Val Val Pro Lys Ser Ala Ala Ala Lys Ala Gly Ile Lys
325 330 335

Ala Gly Asp Ile Ile Val Ser Met Asn Gly Lys Ala Ile Asn Ser Phe
340 345 350

Ala Gly Phe Arg Ala Glu Ile Gly Thr Leu Pro Val Gly Ser Lys Met
355 360 365

Thr Leu Gly Leu Leu Arg Asp Gly Lys Pro Ile Asn Val Asp Val Val
370 375 380

Leu Glu Gln Ser Ser His Ser Gln Val Glu Ser Gly Asn Leu Tyr Thr
385 390 395 400

Gly Ile Glu Gly Ala Glu Leu Ser Asn Ser Asp Val Ser Gly Lys Lys
405 410 415

Gly Val Lys Val Asp Ser Val Lys Pro Gly Thr Ala Ala Ala Arg Ile
420 425 430

Gly Leu Lys Lys Gly Asp Ile Ile Met Gly Ile Asn Gln Gln Pro Val
435 440 445

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

Leu Ala Leu Asn Ile Gln Arg Gly Asp Thr Ser Leu Tyr Leu Leu Met
465 470 475 480

Gln

<210> 103
<211> 1467
<212> DNA
<213> Erwinia carotovora

<400> 103
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agtctggccc ctatgctgga aaatgttatg cttccgtgg tgagcatcta tgtggaaggg 180
cataccacca atgcgggtaa agaaagcaat gcaggcaaag aaggatatacc gccgcagctt 240
cagccgtttt ttggtgaaaa ctcgccgttc tgccaagagg gatcgccgtt ccagtcgtcg 300

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 aatagtcacg tgggtggataa cgccgataaa attcagattc gactcagtga tggccgcaag 480
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 gcgctgcgtg cgaggtcgg ttcgctgccg gtgggcagca aagtcgcact ggggctgctg 1140
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<210> 104
 <211> 488
 <212> PRT
 <213> Erwinia carotovora

<400> 104

Met Lys Arg Lys Ser Leu Val Leu Ser Ala Leu Ala Leu Ser Leu Ala
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Met Ala Met Gly Ser Thr Thr Ala Asn Ala Ala Glu Ser Ala Ala Ser
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Ala Ala Ser Ser Gly Gln Leu Pro Ser Leu Ala Pro Met Leu Glu Asn
35 40 45

Val Met Pro Ser Val Val Ser Ile Tyr Val Glu Gly His Thr Thr Asn
50 55 60

Ala Gly Lys Glu Ser Asn Ala Gly Lys Glu Gly Ile Pro Pro Gln Leu
65 70 75 80

Gln Pro Phe Phe Gly Glu Asn Ser Pro Phe Cys Gln Glu Gly Ser Pro
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Phe Gln Ser Ser₁₀₀ Pro Met Cys Gln Gly₁₀₅ Asp Ser Asp Asp₁₁₀ Asp Ser
 Gly Gln Pro₁₁₅ Gln Pro Lys Gln Glu₁₂₀ Asn Phe Gln Ala₁₂₅ Gly Ala Gly
 Val Val₁₃₀ Ile Asn Ala Glu Lys₁₃₅ Gly Tyr Val Val₁₄₀ Thr Asn Ser His Val
 Val₁₄₅ Asp Asn Ala Asp Lys₁₅₀ Ile Gln Ile Arg Leu₁₅₅ Ser Asp Gly Arg Lys₁₆₀
 Tyr Asp Gly Lys Val₁₆₅ Leu Gly Lys Asp Pro₁₇₀ Arg Ser Asp Ile Ala₁₇₅ Leu
 Val Gln Leu Lys₁₈₀ Asp Phe Lys Asn Leu₁₈₅ Thr Ala Ile Lys Val₁₉₀ Ala Asp
 Ser Asp Gln₁₉₅ Leu Arg Val Gly Asp₂₀₀ Tyr Thr Val Ala₂₀₅ Ile Gly Asn Pro
 Tyr Gly₂₁₀ Leu Gly Glu Thr Ala₂₁₅ Thr Ser Gly Ile Val₂₂₀ Ser Ala Leu Gly
 Arg₂₂₅ Ser Gly Leu Asn Ile₂₃₀ Glu Asn Tyr Glu Asn₂₃₅ Phe Ile Gln Thr Asp₂₄₀
 Ala Ala Ile Asn Arg₂₄₅ Gly Asn Ser Gly Gly₂₅₀ Ala Leu Val Asn₂₅₅ Leu Asn
 Gly Glu Leu Ile₂₆₀ Gly Leu Asn Thr Ala₂₆₅ Ile Leu Ala Pro Asp₂₇₀ Gly Gly
 Asn Ile Gly₂₇₅ Ile Gly Phe Ala Ile₂₈₀ Pro Ser Asn Met Val₂₈₅ Lys Ser Val
 Val Ala Gln Ile Ile Glu Phe₂₉₅ Gly Glu Val Lys Arg₃₀₀ Gly Glu Leu Gly
 Ile₃₀₅ Thr Gly Thr Glu Leu₃₁₀ Asn Ser Glu Leu Ala₃₁₅ Gln Ala Met Lys Val₃₂₀
 Asp Ala Gln Arg Gly₃₂₅ Ala Phe Val Ser Gln₃₃₀ Val Arg Pro Lys Ser₃₃₅ Ala
 Ala Asp Ala Ala Gly Ile Lys Ala Gly₃₄₅ Asp Val Ile Val Thr₃₅₀ Leu Asn
 Gly Lys Ala₃₅₅ Val Ser Ser Phe Ser₃₆₀ Ala Leu Arg Ala Gln₃₆₅ Val Gly Ser

Leu Pro Val Gly Ser Lys Val Ala Leu Gly Leu Leu Arg Asp Gly Lys
370 375 380

Pro Leu Thr Val Asp Val Thr Leu Gln Gln Ser Asn Gln Ala Gln Val
385 390 395 400

Ala Ser Gly Asn Leu Tyr Ser Gly Ile Glu Gly Ala Glu Leu Ser Asn
405 410 415

Thr Gln Ile Asp Asp Lys Lys Gly Val Lys Val Asp Asn Val Lys Pro
420 425 430

Gly Ser Ala Ala Ala Lys Val Gly Leu Lys Lys Asp Asp Ile Ile Leu
435 440 445

Gly Val Asn Gln Gln Val Val Gln Asn Ile Gly Glu Leu Arg Lys Ile
450 455 460

Leu Asp Ser Lys Pro Ala Val Leu Ala Leu Asn Val Arg Arg Gly Asp
465 470 475 480

Ser Thr Ile Tyr Leu Leu Ala Gln
485

<210> 105
<211> 1371
<212> DNA
<213> *Erwinia carotovora*

<400> 105
atgaaaaaaa cgtcattatt atttagtgca ctggcaatga gtatagggtt gaccctgtcc 60
acgcttcccc cagcgaatgc tgcgctacct tccgtgggtc aagggcaaca aacgccaagc 120
ctggcccaaa tgctggaaaa agtcttacca gctgtcgtca gcgtgcatgt tgaagggtaca 180
caggtacagc gccagcgcgt accggaagag ttcaagttct tctttgggcc aaatttcccc 240
acggacaaac aaaattctcg tccgtttgaa gggctgggtt ccggcgtgat tattgatgca 300
gcaaaagggg atgtgctcac caacaatcac gttatcaata atgccgacaa aattcgcgtc 360
cagcttaatg acgggcgtga atatgatgcg aaactgattg gtcgcgacga gcagaccgat 420
attgccctgc tacagctgaa tgacgcaaaa aacctagtat ccgtaaaaat ggcggattcc 480
gatcagttgc gcgtcgggtga ttttgccgtt gccgtgggta acccattcgg cctcggccag 540
accgcgacat ccggcattat ctctgcactg ggacgtagcg gcctgaacct tgaagggctg 600
gaaaacttca tccagaccga tgcttctatc aaccgcggta actccggcgg tgcgctgggt 660
aacctcaacg gcgaactgat cggtatcaac accgcgattc tggctccggg cggaggaaac 720
atcggtatcg gtttcgcat cccagcaac atggctcaga atctggcgca gcagttgggt 780
gaatttggtg aagttaaacg cgggctgctg ggtattaaag gcagcgagat gacgtctgag 840
atggcgaaag cttcaacgt cgatgcacag cgcggcgctt tcgtcagcga agtcttaccg 900

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aaatctgccg cgtccaaagc gggatatcaag gctggcgacg tgttgactac tctggatggg 960
aaaccgatca gcagctttgc agaactgaga gccaaagtcg gcaccaccgc gccgggcaag 1020
accgtgaaaa tcggcctgct gcgtgatggg aaaccacagg aggtttcggg ggtggtggat 1080
aacagcacat cggcatcgac cagcgccgaa acgctttcac cgtcattgca gggatgcacg 1140
ctgatcaatg gtcaattgaa agatggcagc aaaggcgtgc agattgataa cgtcgctaag 1200
gacacgcctg ctgctgaggt tggctctgaa aaaggcgata tcattcattg cgtaaaccgc 1260
gagcgcattg aaaacatcac gcaactgcgc aagctgctgg aagcgaagcc ttccgttctg 1320
gcactgaaca tcgtccgtgg cgaagaaacg atctatctgc tgctacgtta a 1371

<210> 106
<211> 456
<212> PRT
<213> *Erwinia carotovora*

<400> 106

Met Lys Lys Thr Ser Leu Leu Phe Ser Ala Leu Ala Met Ser Ile Gly
1 5 10 15

Leu Thr Leu Ser Thr Leu Pro Ala Ala Asn Ala Ala Leu Pro Ser Val
20 25 30

Val Gln Gly Gln Gln Thr Pro Ser Leu Ala Pro Met Leu Glu Lys Val
35 40 45

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

Gln Arg Val Pro Glu Glu Phe Lys Phe Phe Phe Gly Pro Asn Phe Pro
65 70 75 80

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

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

Asn Asn Ala Asp Lys Ile Arg Val Gln Leu Asn Asp Gly Arg Glu Tyr
115 120 125

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

Gln Leu Asn Asp Ala Lys Asn Leu Val Ser Val Lys Met Ala Asp Ser
145 150 155 160

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

Gly Leu Gly Gln Thr Ala Thr Ser Gly Ile Ile Ser Ala Leu Gly Arg
 180 185 190
 Ser Gly Leu Asn Leu Glu Gly Leu Glu Asn Phe Ile Gln Thr Asp Ala
 195 200 205
 Ser Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu Val Asn Leu Asn Gly
 210 215 220
 Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala Pro Gly Gly Gly Asn
 225 230 235 240
 Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met Ala Gln Asn Leu Ala
 245 250 255
 Gln Gln Leu Val Glu Phe Gly Glu Val Lys Arg Gly Leu Leu Gly Ile
 260 265 270
 Lys Gly Ser Glu Met Thr Ser Glu Met Ala Lys Ala Phe Asn Val Asp
 275 280 285
 Ala Gln Arg Gly Ala Phe Val Ser Glu Val Leu Pro Lys Ser Ala Ala
 290 295 300
 Ser Lys Ala Gly Ile Lys Ala Gly Asp Val Leu Thr Thr Leu Asp Gly
 305 310 315 320
 Lys Pro Ile Ser Ser Phe Ala Glu Leu Arg Ala Lys Val Gly Thr Thr
 325 330 335
 Ala Pro Gly Lys Thr Val Lys Ile Gly Leu Leu Arg Asp Gly Lys Pro
 340 345 350
 Gln Glu Val Ser Val Val Leu Asp Asn Ser Thr Ser Ala Ser Thr Ser
 355 360 365
 Ala Glu Thr Leu Ser Pro Ser Leu Gln Gly Ala Ser Leu Ile Asn Gly
 370 375 380
 Gln Leu Lys Asp Gly Ser Lys Gly Val Gln Ile Asp Asn Val Ala Lys
 385 390 395 400
 Asp Thr Pro Ala Ala Gln Val Gly Leu Gln Lys Gly Asp Ile Ile Ile
 405 410 415
 Gly Val Asn Arg Glu Arg Ile Glu Asn Ile Thr Gln Leu Arg Lys Leu
 420 425 430
 Leu Glu Ala Lys Pro Ser Val Leu Ala Leu Asn Ile Val Arg Gly Glu
 435 440 445
 Glu Thr Ile Tyr Leu Leu Leu Arg

450

455

<210> 107
 <211> 1470
 <212> DNA
 <213> *Saccharomyces bayanus*

<400> 107
 atgtctgctg atttcggttt gattggtttg gccgtcatgg gtcaaaactt gatcttaaac 60
 gctgctgatac acggtttcac tgtttgtgct tacaacagaa ctcaatccaa ggttgaccat 120
 ttcttggcta acgaagccaa aggtaagtct atcattggtg ctacttccat tcaagatttc 180
 atttccaagt tgaagagacc tagaaaggta atgcttttgg ttaaagccgg tgctccagtc 240
 gacgccttga tcaaggaaat tgttccactt ttggaaaagg gcgacatcat catcgatggt 300
 ggtaactccc atttcccaga ctctaacaga cgttacgaag aattgaagaa gcacgggtatt 360
 cttttcgtcg gttccggtgt ctctgggtgg gaagatgggt cccgttatgg tccatctttg 420
 atgccagggt gttctgaaga agcttgacca cacatcaaga acatcttcca atctatctcc 480
 gcaaagtctg atggtgaacc atgttgtgaa tgggtcggcc cagctggtgc cggtcactac 540
 gtcaaaatgg tccacaacgg tatcgaatat ggtgacatgc aattgatttg tgaagcttac 600
 gatatacatga agagattggg tggattcact gacaaagaaa tcagtgaagt tttcaccaca 660
 tggaacaagg gtgtccttga ctctttcttg attgaaatta ccagagatat cttgaaattc 720
 gacgatgtcg acggttaagg attggtggaa aaaatcatgg atactgccgg ccaaagggt 780
 accggttaagt ggactgccat caacgccttg gacttgggta tgccagtcac cttgatcggt 840
 gaagctgtct ttgctcggtg tctatctgcc ttgaagaatg aaagagtcag agcttctaag 900
 gttttgccag gccacaagt tccaaaggac gccgtcaagg acagaaagca atttgtcgat 960
 gatttggaaac aagcttttga cgcttctaag atcatctcct acgctcaagg tttcatgttg 1020
 atccgtgaag ccgctgccac atacggatgg aaactaaaca accctgctat tgctttgatg 1080
 tggagagggt gttgtatcat tagatctgtt ttcttggccg aaatcaccaa ggcttataga 1140
 caagaaccag acctagaaaa cttgttgttc aacaagttct tcgccgatgc tgttaccaag 1200
 gctcaatctg gttggagaaa atccattgca ttggctacca catacgggtat cccaacccca 1260
 gccttttcca ctgctttgac cttctacgac ggttacagat ctgaaagatt accagccaac 1320
 ttactacaag ctcaacgtga ttacttcggt gctcacactt tcagagtctt gccagaatgt 1380
 gcatccgaaa acttgccaga agacaaggat attcatatca actggaccgg tcatggtggt 1440
 aacgtttctt cctcaacata ccaagcttaa 1470

<210> 108
 <211> 489
 <212> PRT
 <213> *Saccharomyces bayanus*

<400> 108

Met Ser Ala Asp Phe Gly Leu Ile Gly Leu Ala Val Met Gly Gln Asn
 1 5 10 15

Leu Ile Leu Asn₂₀ Ala Ala Asp His Gly₂₅ Phe Thr Val Cys Ala₃₀ Tyr Asn
 Arg Thr Gln₃₅ Ser Lys Val Asp His₄₀ Phe Leu Ala Asn Glu₄₅ Ala Lys Gly
 Lys Ser₅₀ Ile Ile Gly Ala Thr₅₅ Ser Ile Gln Asp Phe₆₀ Ile Ser Lys Leu
 Lys Arg Pro Arg Lys Val₇₀ Met Leu Leu Val Lys₇₅ Ala Gly Ala Pro Val₈₀
 Asp Ala Leu Ile Lys₈₅ Glu Ile Val Pro Leu₉₀ Leu Glu Lys Gly Asp₉₅ Ile
 Ile Ile Asp Gly₁₀₀ Gly Asn Ser His Phe₁₀₅ Pro Asp Ser Asn Arg₁₁₀ Arg Tyr
 Glu Glu Leu₁₁₅ Lys Lys His Gly Ile₁₂₀ Leu Phe Val Gly Ser₁₂₅ Gly Val Ser
 Gly Gly₁₃₀ Glu Asp Gly Ala Arg₁₃₅ Tyr Gly Pro Ser Leu₁₄₀ Met Pro Gly Gly
 Ser₁₄₅ Glu Glu Ala Trp Pro₁₅₀ His Ile Lys Asn Ile₁₅₅ Phe Gln Ser Ile Ser₁₆₀
 Ala Lys Ser Asp Gly₁₆₅ Glu Pro Cys Cys Glu₁₇₀ Trp Val Gly Pro Ala₁₇₅ Gly
 Ala Gly His Tyr₁₈₀ Val Lys Met Val His₁₈₅ Asn Gly Ile Glu Tyr₁₉₀ Gly Asp
 Met Gln Leu₁₉₅ Ile Cys Glu Ala Tyr₂₀₀ Asp Ile Met Lys Arg₂₀₅ Leu Gly Gly
 Phe Thr₂₁₀ Asp Lys Glu Ile Ser₂₁₅ Glu Val Phe Thr Thr₂₂₀ Trp Asn Lys Gly
 Val₂₂₅ Leu Asp Ser Phe Leu₂₃₀ Ile Glu Ile Thr Arg₂₃₅ Asp Ile Leu Lys Phe₂₄₀
 Asp Asp Val Asp Gly₂₄₅ Lys Pro Leu Val Glu₂₅₀ Lys Ile Met Asp Thr₂₅₅ Ala
 Gly Gln Lys Gly₂₆₀ Thr Gly Lys Trp Thr₂₆₅ Ala Ile Asn Ala Leu₂₇₀ Asp Leu
 Gly Met Pro₂₇₅ Val Thr Leu Ile Gly₂₈₀ Glu Ala Val Phe Ala₂₈₅ Arg Cys Leu

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Ser Ala Leu Lys Asn Glu Arg Val Arg Ala Ser Lys Val Leu Pro Gly
 290 295 300

Pro Gln Val Pro Lys Asp Ala Val Lys Asp Arg Lys Gln Phe Val Asp
 305 310 315 320

Asp Leu Glu Gln Ala Leu Tyr Ala Ser Lys Ile Ile Ser Tyr Ala Gln
 325 330 335

Gly Phe Met Leu Ile Arg Glu Ala Ala Ala Thr Tyr Gly Trp Lys Leu
 340 345 350

Asn Asn Pro Ala Ile Ala Leu Met Trp Arg Gly Gly Cys Ile Ile Arg
 355 360 365

Ser Val Phe Leu Ala Glu Ile Thr Lys Ala Tyr Arg Gln Glu Pro Asp
 370 375 380

Leu Glu Asn Leu Leu Phe Asn Lys Phe Phe Ala Asp Ala Val Thr Lys
 385 390 395 400

Ala Gln Ser Gly Trp Arg Lys Ser Ile Ala Leu Ala Thr Thr Tyr Gly
 405 410 415

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

Arg Ser Glu Arg Leu Pro Ala Asn Leu Leu Gln Ala Gln Arg Asp Tyr
 435 440 445

Phe Gly Ala His Thr Phe Arg Val Leu Pro Glu Cys Ala Ser Glu Asn
 450 455 460

Leu Pro Glu Asp Lys Asp Ile His Ile Asn Trp Thr Gly His Gly Gly
 465 470 475 480

Asn Val Ser Ser Ser Thr Tyr Gln Ala
 485

<210> 109

<211> 1470

<212> DNA

<213> Saccharomyces castellii

<400> 109

atgtccgctg attttggttt aatcggtttg gccgtcatgg gtcaaaactt gatcttaaatt 60

gccgcagacc acggtttcac cgtctgtgct tacaacagaa ctgtctccaa agtggaacat 120

ttcctagcta acgaagccaa gggtaagtcc attgttggtg ctacttctat cgacgacttt 180

ttgtctaaat tgaagagacc aagaaagggt atgcttcttg ttaaggctgg tgctccagtt 240

gatgctctaa ttaacgaatt ggtcccacgt ctagaaaagg gtgatattat catcgatggt 300

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 ttgtttgttg gttccggtgt ctctgggtgg gaagatgggtg cccgttacgg tccatctttg 420
 atgccagggtg gtgcagaaga agcttgGCCa cacattaagg atattttcca atccatctcc 480
 gctaaatctg atgggtgaacc atgttgtgac tgggtcgggtc cagccgggtgc aggtcattac 540
 gtcaaaatgg tccataacgg tattgaatac ggtgacatgc aattgatttg tgaagcttat 600
 gacattatga agcgtgtcgg tcatttcact gataaggaaa ttggtgatgt ttttgaaacc 660
 tggaacaagg gtgtcttgga ttctttccta attgaaatta ccagagatat cttgaaattc 720
 aatgacgttg atggtaagcc attggttgaa aagattatgg ataccgctgg tcaaaaggggt 780
 actggtaagt ggaccgctat taatgctcta gatttgggta ttccagtcac tttgattgggt 840
 gaagctgtct tctctcgttg tctatctgct ttgaagtctg aaagaattag agcttccaag 900
 actctattgg gtccagaagt tccaaaggat ttgattaagg ataagaagca atttgttgac 960
 gatttggAAC aagccttata cgcttccaaa attatgtcct acgctcaagg tttcatgtta 1020
 atccgtgaag ctggtaagac ttatgggttg aaactaaaca acccagctat tgccttgatg 1080
 tggagagggtg gttgtattat tagatccgtc ttcttgggtg aaattaccaa ggcttacaga 1140
 gaagatccag aactagaaaa tctattattc aacaagttct tctccgatgc tgtcactaag 1200
 gctcaaaccg gttggagaaa gtccattgct ttggctacca cttacgggtat cccaacccca 1260
 gcattctcca ctgctttggc cttctacgat ggttacagat ctgaaagatt accagctaac 1320
 ttgctacaag ctcaaagaga ttacttcgggt gctcacactt tcagagtctt gccagaatgt 1380
 gcctctgaca acttgccatt agacaaggat atccacatta actggaccgg tcacgggtgggt 1440
 aacgtttctt cttctactta ccaagcttaa 1470

<210> 110
 <211> 489
 <212> PRT
 <213> *Saccharomyces castellii*

<400> 110

Met Ser Ala Asp Phe Gly Leu Ile Gly Leu Ala Val Met Gly Gln Asn
 1 5 10 15

Leu Ile Leu Asn Ala Ala Asp His Gly Phe Thr Val Cys Ala Tyr Asn
 20 25 30

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

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

Lys Arg Pro Arg Lys Val Met Leu Leu Val Lys Ala Gly Ala Pro Val
 65 70 75 80

Asp Ala Leu Ile Asn Glu Leu Val Pro Arg Leu Glu Lys Gly Asp Ile
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Ile Ile Asp Gly₁₀₀ Gly Asn Ser His Phe₁₀₅ Pro Asp Thr Asn Arg₁₁₀ Arg Tyr
 Glu Glu Leu₁₁₅ Lys Gln Lys Gly Ile₁₂₀ Leu Phe Val Gly₁₂₅ Ser Gly Val Ser
 Gly Gly₁₃₀ Glu Asp Gly Ala Arg₁₃₅ Tyr Gly Pro Ser Leu₁₄₀ Met Pro Gly Gly
 Ala Glu Glu Ala Trp Pro₁₅₀ His Ile Lys Asp Ile₁₅₅ Phe Gln Ser Ile Ser₁₆₀
 Ala Lys Ser Asp Gly₁₆₅ Glu Pro Cys Cys Asp₁₇₀ Trp Val Gly Pro Ala₁₇₅ Gly
 Ala Gly His Tyr₁₈₀ Val Lys Met Val His₁₈₅ Asn Gly Ile Glu Tyr₁₉₀ Gly Asp
 Met Gln Leu₁₉₅ Ile Cys Glu Ala Tyr₂₀₀ Asp Ile Met Lys Arg₂₀₅ Val Gly His
 Phe Thr₂₁₀ Asp Lys Glu Ile Gly₂₁₅ Asp Val Phe Glu Thr₂₂₀ Trp Asn Lys Gly
 Val₂₂₅ Leu Asp Ser Phe Leu₂₃₀ Ile Glu Ile Thr Arg₂₃₅ Asp Ile Leu Lys Phe₂₄₀
 Asn Asp Val Asp₂₄₅ Gly Lys Pro Leu Val Glu₂₅₀ Lys Ile Met Asp Thr₂₅₅ Ala
 Gly Gln Lys Gly₂₆₀ Thr Gly Lys Trp Thr₂₆₅ Ala Ile Asn Ala Leu₂₇₀ Asp Leu
 Gly Ile Pro₂₇₅ Val Thr Leu Ile Gly₂₈₀ Glu Ala Val Phe Ser₂₈₅ Arg Cys Leu
 Ser Ala₂₉₀ Leu Lys Ser Glu Arg₂₉₅ Ile Arg Ala Ser Lys₃₀₀ Thr Leu Leu Gly
 Pro₃₀₅ Glu Val Pro Lys Asp₃₁₀ Leu Ile Lys Asp Lys₃₁₅ Lys Gln Phe Val Asp₃₂₀
 Asp Leu Glu Gln Ala₃₂₅ Leu Tyr Ala Ser Lys₃₃₀ Ile Met Ser Tyr Ala₃₃₅ Gln
 Gly Phe Met Leu₃₄₀ Ile Arg Glu Ala Gly₃₄₅ Lys Thr Tyr Gly Trp₃₅₀ Lys Leu
 Asn Asn Pro₃₅₅ Ala Ile Ala Leu Met₃₆₀ Trp Arg Gly Gly Cys₃₆₅ Ile Ile Arg

Ser Val Phe Leu Gly Glu Ile Thr Lys Ala Tyr Arg Glu Asp Pro Glu
370 375 380

Leu Glu Asn Leu Leu Phe Asn Lys Phe Phe Ser Asp Ala Val Thr Lys
385 390 395 400

Ala Gln Thr Gly Trp Arg Lys Ser Ile Ala Leu Ala Thr Thr Tyr Gly
405 410 415

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

Arg Ser Glu Arg Leu Pro Ala Asn Leu Leu Gln Ala Gln Arg Asp Tyr
435 440 445

Phe Gly Ala His Thr Phe Arg Val Leu Pro Glu Cys Ala Ser Asp Asn
450 455 460

Leu Pro Leu Asp Lys Asp Ile His Ile Asn Trp Thr Gly His Gly Gly
465 470 475 480

Asn Val Ser Ser Ser Thr Tyr Gln Ala
485

<210> 111
<211> 1470

<212> DNA
<213> Candida glabrata

<400> 111
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attgctgacc acggttacac tggttggtgct tacaacagat ccgttgacaa ggtccaccaa 120
ttcttggaca acgaagccaa gggtaagtcc atcatcggtg ctgagtccat cgaggacttg 180
gtcgccaagt tgaagagacc tagaaagatc atgatgttgg tcaaggccgg tgccccagtc 240
gacggtttga tcgctcaatt ggttcacac ttggaaaagg gtgacatcat cattgacggt 300
ggtaactccc acttcccaga ctctaacaga cgttacgagg agttgaaggc caaggggtatc 360
ttgttcgtcg gctctggtgt ctctggtggt gaagacggtg cccgttacgg tccatctttg 420
atgccagggtg gtgccgaaga agcttgacca cacatcaagg agatcttcca atccatctcc 480
gccaagtccg acggtgagcc atgttgtgac tgggttggtc cagctgggtc tggtcactac 540
gtcaagatgg tccacaacgg tatcgaatac ggtgacatgc agttgatctg tgaagcctac 600
gacatcatga agagaatcgg tggtttcacc gacaaggaaa tctccgaagt cttcggaag 660
tgggacactg gtgttctaga ctctttcttg gtcgaaatta ccaccaacat cctaaagaag 720
gacgacgttg acggttaagcc attggttgaa aagatcatgg actctgctgg tcaaaaggg 780
accggtaagt ggaccgcat caacgccttg gacctaggta tgccagtctc tttgattggt 840
gaagccgtct tcgctagatg tttgtctgct ctaaagtgtg aaagagttaa ggcctccaag 900

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actttgccag gccagaaat tccaaaggac ttgatcaagg acagacaaca attcattgac 960
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atcagagaag ccgctaagac ttacggctgg aagctaaaca acccagctat tgctctaattg 1080
tggagaggtg gttgtatcat cagatccgtc ttcttgggtg aaatcaccaa ggcttacaga 1140
gaaaaccag acttggaataa cttgctattc cacaagttct tcaaggacgc cgtcaccaag 1200
gctcaaggtg gctggagaag atctttggct ttggctgcca cttacggtat cccatcccca 1260
gccttcgcca ccgctttgtc cttctacgat ggttacagat ctgaaagatt gccagctaac 1320
ttgttgcaag ctcaacgtga ctacttcggt gctcacactt tcagagtctt gccagaatgt 1380
gcttccgact ccctaccaa ggacaaggac atccacatca actggaccgg tcacggtggt 1440
aacgtctctt ctaccactta cgatgcttaa 1470

<210> 112
<211> 489
<212> PRT
<213> Candida glabrata
<400> 112

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

Ala Lys Ser Asp Gly₁₆₅ Glu Pro Cys Cys Asp₁₇₀ Trp Val Gly Pro Ala Gly₁₇₅
 Ser Gly His Tyr₁₈₀ Val Lys Met Val His₁₈₅ Asn Gly Ile Glu Tyr₁₉₀ Gly Asp
 Met Gln Leu₁₉₅ Ile Cys Glu Ala Tyr₂₀₀ Asp Ile Met Lys Arg₂₀₅ Ile Gly Gly
 Phe Thr₂₁₀ Asp Lys Glu Ile Ser₂₁₅ Glu Val Phe Gly Lys₂₂₀ Trp Asp Thr Gly
 Val₂₂₅ Leu Asp Ser Phe Leu₂₃₀ Val Glu Ile Thr Thr₂₃₅ Asn Ile Leu Lys Lys₂₄₀
 Asp Asp Val Asp Gly₂₄₅ Lys Pro Leu Val Glu₂₅₀ Lys Ile Met Asp Ser₂₅₅ Ala
 Gly Gln Lys Gly₂₆₀ Thr Gly Lys Trp Thr₂₆₅ Ala Ile Asn Ala Leu₂₇₀ Asp Leu
 Gly Met Pro₂₇₅ Val Ser Leu Ile Gly₂₈₀ Glu Ala Val Phe Ala₂₈₅ Arg Cys Leu
 Ser Ala₂₉₀ Leu Lys Cys Glu Arg₂₉₅ Val Lys Ala Ser Lys₃₀₀ Thr Leu Pro Gly
 Pro Glu Ile Pro Lys Asp₃₁₀ Leu Ile Lys Asp Arg₃₁₅ Gln Gln Phe Ile Asp₃₂₀
 Asp Leu Glu Gln Ala₃₂₅ Leu Tyr Ala Ser Lys₃₃₀ Ile Ile Ser Tyr Ala₃₃₅ Gln
 Gly Phe Met Leu₃₄₀ Ile Arg Glu Ala Ala₃₄₅ Lys Thr Tyr Gly Trp₃₅₀ Lys Leu
 Asn Asn Pro₃₅₅ Ala Ile Ala Leu Met₃₆₀ Trp Arg Gly Gly Cys₃₆₅ Ile Ile Arg
 Ser Val₃₇₀ Phe Leu Gly Glu Ile₃₇₅ Thr Lys Ala Tyr Arg₃₈₀ Glu Asn Pro Asp
 Leu Glu Asn Leu Leu Phe₃₉₀ His Lys Phe Phe Lys₃₉₅ Asp Ala Val Thr Lys₄₀₀
 Ala Gln Gly Gly Trp₄₀₅ Arg Arg Ser Leu Ala₄₁₀ Leu Ala Ala Thr Tyr₄₁₅ Gly
 Ile Pro Ser Pro₄₂₀ Ala Phe Ala Thr Ala₄₂₅ Leu Ser Phe Tyr Asp₄₃₀ Gly Tyr
 Arg Ser Glu Arg Leu Pro Ala Asn Leu Leu Gln Ala Gln Arg Asp Tyr

Phe Gly Ala His Thr Phe Arg Val Leu Pro Glu Cys Ala Ser Asp Ser
450 455 460

Leu Pro Lys Asp Lys Asp Ile His Ile Asn Trp Thr Gly His Gly Gly
465 470 475 480

Asn Val Ser Ser Thr Thr Tyr Asp Ala
485

<210> 113
<211> 1482
<212> DNA
<213> Saccharomyces servazzii

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<400> 113
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aaagtcgacg atttcttagc caacgaagcc aagggcaaat ccacgtcgcg cgccaagtct    180
atcgaagaat tcacgcgcaa attgaaaaga ccaagaaaaa tcacgtctatt agtcaaagcc    240
ggtaaaccag tagactacat catcaacgac ctattaccac atctagaaaa gggatgatct    300
atcatcgatg gtggttaact ccatttccca gacaccaaca gaagatacga agaattgacc    360
aagaagggca ttcttttcgt cggctctggt gtctccgggtg gtgaagacgg ggcccgttac    420
ggtccttcct taatgccagg tgggtgccga gaagcttggc ctcacatcaa ggacatcttc    480
caatccatct ctgctaaagc cgacggtgaa ccttggtgtg actgggtcgg ccctgccggg    540
gccggtcact acgtcaagat ggtccacaac ggtatcgaat acggtgacat gcaattgatc    600
tgtgaagcct acgatcatc gaaacgtatc ggtggcttct cgcacaaaga aatctcagac    660
gtcttcgcca cctggaacaa gggggtccta gattccttct taatcgaaat caccagagat    720
atcctagcct tcaacgacaa agatggtaaa ccattagtcg aaaaaatctt agacagtgtc    780
ggccaaaagg gtaccggtaa atggaccgcc atcaacgccc tagacttagg tatgcctgtc    840
acccttatcg gtgaagccgt ctttgctcgt tgtctatccg ctttaaagag tgaaagaatc    900
ttggcctcca aacaattagc cggcccaacc atcccagccg atgcatcaa ggacaagaaa    960
caattcgtcg acgaattaga acaagcctta tacgcctcca agatcatgtc ctacgcccaa   1020
gggttcattg tgatcagaga agccgccaag acctacggtt ggaaattaaa taaccagct    1080
atcgctttta tgtggagagg tggttgtatc atcagatctg tcttcttagg tgaaattacc   1140
aaagcttata gagaaaacc agatttagaa aacttattat tgaacaaatt cttctcagat   1200
gccgtcacca aggtctaaac cggttggaga aagaccatcg gtttagctac cacctacggt   1260
atcccaaccc caaccttctc tacgccttta gccttctacg atggttacag atctgaaaga   1320
ttaccagcta acttattaca agctcaaaga gattacttcg gtgctcacac tttcagagtc   1380
ttaccagaag aagcttgtga aactttacca gaaggtaagg atatccacat caactggacc   1440

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ggtcacggtg gtaacgtctc ttcttcact tatgatgctt ag

1482

<210> 114
 <211> 493
 <212> PRT
 <213> Saccharomyces servazzii

<400> 114

Met Ser Gln Glu Ala Val Ala Asp Phe Gly Leu Ile Gly Leu Ala Val
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Met Gly Gln Asn Leu Ile Leu Asn Val Ala Asp His Gly Phe Thr Val
 20 25 30

Cys Ala Tyr Asn Arg Thr Val Ser Lys Val Asp Asp Phe Leu Ala Asn
 35 40 45

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

Ile Ala Lys Leu Lys Arg Pro Arg Lys Ile Met Leu Leu Val Lys Ala
 65 70 75 80

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

Lys Gly Asp Ile Ile Ile Asp Gly Gly Asn Ser His Phe Pro Asp Thr
 100 105 110

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

Ser Gly Val Ser Gly Gly Glu Asp Gly Ala Arg Tyr Gly Pro Ser Leu
 130 135 140

Met Pro Gly Gly Ala Glu Glu Ala Trp Pro His Ile Lys Asp Ile Phe
 145 150 155 160

Gln Ser Ile Ser Ala Lys Ala Asp Gly Glu Pro Cys Cys Asp Trp Val
 165 170 175

Gly Pro Ala Gly Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile
 180 185 190

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

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

Trp Asn Lys Gly Val Leu Asp Ser Phe Leu Ile Glu Ile Thr Arg Asp
 225 230 235 240

Ile Leu Ala Phe Asn Asp Lys Asp Gly Lys Pro Leu Val Glu Lys Ile
 245 250 255
 Leu Asp Ser Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ala Ile Asn
 260 265 270
 Ala Leu Asp Leu Gly Met Pro Val Thr Leu Ile Gly Glu Ala Val Phe
 275 280 285
 Ala Arg Cys Leu Ser Ala Leu Lys Ser Glu Arg Ile Leu Ala Ser Lys
 290 295 300
 Gln Leu Ala Gly Pro Thr Ile Pro Ala Asp Ala Ile Lys Asp Lys Lys
 305 310 315 320
 Gln Phe Val Asp Glu Leu Glu Gln Ala Leu Tyr Ala Ser Lys Ile Met
 325 330 335
 Ser Tyr Ala Gln Gly Phe Met Leu Ile Arg Glu Ala Ala Lys Thr Tyr
 340 345 350
 Gly Trp Lys Leu Asn Asn Pro Ala Ile Ala Leu Met Trp Arg Gly Gly
 355 360 365
 Cys Ile Ile Arg Ser Val Phe Leu Gly Glu Ile Thr Lys Ala Tyr Arg
 370 375 380
 Glu Asn Pro Asp Leu Glu Asn Leu Leu Leu Asn Lys Phe Phe Ser Asp
 385 390 395 400
 Ala Val Thr Lys Ala Gln Thr Gly Trp Arg Lys Thr Ile Gly Leu Ala
 405 410 415
 Thr Thr Tyr Gly Ile Pro Thr Pro Thr Phe Ser Thr Ala Leu Ala Phe
 420 425 430
 Tyr Asp Gly Tyr Arg Ser Glu Arg Leu Pro Ala Asn Leu Leu Gln Ala
 435 440 445
 Gln Arg Asp Tyr Phe Gly Ala His Thr Phe Arg Val Leu Pro Glu Glu
 450 455 460
 Ala Cys Glu Thr Leu Pro Glu Gly Lys Asp Ile His Ile Asn Trp Thr
 465 470 475 480
 Gly His Gly Gly Asn Val Ser Ser Ser Thr Tyr Asp Ala
 485 490

<210> 115
 <211> 1479
 <212> DNA
 <213> Kluyveromyces lactis

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<400> 115
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gttgatcatt tcttagcaaa cgaggcaaag ggtaaattcta tcattggtgc tcattctgtg      180
gaagaattgt gccgtaactt gaagagacca agaagaatca ttcttttggg caaggctggg      240
gatgctgtgg atgctttcat tcaacaattg ttgccatttt tggaaaaggg agacattatc      300
atcgatggtg gtaactctca tttcccagat tctaacagac gttacgatga attgaaggaa      360
aagggaaatct actttgtttg ttctggtgtt tctggtgggtg aagaagggtgc tcgttacggg      420
ccttctttga tgccagggtg tgccgaagaa gcttggcctc acattaagga catcttccaa      480
tctatttctg ccaagtctga cggcgaacca tgttgtgact gggttgggtcc agctgggtct      540
ggtcattacg tgaagatggg ccacaacggg atcgaatacg gtgacatgca attgatcact      600
gaagcttacg atatcatgaa gagaattggg ggattcaccg ataaggaaat cgggtgaagtt      660
ttctcccaat ggaacaaggg tgtcttggtt tccttcttgg ttgaaattac aagagacatt      720
ttgctgtacg acgatgtcga tgggtactcct ctagtggaag agatcttggg ttcagctggg      780
caaaagggta ctggtaaatt gactgccatt aacgctttgg atctaggtat gccagttact      840
ttgattggtg aagccgtgtt cgctcgttgt ttgtcctctt tgaaggacga aagagttaga      900
gcctccaagt tgcttccagg ccctcaaatt ccaaaggatg ccgttaagga aagacaacaa      960
ttcgttgacg acttgaaca agctctttac gcttccaaga tcattcttta cgctcaaggt     1020
ttcatgttga tccgtgaagc tggttaagact tacggctgga agttgaacaa ccctgccatc     1080
gctttgatgt ggagaggtgg ttgtatcatc agatccgttt tcttgggtga aattacaaag     1140
gcttatagag aaaaccaga atttgaaaac ttattattca acaaattctt cgctgatgcc     1200
gtcgaagagg ctcaaagcgg ttggagaaag actattgggt tggctgtttc ttacgggtatc     1260
ccaaccccag ctttctccac tgctctatcg ttctacgatg gttacagatc tgaaagattg     1320
ccagctaact tgctacaagc tcaacgtgat tacttcgggt ctcacacttt cagagtcttg     1380
ccagaagctg cttccgaaaa cttgccagct gaccaaaca tccacattaa ctggaccggg     1440
aaagggtgga acgtttcagc ttccagttac caagcttaa                               1479

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<210> 116
<211> 492
<212> PRT
<213> Kluyveromyces lactis

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<400> 116
Met Ser Glu Pro Ala Gly Asp Ile Gly Leu Ile Gly Leu Ala Val Met
1          5          10         15

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

Ala Tyr Asn Arg Thr Val Ser Lys Val Asp His Phe Leu Ala Asn Glu

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Ala Lys Gly Lys Ser Ile Ile Gly Ala His Ser Val Glu Glu Leu Cys
50 55 60

Arg Asn Leu Lys Arg Pro Arg Arg Ile Ile Leu Leu Val Lys Ala Gly
65 70 75 80

Asp Ala Val Asp Ala Phe Ile Gln Gln Leu Leu Pro Phe Leu Glu Lys
85 90 95

Gly Asp Ile Ile Ile Asp Gly Gly Asn Ser His Phe Pro Asp Ser Asn
100 105 110

Arg Arg Tyr Asp Glu Leu Lys Glu Lys Gly Ile Tyr Phe Val Gly Ser
115 120 125

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

Pro Gly Gly Ala Glu Glu Ala Trp Pro His Ile Lys Asp Ile Phe Gln
145 150 155 160

Ser Ile Ser Ala Lys Ser Asp Gly Glu Pro Cys Cys Asp Trp Val Gly
165 170 175

Pro Ala Gly Ser Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu
180 185 190

Tyr Gly Asp Met Gln Leu Ile Thr Glu Ala Tyr Asp Ile Met Lys Arg
195 200 205

Ile Gly Gly Phe Thr Asp Lys Glu Ile Gly Glu Val Phe Ser Gln Trp
210 215 220

Asn Lys Gly Val Leu Asp Ser Phe Leu Val Glu Ile Thr Arg Asp Ile
225 230 235 240

Leu Leu Tyr Asp Asp Val Asp Gly Thr Pro Leu Val Glu Lys Ile Leu
245 250 255

Asp Ser Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ala Ile Asn Ala
260 265 270

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

Arg Cys Leu Ser Ser Leu Lys Asp Glu Arg Val Arg Ala Ser Lys Leu
290 295 300

Leu Pro Gly Pro Gln Ile Pro Lys Asp Ala Val Lys Glu Arg Gln Gln
305 310 315 320

Phe Val Asp Asp Leu Glu Gln Ala Leu Tyr Ala Ser Lys Ile Ile Ser
325 330 335

Tyr Ala Gln Gly Phe Met Leu Ile Arg Glu Ala Gly Lys Thr Tyr Gly
340 345 350

Trp Lys Leu Asn Asn Pro Ala Ile Ala Leu Met Trp Arg Gly Gly Cys
355 360 365

Ile Ile Arg Ser Val Phe Leu Gly Glu Ile Thr Lys Ala Tyr Arg Glu
370 375 380

Asn Pro Glu Leu Glu Asn Leu Leu Phe Asn Lys Phe Phe Ala Asp Ala
385 390 395 400

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

Ser Tyr Gly Ile Pro Thr Pro Ala Phe Ser Thr Ala Leu Ser Phe Tyr
420 425 430

Asp Gly Tyr Arg Ser Glu Arg Leu Pro Ala Asn Leu Leu Gln Ala Gln
435 440 445

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

Ser Glu Asn Leu Pro Ala Asp Gln Asn Ile His Ile Asn Trp Thr Gly
465 470 475 480

Lys Gly Gly Asn Val Ser Ala Ser Ser Tyr Gln Ala
485 490

<210>	117
<211>	1488
<212>	DNA
<213>	Debaryomyces hansenii

<400>	117							
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gtcgacgact	tcttgacaa	cgaggctaag	ggcaaatcag	tcattggtgc	tcactccatc		180	
gaagaattat	gtgctaactt	gaagagacca	agaagaatca	ttttattagt	taaggctggt		240	
aaaccagttg	acgcttttat	tgaacaatta	ttacctcact	tagaaaaggg	tgatatcatc		300	
attgacggtg	gtaactccca	tttcccagat	tctaaccgtc	gttacgaaga	attaaacggt		360	
aagggtatct	tattcgttgg	ttctggtggt	tctggtggtg	aagaagggtgc	tagatacggg		420	
ccatctttga	tgccagggtg	tcacaaggac	gcttggccac	acatcaagga	tatcttccaa		480	
agtattgctg	ccaagtctga	tggtgaacca	tgttgtgact	gggttggtga	tgccggtgct		540	

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ggtcattacg ttaagatggt gcacaatggt attgaatacg gtgacatgca attgatttgt    600
gaagccttatg atttattaaa gagagttagt aaattctcca acaaggaaat cggtgacgtt    660
ttcgctaaat ggaacaaggg tgttttagac tctttcttaa ttgaaattac cagagatatt    720
ttgtacttca atgatccaac tgacaataag ccattattag aaaagatttt ggatactgct    780
ggtcagaagg gtactggtaa gtggactgct atcaatgctt tagatttagg tatgcctgtc    840
accttaattg gtgaagctgt tttctctcgt tgtttatccg ccttgaagga tgaaagagtc    900
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aagcaaaagt tcgttgacga cttagaacaa gctttatatg cttctaagat tatctcttac   1020
gctcaagggt tcatgttgat tagagaagct gctaaggaat acggctggaa attaaataac   1080
ccagctatcg ccttaatgtg gagaggtggt tgtattatca gatctgtttt cttaggtgaa   1140
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aatgatgcca tcaaaaaggc tcaaaagggt tggagatcaa ctattggtaa ggctgttgaa   1260
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caagtgttac caggtgaaga aaatgatttc ttaaagaagg accaatggat ccatgttaac   1440
tggaccggta aggggtgtaa tgtttccgcc tctacttatg atgcttag                   1488

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<210> 118
 <211> 495
 <212> PRT
 <213> Debaryomyces hansenii
 <400> 118

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

Gly Gln Asn Leu Ile Leu Asn Ala Ala Asp Asn Gly Tyr Thr Val Val
          20         25         30

Ala Tyr Asn Arg Thr Val Ala Lys Val Asp Asp Phe Leu Asp Asn Glu
          35         40         45

Ala Lys Gly Lys Ser Val Ile Gly Ala His Ser Ile Glu Glu Leu Cys
          50         55         60

Ala Asn Leu Lys Arg Pro Arg Arg Ile Ile Leu Leu Val Lys Ala Gly
65          70          75          80

Lys Pro Val Asp Ala Phe Ile Glu Gln Leu Leu Pro His Leu Glu Lys
          85          90          95

Gly Asp Ile Ile Ile Asp Gly Gly Asn Ser His Phe Pro Asp Ser Asn
          100         105         110

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Arg Arg Tyr Glu Glu Leu Asn Gly Lys Gly Ile Leu Phe Val Gly Ser
 115 120 125
 Gly Val Ser Gly Gly Glu Glu Gly Ala Arg Tyr Gly Pro Ser Leu Met
 130 135 140
 Pro Gly Gly His Lys Asp Ala Trp Pro His Ile Lys Asp Ile Phe Gln
 145 150 155 160
 Ser Ile Ala Ala Lys Ser Asp Gly Glu Pro Cys Cys Asp Trp Val Gly
 165 170 175
 Asp Ala Gly Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu
 180 185 190
 Tyr Gly Asp Met Gln Leu Ile Cys Glu Ala Tyr Asp Leu Leu Lys Arg
 195 200 205
 Val Gly Lys Phe Ser Asn Lys Glu Ile Gly Asp Val Phe Ala Lys Trp
 210 215 220
 Asn Lys Gly Val Leu Asp Ser Phe Leu Ile Glu Ile Thr Arg Asp Ile
 225 230 235 240
 Leu Tyr Phe Asn Asp Pro Thr Asp Asn Lys Pro Leu Leu Glu Lys Ile
 245 250 255
 Leu Asp Thr Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ala Ile Asn
 260 265 270
 Ala Leu Asp Leu Gly Met Pro Val Thr Leu Ile Gly Glu Ala Val Phe
 275 280 285
 Ser Arg Cys Leu Ser Ala Leu Lys Asp Glu Arg Val Arg Ala Ser Lys
 290 295 300
 Ser Leu Ala Gly Pro Ser Val Glu Asp Asp Glu Ser Pro Ile Gln Asp
 305 310 315 320
 Lys Gln Lys Phe Val Asp Asp Leu Glu Gln Ala Leu Tyr Ala Ser Lys
 325 330 335
 Ile Ile Ser Tyr Ala Gln Gly Phe Met Leu Ile Arg Glu Ala Ala Lys
 340 345 350
 Glu Tyr Gly Trp Lys Leu Asn Asn Pro Ala Ile Ala Leu Met Trp Arg
 355 360 365
 Gly Gly Cys Ile Ile Arg Ser Val Phe Leu Gly Glu Ile Thr Ser Ala
 370 375 380
 Tyr Arg Glu Thr Pro Asp Leu Glu Asn Leu Leu Phe His Pro Phe Phe

385 390 395 400

Asn Asp Ala Ile Lys Lys Ala Gln Lys Gly Trp Arg Ser Thr Ile Gly
405 410 415

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

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

Gln Ala Gln Arg Asp Tyr Phe Gly Ala His Thr Phe Gln Val Leu Pro
450 455 460

Gly Glu Glu Asn Asp Phe Leu Lys Lys Asp Gln Trp Ile His Val Asn
465 470 475 480

Trp Thr Gly Lys Gly Asn Val Ser Ala Ser Thr Tyr Asp Ala
485 490 495

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<210> 119
<211> 1470
<212> DNA
<213> Aspergillus nidulans
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gaattctgct	ccaagctcaa	gcgccctcgc	cgtatcatgc	tccttgatcat	ggccggaaac		240
cccgttgacc	agttcatcga	gtctcttctg	ccccacctcg	aggaggggtga	tattatcatc		300
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ggcatccgct	tcgtcggcag	cggtgtctcc	ggtggtgagg	agggtgccc	ctacggtccc		420
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gcttacgaca	tcctcaagcg	tggtgtcggc	ctctcctcca	aggagattgc	cgatgttttc		660
gccaaagtga	acaacggtgt	tcttgactct	ttcctgattg	aaatcactcg	tgacattctc		720
tacttcaacg	acgacgatgg	aacccccatg	gttgagaaga	tcctcgacaa	ggctggtcag		780
aagggtaccg	gcaagtggac	cgccgtcaac	gctctcgacc	tcggcatgcc	cgtcaccctg		840
attggcgagt	ccgtcttcgc	tcgctgcctc	tctgctctca	aggacgagcg	tatccgcgcc		900
agcagcctcc	tcaacggccc	cactcccag	ttcaccggtg	acaaggagga	gttcattgcc		960
gatctcgagc	aggctctcta	cgcttccaag	atcatctcct	acgccagg	tttcatgctc		1020
atccagaacg	ctgccaagga	gtacggctgg	aagctcaaca	agcccgccat	tgccctcatg		1080

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 aaggaccccg acctggagaa cctgctcttc aacgacttct tcaacaaggc catccacaac 1200
 gccagaagg gctggagaaa cggtgtcagc aagggtgctc tctgggggtat cccactccc 1260
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<210> 120
 <211> 489
 <212> PRT
 <213> *Aspergillus nidulans*
 <400> 120

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Gln Asn Leu Ile Leu Asn Ala Ala Asp His Gly Phe Thr Val Cys Ala
20 25 30

Tyr Asn Arg Thr Thr Ser Lys Val Asp Arg Phe Leu Glu Asn Glu Ala
35 40 45

Lys Gly Lys Ser Ile Val Gly Ala His Ser Val Glu Glu Phe Cys Ser
50 55 60

Lys Leu Lys Arg Pro Arg Arg Ile Met Leu Leu Val Met Ala Gly Asn
65 70 75 80

Pro Val Asp Gln Phe Ile Glu Ser Leu Leu Pro His Leu Glu Glu Gly
85 90 95

Asp Ile Ile Ile Asp Gly Gly Asn Ser His Phe Pro Asp Ser Asn Arg
100 105 110

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

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

Gly Gly Asn Glu Glu Ala Trp Pro Tyr Ile Lys Asp Ile Phe Gln Ser
145 150 155 160

Ile Ala Ala Lys Ser Asp Gly Glu Ala Cys Cys Asp Trp Val Gly Asp
165 170 175

Glu Gly Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu Tyr
180 185 190

Gly Asp Met Gln Leu Ile Cys Glu Ala Tyr Asp Ile Leu Lys Arg Gly
 195 200 205
 Val Gly Leu Ser Ser Lys Glu Ile Ala Asp Val Phe Ala Lys Trp Asn
 210 215 220
 Asn Gly Val Leu Asp Ser Phe Leu Ile Glu Ile Thr Arg Asp Ile Leu
 225 230 235 240
 Tyr Phe Asn Asp Asp Asp Gly Thr Pro Met Val Glu Lys Ile Leu Asp
 245 250 255
 Lys Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ala Val Asn Ala Leu
 260 265 270
 Asp Leu Gly Met Pro Val Thr Leu Ile Gly Glu Ser Val Phe Ala Arg
 275 280 285
 Cys Leu Ser Ala Leu Lys Asp Glu Arg Ile Arg Ala Ser Ser Leu Leu
 290 295 300
 Asn Gly Pro Thr Pro Glu Phe Thr Gly Asp Lys Glu Glu Phe Ile Ala
 305 310 315 320
 Asp Leu Glu Gln Ala Leu Tyr Ala Ser Lys Ile Ile Ser Tyr Ala Gln
 325 330 335
 Gly Phe Met Leu Ile Gln Asn Ala Ala Lys Glu Tyr Gly Trp Lys Leu
 340 345 350
 Asn Lys Pro Ala Ile Ala Leu Met Trp Arg Gly Gly Cys Ile Ile Arg
 355 360 365
 Ser Val Phe Leu Lys Asp Ile Thr Glu Ala Tyr Arg Lys Asp Pro Asp
 370 375 380
 Leu Glu Asn Leu Leu Phe Asn Asp Phe Phe Asn Lys Ala Ile His Asn
 385 390 395 400
 Ala Gln Lys Gly Trp Arg Asn Val Val Ser Lys Gly Ala Leu Trp Gly
 405 410 415
 Ile Pro Thr Pro Ala Phe Ser Thr Ala Leu Ser Phe Tyr Asp Gly Tyr
 420 425 430
 Arg Thr Lys Ala Leu Pro Ala Asn Leu Leu Gln Ala Gln Arg Asp Tyr
 435 440 445
 Phe Gly Ala His Thr Phe Arg Ile Lys Pro Glu His Ala Ser Glu Lys
 450 455 460

Tyr Pro Ala Asp Lys Asp Ile His Val Asn Trp Thr Gly Arg Gly Gly
 465 470 475 480

Gln Val Ser Ala Ser Thr Tyr Thr Ala
 485

<210> 121
 <211> 1476
 <212> DNA
 <213> *Aspergillus oryzae*

<400> 121
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 aaggttgacc gcttccttga aaatgaggcc aagggcaagt ccattgtcgg tgctcactcc 180
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 gagaagggca tccgcttcgt cggtagcggg gtctctgggt gtgaggaggg tgcccgttac 420
 ggtccctctc tcatgcccgg tggtaacgag gaggcctggc ctttcattaa ggatatcttc 480
 cagagcattg ccgccaagag cgaagggtgag gcttgctgcg actgggtcgg tgatgagggt 540
 gccggccact acgtcaagat ggtccacaac ggtatcgagt atggtgacat gcagctgata 600
 tgtgaggcct atgatattct caagcgtggg gttggcatgc ccgtcaacga aatcgccgaa 660
 gtcttcgaca agtgaacaa ggggtgtcttg gactccttct tgatcgaaat caccgcgat 720
 gtcctccgct tcaacgatga cgacggcact cccctcgttg agaagatcct tgacaaggcc 780
 ggccagaagg gaaccggcaa gtggaccgcc atcaacgctc ttgaccttggt tatgcctgtc 840
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 cttatgtggc gtggtggctg catcatccgc tctgtcttcc tgaaggacat caccaacgcc 1140
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 gccaacctgc tgcaggctca gcgtgactac ttcggtgccc acaccttcg cgtcaagccc 1380
 gagcacgcca acgagaccta ccctgagggc aaggacatcc acgtcaactg gactggacgt 1440
 ggtggtaatg tgtccgcctc tacctacatt gcttaa 1476

<210> 122
 <211> 491
 <212> PRT
 <213> *Aspergillus oryzae*

<400> 122

Met Ala Asp Gln Ala Val Ala Asp Phe Gly Leu Ile Gly Leu Ala Val
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Met Gly Gln Asn Leu Ile Met Asn Val Ala Asp His Gly Phe Thr Val
 20 25 30

Cys Ala Tyr Asn Arg Thr Thr Ser Lys Val Asp Arg Phe Leu Glu Asn
 35 40 45

Glu Ala Lys Gly Lys Ser Ile Val Gly Ala His Ser Ile Glu Glu Phe
 50 55 60

Cys Ala Lys Leu Lys Arg Pro Arg Arg Ile Met Leu Leu Val Met Ala
 65 70 75 80

Gly Lys Pro Val Asp Gln Phe Ile Glu Ser Leu Leu Pro His Leu Glu
 85 90 95

Lys Gly Asp Ile Ile Ile Asp Gly Gly Asn Ser His Phe Pro Asp Ser
 100 105 110

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

Ser Gly Val Ser Gly Gly Glu Glu Gly Ala Arg Tyr Gly Pro Ser Leu
 130 135 140

Met Pro Gly Gly Asn Glu Glu Ala Trp Pro Phe Ile Lys Asp Ile Phe
 145 150 155 160

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

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

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

Arg Gly Val Gly Met Pro Val Asn Glu Ile Ala Glu Val Phe Asp Lys
 210 215 220

Trp Asn Lys Gly Val Leu Asp Ser Phe Leu Ile Glu Ile Thr Arg Asp
 225 230 235 240

Val Leu Arg Phe Asn Asp Asp Asp Gly Thr Pro Leu Val Glu Lys Ile
 245 250 255

Leu Asp Lys Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ala Ile Asn
 260 265 270

Ala Leu Asp₂₇₅ Leu Gly Met Pro Val₂₈₀ Thr Leu Ile Gly Glu₂₈₅ Ala Val Phe

Ser Arg₂₉₀ Cys Leu Ser Ala Leu₂₉₅ Lys Asp Glu Arg Val₃₀₀ Arg Ala Ser Ser

Leu₃₀₅ Leu Pro Gly Pro Thr₃₁₀ Pro Gln Phe Thr Gly₃₁₅ Asp Lys Gln Ala Phe₃₂₀

Val Asp Asp Leu Glu₃₂₅ Gln Ala Leu Tyr Ala₃₃₀ Ser Lys Ile Ile Ser₃₃₅ Tyr

Ala Gln Gly Phe₃₄₀ Met Leu Met Gln Glu₃₄₅ Ala Ala Lys Glu Tyr₃₅₀ Gly Trp

Lys Leu Asn₃₅₅ Lys Pro Ser Ile Ala₃₆₀ Leu Met Trp Arg Gly₃₆₅ Gly Cys Ile

Ile Arg₃₇₀ Ser Val Phe Leu Lys₃₇₅ Asp Ile Thr Asn Ala₃₈₀ Tyr Arg Gln Asn

Pro Asp Leu Glu Asn Leu₃₉₀ Leu Phe Asp Lys Phe₃₉₅ Phe Asn Glu Ala Ile₄₀₀

Ala Lys Ala Gln Asn₄₀₅ Gly Trp Arg Asn Val₄₁₀ Val Ser Lys Gly Ala₄₁₅ Leu

Trp Gly Ile Pro₄₂₀ Thr Pro Ala Phe Ser₄₂₅ Thr Ala Leu Ser Phe₄₃₀ Tyr Asp

Gly Tyr Arg₄₃₅ Thr Arg Asp Leu Pro Ala Asn Leu Leu Gln Ala Gln Arg₄₄₅

Asp Tyr₄₅₀ Phe Gly Ala His Thr₄₅₅ Phe Arg Val Lys Pro₄₆₀ Glu His Ala Asn

Glu Thr Tyr Pro Glu Gly₄₇₀ Lys Asp Ile His Val₄₇₅ Asn Trp Thr Gly Arg₄₈₀

Gly Gly Asn Val Ser₄₈₅ Ala Ser Thr Tyr Ile₄₉₀ Ala

<210> 123

<211> 1470

<212> DNA

<213> Yarrowia lipolytica

<400> 123

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atgggccaga acctgacat caacatggcc gaccacggct acgaggttgt tgcctacaac 120

cgaaccacct ccaaggtcga ccacttcctc gagaacgagg ccaagggaaa gtccattatt 180

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aagggtgata tcatcattga cgggtggaac tcccacttcc ccgactccaa ccgacgatac 360
gaggagctta acgagaaggg aatcctcttt gttggttccg gtgtttccgg cggtgaggag 420
ggtgcccgat acggtccctc catcatgccc ggtggaaaca aggaggcctg gccccacatt 480
aagaagattt tccaggacat ctctgctaag gctgatggtg agccctgctg tgactgggtc 540
ggtgacgctg gtgccggcca ctttgtcaag atggttcaca acggtattga gtatggtgac 600
atgcagctta tctgcgaggc ttacgacctc atgaagcgag gtgctgggtt caccaatgag 660
gagattggag acgttttcgc caagtggaac aacggtatcc tcgactcctt cctcattgag 720
atcacccgag acatcttcaa gtacgacgac ggctctggaa ctctctcgt tgagaagatc 780
tccgacactg ctggccagaa gggactgga aagtggaccg ctatcaacgc tcttgacctt 840
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gaggtttctt cttccactta cgatgcttaa 1470

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<210> 124
 <211> 489
 <212> PRT
 <213> Yarrowia lipolytica

<400> 124

Met Thr Asp Thr Ser Asn Ile Lys Pro Val Ala Asp Ile Ala Leu Ile
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Gly Leu Ala Val Met Gly Gln Asn Leu Ile Leu Asn Met Ala Asp His
 20 25 30

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

Phe Leu Glu Asn Glu Ala Lys Gly Lys Ser Ile Ile Gly Ala His Ser
 50 55 60

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

340

345

350

Lys Thr Tyr Gly Trp Glu Leu Asn Asn Ala Gly Ile Ala Leu Met Trp
 355 360 365

Arg Gly Gly Cys Ile Ile Arg Ser Val Phe Leu Ala Asp Ile Thr Lys
 370 375 380

Ala Tyr Arg Gln Asp Pro Asn Leu Glu Asn Leu Leu Phe Asn Asp Phe
 385 390 395 400

Phe Lys Asn Ala Ile Ser Lys Ala Asn Pro Ser Trp Arg Ala Thr Val
 405 410 415

Ala Lys Ala Val Thr Trp Gly Val Pro Thr Pro Ala Phe Ala Ser Ala
 420 425 430

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

Leu Gln Ala Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Gln Leu Leu
 450 455 460

Asp Gly Asp Gly Lys Trp Ile His Thr Asn Trp Thr Gly Arg Gly Gly
 465 470 475 480

Glu Val Ser Ser Ser Thr Tyr Asp Ala
 485

<210> 125
 <211> 1479
 <212> DNA
 <213> Ustilago maydis

<400> 125
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 ctgacacctca acatgaacga caagggcttc accgtctgcg cctacaaccg taccaccagc 120
 aaggtggacg acttcctcgc caacgaggct aagggcacca acgtcgttgg cgccaagtcg 180
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 ggtccccgccg tcgacgcttt cattgagcag ctctctcccc acctcgagca gggtgacatt 300
 gtcattgacg gtggtaactc gcactacccc gactcgatcc gccgctgcaa ggagctcgag 360
 gccaagggaa tcctctttgt cggctccggt gtatccggtg gtgaggaggg tgcgcgtcac 420
 ggcccttcgc tcatgcccgg tggttcggat gctgcatggc cccacatcaa ggagattttc 480
 cagaagaccg ctgctcagtc ggatggcgag ccatgctgtg actgggtcgg ccaaaccggt 540
 gccggccact acgtcaagat ggtccacaac ggtatcgagt acggcgatat gcagctcatc 600
 tgcgaggcct acgacatcct taagcacggc cttggtctca aggagggcga gattggtgac 660
 attttcacca agtgaacac tgggtgtctc gactcgttcc tcatcgagat caccggtgac 720

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 accctcatcg gcgaggccgt ctttgcccga tgcctttcgt cgctcaaggg cgagcgtact 900
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 cccgccaacc tgctgcaggc ccagcgtgac tactttggtg ctcacacctt ccgtgttctg 1380
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 cgtggtggta acgtctcggc ttccacctac caggcataa 1479

<210> 126
 <211> 492
 <212> PRT
 <213> Ustilago maydis

<400> 126

Met Ser Ser Gln Ala Val Ala Asp Ile Gly Leu Ile Gly Leu Ala Val
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Met Gly Gln Asn Leu Ile Leu Asn Met Asn Asp Lys Gly Phe Thr Val
 20 25 30

Cys Ala Tyr Asn Arg Thr Thr Ser Lys Val Asp Asp Phe Leu Ala Asn
 35 40 45

Glu Ala Lys Gly Thr Asn Val Val Gly Ala Lys Ser Ile Glu Glu Phe
 50 55 60

Val Ala Lys Leu Lys Arg Pro Arg Lys Met Ile Leu Leu Val Lys Ala
 65 70 75 80

Gly Pro Ala Val Asp Ala Phe Ile Glu Gln Leu Leu Pro His Leu Glu
 85 90 95

Gln Gly Asp Ile Val Ile Asp Gly Gly Asn Ser His Tyr Pro Asp Ser
 100 105 110

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

Ser Gly Val Ser Gly Gly Glu Glu Gly Ala Arg His Gly Pro Ser Leu
 130 135 140

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Met Pro Gly Gly Ser Asp Ala Ala Trp Pro His Ile Lys Glu Ile Phe
 145 150 155 160
 Gln Lys Thr Ala Ala Gln Ser Asp Gly Glu Pro Cys Cys Asp Trp Val
 165 170 175
 Gly Gln Thr Gly Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile
 180 185 190
 Glu Tyr Gly Asp Met Gln Leu Ile Cys Glu Ala Tyr Asp Ile Leu Lys
 195 200 205
 His Gly Leu Gly Leu Lys Glu Gly Glu Ile Gly Asp Ile Phe Thr Lys
 210 215 220
 Trp Asn Thr Gly Val Leu Asp Ser Phe Leu Ile Glu Ile Thr Arg Asp
 225 230 235 240
 Ile Leu Lys Tyr Asn Asp Glu Asp Gly Ala Pro Leu Leu Thr Lys Ile
 245 250 255
 Met Asp Ser Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ala Ile Asn
 260 265 270
 Ala Leu Asp Leu Gly Gln Pro Val Thr Leu Ile Gly Glu Ala Val Phe
 275 280 285
 Ala Arg Cys Leu Ser Ser Leu Lys Gly Glu Arg Thr Arg Ala Ser Lys
 290 295 300
 Ile Leu Gly Gly Pro Gln Ile Lys Pro Phe Glu Gly Asn Lys Glu Gln
 305 310 315 320
 Phe Ile Ala Asp Leu Glu Gln Ala Leu Tyr Ala Ser Lys Ile Val Ser
 325 330 335
 Tyr Ala Gln Gly Phe Met Leu Met Arg Glu Ala Ala Lys Glu Tyr Asp
 340 345 350
 Trp Lys Leu Asn Asn Pro Ser Ile Ala Leu Met Trp Arg Gly Gly Cys
 355 360 365
 Ile Ile Arg Ser Val Phe Leu Lys Asp Ile Thr Ala Ala Phe Arg Lys
 370 375 380
 Asn Pro Glu Leu Glu Asn Leu Leu Phe Asp Asp Phe Phe Asn Lys Ala
 385 390 395 400
 Ile His Asn Ala Gln Glu Gly Trp Arg Arg Val Val Ala Gln Ala Ile
 405 410 415

Leu Trp Gly Ile Pro Thr Pro Ala Phe Ser Thr Ala Leu Ala Phe Phe
 420 425 430

Asp Gly Tyr Arg Arg Glu Leu Leu Pro Ala Asn Leu Leu Gln Ala Gln
 435 440 445

Arg Asp Tyr Phe Gly Ala His Thr Phe Arg Val Leu Pro Gln Phe Ala
 450 455 460

Ser Glu Lys Leu Pro Glu Gly Gln Asp Ile His Ile Asn Trp Thr Gly
 465 470 475 480

Arg Gly Gly Asn Val Ser Ala Ser Thr Tyr Gln Ala
 485 490

<210> 127
 <211> 1554
 <212> DNA
 <213> Candida albicans

<400> 127
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 caaaacttga ttcttaacat ggccgaccat ggttacactg ttgttgctta caacagaacc 180
 actgccaaag ttgatcggtt cttagaaaac gaagctaaag gtaaattccat cctcgggtgct 240
 cactccatca aggaattggg tgatcaatta aagagaccaa gaagaattat gcttttggtc 300
 aaagctgggtg ctccagttga tgaattcatt aaccaattat tgccatactt ggaagaagggt 360
 gatatcatca ttgacgggtg taactcccat ttcccagatt ctaacagaag atacgaagaa 420
 ttggccaaga aaggatatttt gtttggttggg tccgggtgtt ctgggtgggtga agaagggtgct 480
 agaactgggtc catctttgat gccaggtggg aacgaaaaag cttggccaca cattaaagac 540
 atcttccaag atgttgccgc caagagtgat ggtgaaccat gttgtgactg ggttggtgat 600
 gccggtgctg gtcattacgt caagatgggt cacaatggta ttgaatatgg tgatatgcaa 660
 ttgattttgtg aagcttacga tcttatgaag agagttggta aatttgaaga caaagaaatt 720
 ggtgacgtgt ttgccacatg gaacaaagggt gttttggatt ctttcttgat tgaaatcacc 780
 agagacattt tatactacaa tgacccaact gacggtaaac cattgggttg aaaaatcttg 840
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 atcccagtta ctttgattgg tgaagctgtc ttttctagat gtctttctgc catgaaagcc 960
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 aacaatgctg gtattgcctt gatgtggaga ggtggttgta ttatcagatc agttttcttg 1200
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<210> 128
 <211> 517
 <212> PRT
 <213> Candida albicans
 <400> 128

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Leu Ser Phe Asn Asn Thr Asn Ser Ser Ile Ala Arg Gly Asp Ile Gly
 20 25 30

Leu Ile Gly Leu Ala Val Met Gly Gln Asn Leu Ile Leu Asn Met Ala
 35 40 45

Asp His Gly Tyr Thr Val Val Ala Tyr Asn Arg Thr Thr Ala Lys Val
 50 55 60

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

His Ser Ile Lys Glu Leu Val Asp Gln Leu Lys Arg Pro Arg Arg Ile
 85 90 95

Met Leu Leu Val Lys Ala Gly Ala Pro Val Asp Glu Phe Ile Asn Gln
 100 105 110

Leu Leu Pro Tyr Leu Glu Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn
 115 120 125

Ser His Phe Pro Asp Ser Asn Arg Arg Tyr Glu Glu Leu Ala Lys Lys
 130 135 140

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

Arg Thr Gly Pro Ser Leu Met Pro Gly Gly Asn Glu Lys Ala Trp Pro
 165 170 175

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

Pro Cys Cys Asp Trp Val Gly Asp Ala Gly Ala Gly His Tyr Val Lys
 195 200 205

Met Val His Asn Gly Ile Glu Tyr Gly Asp Met Gln Leu Ile Cys Glu
 210 215 220
 Ala Tyr Asp Leu Met Lys Arg Val Gly Lys Phe Glu Asp Lys Glu Ile
 225 230 235 240
 Gly Asp Val Phe Ala Thr Trp Asn Lys Gly Val Leu Asp Ser Phe Leu
 245 250 255
 Ile Glu Ile Thr Arg Asp Ile Leu Tyr Tyr Asn Asp Pro Thr Asp Gly
 260 265 270
 Lys Pro Leu Val Glu Lys Ile Leu Asp Thr Ala Gly Gln Lys Gly Thr
 275 280 285
 Gly Lys Trp Thr Ala Val Asn Ala Leu Asp Leu Gly Ile Pro Val Thr
 290 295 300
 Leu Ile Gly Glu Ala Val Phe Ser Arg Cys Leu Ser Ala Met Lys Ala
 305 310 315 320
 Glu Arg Val Glu Ala Ser Lys Ala Leu Lys Gly Pro Gln Val Thr Gly
 325 330 335
 Glu Ser Pro Ile Thr Asp Lys Lys Gln Phe Ile Asp Asp Leu Glu Gln
 340 345 350
 Ala Leu Tyr Ala Ser Lys Ile Ile Ser Tyr Thr Gln Gly Phe Met Leu
 355 360 365
 Met Asn Gln Ala Ala Lys Asp Tyr Gly Trp Lys Leu Asn Asn Ala Gly
 370 375 380
 Ile Ala Leu Met Trp Arg Gly Gly Cys Ile Ile Arg Ser Val Phe Leu
 385 390 395 400
 Ala Glu Ile Thr Ala Ala Tyr Arg Lys Lys Pro Asp Leu Glu Asn Leu
 405 410 415
 Leu Leu Tyr Pro Phe Phe Asn Asp Ala Ile Thr Lys Ala Gln Ser Gly
 420 425 430
 Trp Arg Ala Ser Val Gly Lys Ala Ile Gln Tyr Gly Ile Pro Thr Pro
 435 440 445
 Ala Phe Ser Thr Ala Leu Ala Phe Tyr Asp Gly Leu Arg Ser Glu Arg
 450 455 460
 Leu Pro Ala Asn Leu Leu Gln Ala Gln Arg Asp Tyr Phe Gly Ala His
 465 470 475 480
 Thr Phe Lys Val Leu Pro Gly Gln Glu Asn Glu Leu Leu Lys Lys Asp
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Glu Trp Ile His Ile Asn Trp Thr Gly Arg Gly Gly Asp Val Ser Ser
 500 505 510

Thr Thr Tyr Asp Ala
 515

<210> 129
 <211> 1554
 <212> DNA
 <213> Candida albicans

<400> 129
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 caaaacttga ttcttaacat ggccgaccat ggttacactg ttgttgctta caacagaacc 180
 actgccaaag ttgatcgttt cttagaaaac gaagctaaag gtaaattccat cctcgggtgct 240
 cactccatca aggaattgggt tgatcaatta aagagaccaa gaagaattat gcttttggtc 300
 aaagctgggtg ctccagttga tgaattcatt aaccaattat tgccatactt ggaagaaggt 360
 gatatcatca ttgacgggtg taactcccat ttcccagatt ctaacagaag atacgaagaa 420
 ttggccaaga aaggtatttt gtttggttgg tccggtgttt ctggtggtga agaaggtgct 480
 agaactgggtc catctttgat gccagggtgg aacgaaaaag cttggccaca cattaagag 540
 atcttccaag atgttgccgc caagagtgat ggtgaaccat gttgtgactg gggtggtgat 600
 gccggtgctg gtcattacgt caagatgggt cacaatggta ttgaatatgg tgatatgcaa 660
 ttgattttgtg aagcttacga tcttatgaag agagttggta aatttgaaga caaagaaatt 720
 ggtgacgtgt ttgccacatg gaacaaaggt gttttggatt ctttcttgat tgaaatcacc 780
 agagacattt tatactacaa tgaccaact gacggtaaac cattgggtga aaaaatcttg 840
 gatactgctg gtcaaaaagg tactggtaaa tggactgctg tcaatgccct tgatttggtg 900
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 agatctgaaa gattaccagc taacttggtta caagctcaaa gagattactt tgggtgctcat 1440
 actttcaagg tcttgccagg tcaagaaaat gaattgttga agaaagatga atggattcac 1500
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<210> 130
 <211> 517
 <212> PRT
 <213> Candida albicans

<400> 130

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Leu Ile Gly Leu Ala Val Met Gly Gln Asn Leu Ile Leu Asn Met Ala
 35 40 45

Asp His Gly Tyr Thr Val Val Ala Tyr Asn Arg Thr Thr Ala Lys Val
 50 55 60

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

His Ser Ile Lys Glu Leu Val Asp Gln Leu Lys Arg Pro Arg Arg Ile
 85 90 95

Met Leu Leu Val Lys Ala Gly Ala Pro Val Asp Glu Phe Ile Asn Gln
 100 105 110

Leu Leu Pro Tyr Leu Glu Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn
 115 120 125

Ser His Phe Pro Asp Ser Asn Arg Arg Tyr Glu Glu Leu Ala Lys Lys
 130 135 140

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

Arg Thr Gly Pro Ser Leu Met Pro Gly Gly Asn Glu Lys Ala Trp Pro
 165 170 175

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

Pro Cys Cys Asp Trp Val Gly Asp Ala Gly Ala Gly His Tyr Val Lys
 195 200 205

Met Val His Asn Gly Ile Glu Tyr Gly Asp Met Gln Leu Ile Cys Glu
 210 215 220

Ala Tyr Asp Leu Met Lys Arg Val Gly Lys Phe Glu Asp Lys Glu Ile
 225 230 235 240

Gly Asp Val Phe Ala Thr Trp Asn Lys Gly Val Leu Asp Ser Phe Leu
 Seite 133

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

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

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

Leu Ile Gly Glu Ala Val Phe Ser Arg Cys Leu Ser Ala Met Lys Ala
 305 310 315 320

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

Glu Ser Pro Ile Thr Asp Lys Lys Gln Phe Ile Asp Asp Leu Glu Gln
 340 345 350

Ala Leu Tyr Ala Ser Lys Ile Ile Ser Tyr Thr Gln Gly Phe Met Leu
 355 360 365

Met Asn Gln Ala Ala Lys Asp Tyr Gly Trp Lys Leu Asn Asn Ala Gly
 370 375 380

Ile Ala Leu Met Trp Arg Gly Gly Cys Ile Ile Arg Ser Val Phe Leu
 385 390 395 400

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

Leu Leu Tyr Pro Phe Phe Asn Asp Ala Ile Thr Lys Ala Gln Ser Gly
 420 425 430

Trp Arg Ala Ser Val Gly Lys Ala Ile Gln Tyr Gly Ile Pro Thr Pro
 435 440 445

Ala Phe Ser Thr Ala Leu Ala Phe Tyr Asp Gly Leu Arg Ser Glu Arg
 450 455 460

Leu Pro Ala Asn Leu Leu Gln Ala Gln Arg Asp Tyr Phe Gly Ala His
 465 470 475 480

Thr Phe Lys Val Leu Pro Gly Gln Glu Asn Glu Leu Leu Lys Lys Asp
 485 490 495

Glu Trp Ile His Ile Asn Trp Thr Gly Arg Gly Gly Asp Val Ser Ser
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Thr Thr Tyr Asp Ala
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<210> 131
 <211> 1479
 <212> DNA
 <213> Schizosaccharomyces pombe

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 agagttgacg agTTTTtggc aaacgaagcc aaaggtaaT ctattgttgg tgctcactcc 180
 cttgaggaat ttgtttccaa gcttaagaag cctcgtgttt gtatTTTtgct tgTTaaggct 240
 ggtaagcctg ttgattacct tattgaggga ttggctcctc tcctcgagaa gggcgatata 300
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 aagaagggca ttctTTTTgt tggttccggT gtttctggTg gtgaagaggg tgctcgTTac 420
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 atttgcgaaa cttatgacat tatgaaacgt ggccttggTa tgtcttTgTa tgagattgcc 660
 gatgtTTTTg agaagtggaa cactggTaaa cttgactctt tcttaattga aatcactcgc 720
 gatgtTTTTgc gttacaaggc tgatgacggc aagcccttgg ttgagaagat tctcgacgct 780
 gctggacaga agggTactgg taagtggact gTcaaaacg ctttggaaat gggTaccctt 840
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 gctttgatgt ggcgtggTgg ttgtattatc cgTtccgtct tccttaagga tatcactgag 1140
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 ccagtccctg ccacttctac cggTctttcc ttctacgacg gttatcgtag tgctgttttg 1320
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 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 132

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 Cys Cys Tyr₃₅ Asn Arg Thr Thr Ser₄₀ Arg Val Asp Glu Phe₄₅ Leu Ala Asn
 Glu Ala₅₀ Lys Gly Lys Ser Ile₅₅ Val Gly Ala His Ser₆₀ Leu Glu Glu Phe
 Val₆₅ Ser Lys Leu Lys Lys₇₀ Pro Arg Val Cys Ile₇₅ Leu Leu Val Lys Ala₈₀
 Gly Lys Pro Val₈₅ Asp Tyr Leu Ile Glu Gly₉₀ Leu Ala Pro Leu₉₅ Glu
 Lys Gly Asp Ile₁₀₀ Ile Val Asp Gly Gly₁₀₅ Asn Ser His Tyr Pro₁₁₀ Asp Thr
 Thr Arg Arg₁₁₅ Cys Glu Glu Leu Ala₁₂₀ Lys Lys Gly Ile Leu₁₂₅ Phe Val Gly
 Ser Gly₁₃₀ Val Ser Gly Gly Glu₁₃₅ Glu Gly Ala Arg Tyr₁₄₀ Gly Pro Ser Leu
 Met₁₄₅ Pro Gly Gly Asn₁₅₀ Ala Ala Trp Pro Arg₁₅₅ Ile Lys Pro Ile Phe₁₆₀
 Gln Thr Leu Ala Ala₁₆₅ Lys Ala Gly Asn Asn₁₇₀ Glu Pro Cys Cys Asp₁₇₅ Trp
 Val Gly Glu Gln₁₈₀ Gly Ala Gly His Tyr₁₈₅ Val Lys Met Val His₁₉₀ Asn Gly
 Ile Glu Tyr₁₉₅ Gly Asp Met Gln₂₀₀ Ile Cys Glu Thr Tyr₂₀₅ Asp Ile Met
 Lys Arg₂₁₀ Gly Leu Gly Met Ser₂₁₅ Cys Asp Glu Ile Ala₂₂₀ Asp Val Phe Glu
 Lys₂₂₅ Trp Asn Thr Gly Lys₂₃₀ Leu Asp Ser Phe Leu₂₃₅ Ile Glu Ile Thr Arg₂₄₀
 Asp Val Leu Arg Tyr₂₄₅ Lys Ala Asp Asp Gly₂₅₀ Lys Pro Leu Val Glu₂₅₅ Lys
 Ile Leu Asp Ala₂₆₀ Ala Gly Gln Lys Gly₂₆₅ Thr Gly Lys Trp Thr₂₇₀ Ala Gln
 Asn Ala Leu₂₇₅ Glu Met Gly Thr Pro₂₈₀ Val Ser Leu Ile Thr₂₈₅ Glu Ala Val

Phe Ala Arg Cys Leu Ser Ser Leu Lys Ser Glu Arg Val Arg Ala Ser
 290 295 300

Lys Lys Leu Thr Gly Pro Asn Thr Lys Phe Thr Gly Asp Lys Lys Gln
 305 310 315 320

Leu Ile Asp Asp Leu Glu Asp Ala Leu Tyr Ala Ser Lys Ile Ile Ser
 325 330 335

Tyr Ala Gln Gly Phe Met Leu Met Arg Glu Ala Ala Lys Glu Tyr Gly
 340 345 350

Trp Lys Leu Asn Asn Ala Gly Ile Ala Leu Met Trp Arg Gly Gly Cys
 355 360 365

Ile Ile Arg Ser Val Phe Leu Lys Asp Ile Thr Glu Ala Phe Arg Glu
 370 375 380

Asp Pro Asn Leu Glu Ser Ile Leu Phe His Pro Phe Phe Thr Asn Gly
 385 390 395 400

Val Glu Lys Ala Gln Ala Gly Trp Arg Arg Val Val Ala Gln Ala Ala
 405 410 415

Met Leu Gly Ile Pro Val Pro Ala Thr Ser Thr Gly Leu Ser Phe Tyr
 420 425 430

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

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

Asp Lys Ser Leu Pro Ala Asp Lys Asp Ile His Ile Asn Trp Thr Gly
 465 470 475 480

His Gly Gly Asn Ile Ser Ala Thr Thr Tyr Asp Ala
 485 490

<210> 133
 <211> 1536
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 133
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 ctgaccta acgttgctga tcacggtttc acggtctgct cttacaaccg tacgacctcc 180
 aaggtcgacc gcttcctagc aaatgaggcc aagggcaagt ccattgtcgg tgctcactcc 240
 gtcgaggaat tctgcgcaa gctgaagcgc cctcgccgta tcatgctgct gggttatggct 300
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cagagcattg ccgccaagag cgacggcgag gcttgctgtg actgggtggg tgacgagggc    600
gctggtcact tcgtcaagat ggtccacaac ggtatcgagt acggtgacat gcagctgac    660
tgcgaggctt atgacatcat gaagcgtggg ctgggcatgc ccgtcaacga gatcgccgat    720
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ggccagaagg gtaccggcaa gtggaccgcc atcaacgctc tcgaccttgg catgcccggt    900
accctgatcg gtgaggccgt cttcgcccgt tgcctgagcg ccatcaagga cgagcgtatc    960
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cagaaggctc agcagggtg gagaaacgtg gtcagcaagg gcgccctctg gggtatcccc   1320
actcccgctc tcagcactgc tctgagcttc tacgacggat accgcacccg agacctccct   1380
gccaacctgc tgcaggctca gcgtgactac ttcggtgctc acaccttcg cgtcaagccc   1440
gagtgcgcca acgagaacta ccccgagggc aaggatatcc acgtcaactg gaccggctcg   1500
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<210> 134
<211> 511
<212> PRT
<213> Aspergillus fumigatus
<400> 134

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

Gly Leu Ala Val Met Gly Gln Asn Leu Ile Leu Asn Val Ala Asp His
          35         40         45

Gly Phe Thr Val Cys Ala Tyr Asn Arg Thr Thr Ser Lys Val Asp Arg
          50         55         60

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

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Val Glu Glu Phe Cys₈₅ Ala Lys Leu Lys Arg₉₀ Pro Arg Arg Ile Met₉₅ Leu
 Leu Val Met Ala₁₀₀ Gly Lys Pro Val Asp₁₀₅ Asp Phe Ile Glu Ser₁₁₀ Leu Leu
 Pro His Leu₁₁₅ Glu Glu Gly Asp Ile₁₂₀ Ile Ile Asp Gly₁₂₅ Gly Asn Ser His
 Phe Pro₁₃₀ Asp Ser Asn Arg Arg₁₃₅ Thr Lys Tyr Leu Lys₁₄₀ Glu Lys Gly Ile
 Arg₁₄₅ Phe Val Gly Ser Gly₁₅₀ Val Ser Gly Gly Glu₁₅₅ Glu Gly Ala Arg Tyr₁₆₀
 Gly Pro Ser Leu Met₁₆₅ Pro Gly Gly Asn Glu₁₇₀ Glu Ala Trp Pro Phe₁₇₅ Ile
 Lys Asp Ile Phe₁₈₀ Gln Ser Ile Ala Ala₁₈₅ Lys Ser Asp Gly Glu₁₉₀ Ala Cys
 Cys Asp Trp₁₉₅ Val Gly Asp Glu Gly₂₀₀ Ala Gly His Phe Val₂₀₅ Lys Met Val
 His Asn₂₁₀ Gly Ile Glu Tyr Gly₂₁₅ Asp Met Gln Leu Ile₂₂₀ Cys Glu Ala Tyr
 Asp₂₂₅ Ile Met Lys Arg Gly₂₃₀ Leu Gly Met Pro Val₂₃₅ Asn Glu Ile Ala Asp₂₄₀
 Val Phe Ala Lys Trp₂₄₅ Asn Lys Gly Val Leu₂₅₀ Asp Ser Phe Leu Ile₂₅₅ Glu
 Ile Thr Arg Asp₂₆₀ Val Leu Tyr Phe Asn₂₆₅ Asp Asn Asp Gly Thr₂₇₀ Pro Leu
 Val Glu Lys₂₇₅ Ile Leu Asp Lys Ala₂₈₀ Gly Gln Lys Gly Thr₂₈₅ Gly Lys Trp
 Thr Ala₂₉₀ Ile Asn Ala Leu Asp₂₉₅ Leu Gly Met Pro Val₃₀₀ Thr Leu Ile Gly
 Glu₃₀₅ Ala Val Phe Ala Arg₃₁₀ Cys Leu Ser Ala Ile₃₁₅ Lys Asp Glu Arg Ile₃₂₀
 Arg Ala Ser Ser Leu₃₂₅ Leu Asp Gly Pro Thr₃₃₀ Pro Gln Phe Thr Gly₃₃₅ Asp
 Lys Gln Ala Phe₃₄₀ Ile Asp Asp Leu Glu₃₄₅ Gln Ala Leu Tyr Ala₃₅₀ Ser Lys
 Ile Ile Ser Tyr Ala Gln Gly Phe Met Leu Ile Gln Glu Ala Ala Arg

Glu Tyr Gly Trp Lys Leu Asn Lys Pro Ser Ile Ala Leu Met Trp Arg
370 375 380

Gly Gly Cys Ile Ile Arg Ser Val Phe Leu Lys Asp Ile Thr Asn Ala
385 390 395 400

Tyr Arg Asn Asn Pro Asp Leu Glu Asn Leu Leu Phe Asp Asp Phe Phe
405 410 415

Lys Ala Ala Ile Gln Lys Ala Gln Gln Gly Trp Arg Asn Val Val Ser
420 425 430

Lys Gly Ala Leu Trp Gly Ile Pro Thr Pro Ala Phe Ser Thr Ala Leu
435 440 445

Ser Phe Tyr Asp Gly Tyr Arg Thr Arg Asp Leu Pro Ala Asn Leu Leu
450 455 460

Gln Ala Gln Arg Asp Tyr Phe Gly Ala His Thr Phe Arg Val Lys Pro
465 470 475 480

Glu Cys Ala Asn Glu Asn Tyr Pro Glu Gly Lys Asp Ile His Val Asn
485 490 495

Trp Thr Gly Arg Gly Gly Asp Val Ser Ala Ser Thr Tyr Val Val
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<211> 2367
<212> DNA
<213> Saccharomyces cerevisiae

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acgggaacac cctctgctca gtcagcagag gcaacattga caaaaccaag aactaatatt 660

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 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 136

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

Leu Glu Glu Thr Val Arg Lys Ser Lys Leu Tyr Gly Asn Asn Asn Asn
 290 295 300
 Asp Asp Asp Arg Asn Ile Asn Ser Ala Glu Asn Lys Gly Lys Ser Ile
 305 310 315 320
 Asp Asp Val Ser Lys Ala Ser Pro Leu Ala Lys Thr Pro Leu Pro Ile
 325 330 335
 Glu Asn Val Arg Ala Ser Pro Arg Arg Leu Ser Ser Val Val Thr Thr
 340 345 350
 Ser Pro Asp Lys Ala Met Asn Gly Thr Cys Pro Val Phe Leu Arg Ile
 355 360 365
 Gly Asp Lys Thr Lys Lys Cys His Val Gln Leu Pro Thr Thr Lys Asn
 370 375 380
 Ala Leu Arg Leu Leu Phe Ile Glu Arg Phe Ala Tyr Ser Pro Gly Ala
 385 390 395 400
 Asn Ser Phe Pro Asp Ile Tyr Ile Met Asp Pro Gln Tyr Gly Val Phe
 405 410 415
 Tyr Glu Leu Glu Glu Leu Asn Leu Leu Asp Ile Lys Glu Gly Phe Val
 420 425 430
 Ile Glu Leu Lys Leu Glu Glu Asn Pro Asn Asn Thr Ile Lys Glu Phe
 435 440 445
 Ile Asp Thr Val Lys Met Glu Ile Ser Asn Ser Gln Asn Asp Ile Ile
 450 455 460
 Arg His Leu Lys Glu Met Ser Phe Gly Ser Ala Ile Ser Gly Lys Gln
 465 470 475 480
 Thr Glu Val Leu Pro Gln Pro Gly Leu Glu Ala Asn Lys His Asp Leu
 485 490 495
 Val Gly Gln Asn Lys Lys Asp Asp Asp Lys Thr Ile Lys Asp Ile Gln
 500 505 510
 Tyr Glu Leu Gly Lys Ile Lys Gln Val His Asn Ile Asn Arg Ser Asn
 515 520 525
 Ile Asn Glu Thr Ile Phe Asn Ile Leu Arg Lys Val Asp Asn Phe Lys
 530 535 540
 Ser Leu Ser Phe Ser Ala Lys Asn Ser Ser Asn Arg Met Tyr Met Glu
 545 550 555 560
 Lys Ser Gln Thr Glu Leu Gly Asp Leu Ser Asp Thr Leu Leu Ser Lys

Val Asp Asp Leu Gln Asp Val Ile Glu Ile Met Arg Lys Asp Val Ala
580 585 590

Glu Arg Arg Ser Gln Pro Ala Lys Lys Lys Leu Glu Thr Val Ser Lys
595 600 605

Asp Leu Glu Asn Ala Gln Ala Asp Val Leu Lys Leu Gln Glu Phe Ile
610 615 620

Asp Thr Glu Lys Pro His Trp Lys Lys Thr Trp Glu Ala Glu Leu Asp
625 630 635 640

Lys Val Cys Glu Glu Gln Gln Phe Leu Thr Leu Gln Glu Glu Leu Ile
645 650 655

Leu Asp Leu Lys Glu Asp Leu Gly Lys Ala Leu Glu Thr Phe Asp Leu
660 665 670

Ile Lys Leu Cys Cys Glu Glu Gln Glu Lys Asn Pro Ser Arg Ser Lys
675 680 685

Ser Asn Pro Ile Leu Pro Ile Met Arg Pro Gly Thr Phe Asn Gln Val
690 695 700

Arg Glu Gln Val Met Val Ala Val Gln Ser Leu Asn Pro Asp His Asp
705 710 715 720

Ser Arg Val Glu Ala Ile Asp Lys Ala Glu Lys Met Trp Glu Met Glu
725 730 735

Arg Lys Leu Lys Ala Ser Asn Glu Phe Asp Asp Glu Leu Glu Asn Phe
740 745 750

Val Gly Asn Ser Asn Leu Lys Lys Ser Gly Gly Phe Glu Glu Val Glu
755 760 765

Arg Ile Arg Lys Gln Lys Asp Glu Ala Asn Leu Arg Ala Tyr Phe Gly
770 775 780

Pro Gly Phe Thr
785

<210> 137
<211> 990
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 137
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gttgctgtga ctgtcacgca acatgtccac caagctgcca ctgtagtggg acaaggtata 120

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 tctgctagtc ccgttgccac aacatcagct cctattgtgg ttgctaatgc tcaagtggac 240
 agcatagcta cttccgttat ccaagaaagc gctgtcgtgg ctgaatctgc aacatttgaa 300
 gaatcctcta cagaaacatc tgaagcattt tctacagcaa ctgcaaccat acaagcgggtg 360
 caaacctccg caagtgccac acaggatgat gtaaccacaa ctttaacatc ttcaacacaa 420
 cctaccagca caactactcc aacaaccact accactagcc caaccactac cactagccca 480
 actactaccg ctagtccaac tactactgct agcccaacca ccgctaccac cactcaatct 540
 accgcctcaa gcactcaatc ctcaagctcc gattttctcaa cgtcaatggg taacgaacac 600
 aacactaaaa gggcgttgca caaggatacc ggttctttga catgggtctga cacactagca 660
 acatatgcac aaaactacgc tgactcctac gattgttcag gcaacctagt ccactccggc 720
 ggtccatacg gtgaaaactt ggcacttggt tacggtacga ccggctctgt tgatgcctgg 780
 tataacgaaa ttaccagcta cgactattcc aaccctgggt ttagtgaaag cgcagggtcac 840
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 tttgctgaca acgttatgcc attagcttaa 990

<210> 138
 <211> 329
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 138

Met Lys Phe Ser Lys Val Ser Leu Leu Ala Ala Ser Ala Ser Val Ala
1 5 10 15

Leu Ser Ala Pro Val Ala Val Thr Val Thr Gln His Val His Gln Ala
20 25 30

Ala Thr Val Val Val Gln Gly Ile Val Arg Val Glu Asn Gly Gln Thr
35 40 45

Leu Thr Thr Phe Ile Thr Lys Gly Thr Gln Thr Ala Ser Ala Ser Pro
50 55 60

Val Ala Thr Thr Ser Ala Pro Ile Val Val Ala Asn Ala Gln Val Asp
65 70 75 80

Ser Ile Ala Thr Ser Val Ile Gln Glu Ser Ala Val Val Ala Glu Ser
85 90 95

Ala Thr Phe Glu Glu Ser Ser Thr Glu Thr Ser Glu Ala Phe Ser Thr
100 105 110

Ala Thr Ala Thr Ile Gln Ala Val Gln Thr Ser Ala Ser Ala Thr Gln
115 120 125

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Asp Asp Val Thr Thr Thr Leu Thr Ser Ser Thr Gln Pro Thr Ser Thr
130 135 140

Thr Thr Pro Thr Thr Thr Thr Thr Ser Pro Thr Thr Thr Thr Ser Pro
145 150 155 160

Thr Thr Thr Ala Ser Pro Thr Thr Thr Ala Ser Pro Thr Thr Ala Thr
165 170 175

Thr Thr Gln Ser Thr Ala Ser Ser Thr Gln Ser Ser Ser Ser Asp Phe
180 185 190

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

Asp Thr Gly Ser Leu Thr Trp Ser Asp Thr Leu Ala Thr Tyr Ala Gln
210 215 220

Asn Tyr Ala Asp Ser Tyr Asp Cys Ser Gly Asn Leu Val His Ser Gly
225 230 235 240

Gly Pro Tyr Gly Glu Asn Leu Ala Leu Gly Tyr Gly Thr Thr Gly Ser
245 250 255

Val Asp Ala Trp Tyr Asn Glu Ile Thr Ser Tyr Asp Tyr Ser Asn Pro
260 265 270

Gly Phe Ser Glu Ser Ala Gly His Phe Thr Gln Val Val Trp Lys Gly
275 280 285

Thr Ser Glu Val Gly Cys Gly Leu Lys Ser Cys Gly Gly Glu Trp Gly
290 295 300

Asp Tyr Ile Ile Cys Ser Tyr Lys Ala Ala Gly Asn Val Ile Gly Glu
305 310 315 320

Phe Ala Asp Asn Val Met Pro Leu Ala
325

<210> 139
<211> 1896
<212> DNA
<213> Escherichia coli

<400> 139
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ggcgtgcgcg tgccgatgcg tgagatccag cttagcccga cgctaattgg cggtagcaaa 180
gaacagccgc agtacgaaga aaacgaagcg attccggtct acgacacctc cggcccgtat 240
ggtgatccgc agattgccat taacgtgcag caagggctgg caaaactacg ccagccgtgg 300

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cggctggcag atgatggcct cgacgaactg cgttttagcg gcgtactaac accaaaacgc 420
gccaaagcag gacgccgtgt caccgaactg cactacgccc gccagggcat catcacgccg 480
gaaatggaat tcatcgccat ccgcgagaat atggggccgc agcgcatccg tagcgaggtt 540
ttacgccacc agcatccggg aatgagcttt ggcgcacatc tgccggaaaa tatcactgcg 600
gaatttgctc gtgatgaagt tgctgccgga cgtgcgatta tcccggccaa cattaatcat 660
ccggaatcgg agccgatgat tattggtcgc aatttcctgg taaaagttaa cgccaatatc 720
ggcaactcgg cggtcacctc ttccatcgaa gaagaagtgg aaaagctggg atgggtccacg 780
cgctggggag cggatacggg gatggatctc tccaccgggc gctatattca cgaaacccgc 840
gagtggattt tgcgtaacag cccggtgccg atcggtagag tgccgatcta ccaggcgctg 900
gagaaggtta acgggatcgc cgaagatctt acctgggaag cgttccgcga cacgtgctg 960
gaacaggccg agcaagggtg ggattacttc actatccatg cgggcgtact gctgctctat 1020
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gaaatctgtg ccgcttatga cgtttcgctg tcgctgggag acggtctgag ccccggttct 1200
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catctgggtc tgccaataa agaagatgtt aagcaggggc ttatcaccta taagattgct 1560
gccacgccg ctgacctggc gaaagggcat ccgggcgcgc aaattcgcga taacgccatg 1620
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accgcccgcg cttatcacga tgaaaccctg ccgcaagagt caggtaaagt cgcccatttt 1740
tgctccatgt gtgggccgaa attctgctcg atgaaaatca gccaggaagt gcgtgattac 1800
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ggcggagaaa tctacctgag taaggaggaa gcgtaa 1896

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<210> 140
 <211> 631
 <212> PRT
 <213> Escherichia coli

<400> 140

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

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

Gly Ile Ala Glu Asp Leu Thr Trp Glu Ala Phe Arg Asp Thr Leu Leu
 305 310 315 320
 Glu Gln Ala Glu Gln Gly Val Asp Tyr Phe Thr Ile His Ala Gly Val
 325 330 335
 Leu Leu Arg Tyr Val Pro Met Thr Ala Lys Arg Leu Thr Gly Ile Val
 340 345 350
 Ser Arg Gly Gly Ser Ile Met Ala Lys Trp Cys Leu Ser His His Gln
 355 360 365
 Glu Asn Phe Leu Tyr Gln His Phe Arg Glu Ile Cys Glu Ile Cys Ala
 370 375 380
 Ala Tyr Asp Val Ser Leu Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser
 385 390 395 400
 Ile Gln Asp Ala Asn Asp Glu Ala Gln Phe Ala Glu Leu His Thr Leu
 405 410 415
 Gly Glu Leu Thr Lys Ile Ala Trp Glu Tyr Asp Val Gln Val Met Ile
 420 425 430
 Glu Gly Pro Gly His Val Pro Met Gln Met Ile Arg Arg Asn Met Thr
 435 440 445
 Glu Glu Leu Glu His Cys His Glu Ala Pro Phe Tyr Thr Leu Gly Pro
 450 455 460
 Leu Thr Thr Asp Ile Ala Pro Gly Tyr Asp His Phe Thr Ser Gly Ile
 465 470 475 480
 Gly Ala Ala Met Ile Gly Trp Phe Gly Cys Ala Met Leu Cys Tyr Val
 485 490 495
 Thr Pro Lys Glu His Leu Gly Leu Pro Asn Lys Glu Asp Val Lys Gln
 500 505 510
 Gly Leu Ile Thr Tyr Lys Ile Ala Ala His Ala Ala Asp Leu Ala Lys
 515 520 525
 Gly His Pro Gly Ala Gln Ile Arg Asp Asn Ala Met Ser Lys Ala Arg
 530 535 540
 Phe Glu Phe Arg Trp Glu Asp Gln Phe Asn Leu Ala Leu Asp Pro Phe
 545 550 555 560
 Thr Ala Arg Ala Tyr His Asp Glu Thr Leu Pro Gln Glu Ser Gly Lys
 565 570 575
 Val Ala His Phe Cys Ser Met Cys Gly Pro Lys Phe Cys Ser Met Lys
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Ile Ser Gln Glu Val Arg Asp Tyr Ala Ala Thr Gln Thr Ile Glu Met
 595 600 605

Gly Met Ala Asp Met Ser Glu Asn Phe Arg Ala Arg Gly Gly Glu Ile
 610 615 620

Tyr Leu Arg Lys Glu Glu Ala
 625 630

<210> 141
 <211> 1371
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 141
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 cctggaaatg tgcccttgct tgacactaca gcgagattaa agaagttgaa tattgcggac 180
 gaatccaaga caaaaatggg gctggatagc tcccatgtgg gcgtttagacc ttctcctgca 240
 acctctcagc cgacgacatc aactgggagt gctgacctgg acagtatact aggccatatg 300
 gggctgccgc tgggaaactc tgtactagta gaggagcaga gcacgacaga atttcactct 360
 attctcggta aactgtttgc cgcacagggg atcgttcata atagaatttc agatagcagt 420
 gctgataaaa ctagaaacgg cgacactcat gtcattgtct tgtcattgaa ccaaattgttt 480
 gcaaaggagc tacctggtat ctacaaggga tcacgtaaac aaatgaagaa aaacctaatc 540
 tctgaagaag aatcaaaagt tactgttcaa aatttgaacg agaccagag atcgacgcct 600
 tccagggtaca aagacctgaa aattgcatgg aaatataaac tggcagatga aaagagattg 660
 ggttctccgg atcgagatga catccaacaa aattctgagt acaaggacta caatcatcag 720
 tttgatatta caacgcgtct gatgcccgtc cccatagcat ctgaactgac atttatcgcc 780
 ccaactcaac ctgtctccac tattttgagc caatagaac agactattaa aaggaatgac 840
 aagaaactga taagaattgt tattccttcc cttctacatc cggcaatgta tccgccccaa 900
 atgtttgaat catctgaaat aatagggtta atgcacggtg tgaggagtct tgtcaagaaa 960
 tactatgagc gggttgtact gtttgcttcc atatccatag acattatcac tccccatta 1020
 ctggtattgc tgagaaacat gttcgattct gttatcaatc tagaaccctt taaccaggag 1080
 atgactgagt tcttagaacg tgtttataaa tcgcaaccgg ggaagattca acatgggcta 1140
 gtccacatat tgaaattacc agttttcacg gaccgtggag agatgagagt tttaaagtct 1200
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 gatgatgctg aaggttcagc tgcctcgga cagtcacatt cacactcgca ctcggatgaa 1320
 atctcacata atatacctgc aaagaagacc aagatatctt tagactatta a 1371

<210> 142

<211> 456
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 142

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

Thr Phe Ile Ala Pro Thr Gln Pro Val Ser Thr Ile Leu Ser Gln Ile
260 265 270

Glu Gln Thr Ile Lys Arg Asn Asp Lys Lys Leu Ile Arg Ile Val Ile
275 280 285

Pro Ser Leu Leu His Pro Ala Met Tyr Pro Pro Lys Met Phe Glu Ser
290 295 300

Ser Glu Ile Ile Gly Leu Met His Gly Val Arg Ser Leu Val Lys Lys
305 310 315 320

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

Thr Pro Pro Leu Leu Val Leu Leu Arg Asn Met Phe Asp Ser Val Ile
340 345 350

Asn Leu Glu Pro Phe Asn Gln Glu Met Thr Glu Phe Leu Glu Arg Val
355 360 365

Tyr Lys Ser Gln Pro Gly Lys Ile Gln His Gly Leu Val His Ile Leu
370 375 380

Lys Leu Pro Val Phe Thr Asp Arg Gly Glu Met Arg Val Leu Lys Ser
385 390 395 400

Glu Trp Ala Phe Lys Asn Gly Arg Lys Lys Phe Glu Ile Glu Gln Trp
405 410 415

Gly Ile Pro Val Asp Asp Ala Glu Gly Ser Ala Ala Ser Glu Gln Ser
420 425 430

His Ser His Ser His Ser Asp Glu Ile Ser His Asn Ile Pro Ala Lys
435 440 445

Lys Thr Lys Ile Ser Leu Asp Tyr
450 455

<210> 143
<211> 1035
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 143
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tcattgagtt tattggctgc tgcacaaaag ttgtctaacc ctatcacagc tgtaatcaca 180
ggtagcaaag ctgaaaaaac tgctgaggcg ctaaaatctt catattcatg cagcaattta 240
gaaaagcttg tcatatttga agattcaaaa ttagatacct gtcttcccga acaactaact 300

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ccgttattag tgaactatt aaaaggcggc gactattcac attttgttgt ctcaaactcc 360
tctgttgga aaagtgtttt acctcgggtg ggtgcgctct tggacgtcca acctgtttgt 420
gaggttactg taatcaaaga tcctaagacc ttataaggc caatttatgc aggtaacatt 480
atttctacaa tagaatgcca ggcagaaaaa aaactgttga ttattagggc atcagctttt 540
ccaccaattg cagagggtag tatggattct gttaccattg agaagagaac tgatattcct 600
ccttgtgact taaatgttac ctgggttaaa actattctta ccaagagtga aaggcctgaa 660
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<210> 144
 <211> 344
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 144

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1 5 10 15

Phe Leu Gln Lys Asn Tyr Ala Ser Thr Leu Ala Phe Ile Glu Ser Ser
20 25 30

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

Gln Lys Leu Ser Asn Pro Ile Thr Ala Val Ile Thr Gly Ser Lys Ala
50 55 60

Glu Lys Thr Ala Glu Ala Leu Lys Ser Ser Tyr Ser Cys Ser Asn Leu
65 70 75 80

Glu Lys Leu Val Ile Phe Glu Asp Ser Lys Leu Asp Thr Cys Leu Pro
85 90 95

Glu Gln Leu Thr Pro Leu Leu Val Lys Leu Leu Lys Gly Gly Asp Tyr
100 105 110

Ser His Phe Val Val Ser Asn Ser Ser Val Gly Lys Ser Val Leu Pro
115 120 125

Arg Val Gly Ala Leu Leu Asp Val Gln Pro Val Cys Glu Val Thr Val
130 135 140

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

Ile Ser Thr Ile Glu Cys Gln Ala Glu Lys Lys Leu Leu Ile Ile Arg
165 170 175

Ala Ser Ala Phe Pro Pro Ile Ala Glu Gly Ser Met Asp Ser Val Thr
180 185 190

Ile Glu Lys Arg Thr Asp Ile Pro Pro Cys Asp Leu Asn Val Thr Trp
195 200 205

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

Gln Asn Val Val Thr Gly Gly Arg Ala Leu Lys Asp Lys Glu Thr Phe
225 230 235 240

Glu Lys Leu Leu Ser Pro Leu Ala Asp Val Leu His Ala Ala Ile Gly
245 250 255

Ala Thr Arg Ala Ser Val Asp Asn Gly Leu Cys Asp Asn Ser Leu Gln
260 265 270

Ile Gly Gln Thr Gly Lys Val Val Ala Pro Asn Leu Tyr Ile Ala Ile
275 280 285

Gly Val Ser Gly Ala Val Gln His Leu Ala Gly Met Lys Asp Ser Lys
290 295 300

Val Ile Val Ala Ile Asn Asn Asp Pro Asp Ala Pro Ile Phe Asn Val
305 310 315 320

Ala Asp Tyr Gly Leu Gln Gly Asp Leu Tyr Lys Ile Val Pro Glu Leu
325 330 335

Thr Glu Lys Leu Gly Lys Tyr Lys
340

<210> 145
<211> 1512
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 145
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gggttgactt acaaggggtgt ttacgagtat caatcagttt cctactgtca aaatgaatgc 180
cctggtcagg ctgtcgttgc tcttttcaac ggtacaggtt gctactgtgg tggttccgta 240
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 tccacgcatt acactaccg tgtggtgacg cagtccgtgg tttctcaagc taaccaacaa 840
 gcaagcacga tctttaccac caggacctct gtttatgcaa cagtatcgtc tacgtcctcc 900
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 ggcgccatcg cagggtgctg agtaggtgtg gtttgtggtta cagttgcctt gttggctctg 1020
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 gagacaaagc agtaccagcc gtactcactg ggtgatgctg acgctaacc tgttattcca 1140
 ccgtctgctt cgagcactaa ctggcacata ccctctagga ataatacagc attgtccaag 1200
 aatacagcgt ctacttttgc cacttatgat ctgccgacaa gggcgccggg cggcagagat 1260
 tctattatta ctggtgatgc acataatatc agcaaaagaa gtcactttcc ctcggtagt 1320
 tacgaggagc ctcttcgat ctataacggg aaccaaagg tcatgtgtac ttcgctgccc 1380
 gatatgatgg aagaaagaca actacacatt gtcaaccccg ataatgtgag ttcaaata 1440
 gggagtaatg tctcagatgg tgatgatgat tacgatgatg caaaggattc caataatagt 1500
 tctttgcgct ga 1512

<210> 146
 <211> 503
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 146

Met His Leu Asp Leu Ile His Lys Ser Phe Ile Leu Val Trp Leu Ile
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Tyr Ile Arg Ala Ala Leu Ala Asp Gln Phe Thr Tyr Lys Ala Cys Tyr
 20 25 30

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

Glu Tyr Gln Ser Val Ser Tyr Cys Gln Asn Glu Cys Pro Gly Gln Ala
 50 55 60

Val Val Ala Leu Phe Asn Gly Thr Gly Cys Tyr Cys Gly Gly Ser Val
 65 70 75 80

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Ala Gln Leu Gln Ser₈₅ Leu Thr Gln Val Asp₉₀ Ser Ser Lys Cys Asp₉₅ Val
 Ser Cys Ala Gly₁₀₀ Trp Pro Tyr Gln Asn₁₀₅ Cys Gly Gly Ser₁₁₀ Ala Met
 Asn Val Tyr₁₁₅ Ile Asn Asn Ala Ala₁₂₀ Ser Thr Ala Asp₁₂₅ Ser Thr Ser Ser
 Thr Ala₁₃₀ Thr Ser Thr Ser Thr₁₃₅ Thr Ser Ser Ser Ser₁₄₀ Thr Ser Val Ser
 Ser₁₄₅ Lys Thr Ser Thr Lys₁₅₀ Leu Asp Thr Lys Thr₁₅₅ Ser Thr Ser Ser Ser₁₆₀
 Ala Thr His Ser Ser₁₆₅ Ser Ser Ser Ser Ser Thr₁₇₀ Thr Ser Thr Thr Thr₁₇₅ Ser
 Ser Ser Glu Thr₁₈₀ Thr Thr Ser Ser Ser₁₈₅ Ser Ser Ser Ser Ser₁₉₀ Ser Ser
 Thr Ser Thr₁₉₅ Thr Ser Thr Thr Ser₂₀₀ Thr Thr Ser Ser Thr₂₀₅ Thr Ser Thr
 Ser Ser₂₁₀ Ser Pro Ser Thr Thr₂₁₅ Ser Ser Ser Thr Ser₂₂₀ Ala Ser Ser Ser
 Ser₂₂₅ Glu Thr Ser Ser Thr₂₃₀ Gln Ala Thr Ser Ser₂₃₅ Ser Thr Thr Ser Thr₂₄₀
 Ser Ser Ser Thr Ser₂₄₅ Thr Ala Thr Val Thr₂₅₀ Ser Thr Pro Ser Ser₂₅₅ Thr
 Ser Ile Gly Thr₂₆₀ Ser Thr His Tyr Thr₂₆₅ Thr Arg Val Val Thr₂₇₀ Gln Ser
 Val Val Ser₂₇₅ Gln Ala Asn Gln Gln₂₈₀ Ala Ser Thr Ile Phe₂₈₅ Thr Thr Arg
 Thr Ser₂₉₀ Val Tyr Ala Thr Val₂₉₅ Ser Ser Thr Ser Ser₃₀₀ Ser Thr Ser Ser
 Leu₃₀₅ Leu Asn Gly Lys Ser₃₁₀ Ser Ser Ser Lys Ser₃₁₅ Lys Gly Leu Ser Gly₃₂₀
 Gly Ala Ile Ala Gly₃₂₅ Val Val Val Gly Val₃₃₀ Val Cys Gly Thr Val₃₃₅ Ala
 Leu Leu Ala Leu₃₄₀ Ala Leu Phe Phe Phe₃₄₅ Val Trp Lys Lys Arg₃₅₀ Arg Gln

Ser Ser Gln His Val Asp Leu Glu Glu Thr Lys Gln Tyr Gln Pro Tyr
 355 360 365

Ser Leu Gly Asp Ala Asp Ala Asn Pro Val Ile Pro Pro Ser Ala Ser
 370 375 380

Ser Thr Asn Trp His Ile Pro Ser Arg Asn Asn Thr Ala Leu Ser Lys
 385 390 395 400

Asn Thr Ala Ser Thr Phe Ala Thr Tyr Asp Leu Pro Thr Arg Ala Pro
 405 410 415

Gly Gly Arg Asp Ser Ile Ile Thr Gly Asp Ala His Asn Ile Ser Lys
 420 425 430

Arg Ser His Phe Pro Ser Val Val Tyr Glu Glu Pro Pro Ser Ile Tyr
 435 440 445

Asn Gly Asn Gln Arg Phe Ser Ala Thr Ser Leu Pro Asp Met Met Glu
 450 455 460

Glu Arg Gln Leu His Ile Val Asn Pro Asp Asn Val Ser Ser Asn Ile
 465 470 475 480

Gly Ser Asn Val Ser Asp Gly Asp Asp Asp Tyr Asp Asp Ala Lys Asp
 485 490 495

Ser Asn Asn Ser Ser Leu Arg
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<210> 147
 <211> 1494
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 147
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 tctcaagatg aagatagtct acctaacaat acaaacttaa tcaaagaaat tgactggcag 180
 ggcgagaaaag ttaaaacata tccactaaac tatcaaactg taccactagt aaagctgcag 240
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 ttagcaactg caccttctag tttctatggt tgatgttttt gtggccttcc tcttggttta 540
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 aatgaactca tgggtatcat gcatggtctt tacggggcag cagctatggt tactcctccc 660
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gataactcgc tgatggaatc taccaaggcg agcccaggat tttttgaact ttttaagaaat      900
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gccgtcgccg ttggtggttg tgggtgtgca gccattccat atttggctgg agttattgca     1380
cacacagtgg gaatccagta tatcccacta ttgtgttgga ttatggttgc gttatttaca     1440
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<210> 148
 <211> 497
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 148

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Thr Thr Glu Ile Ser His His Asn Pro Ile Glu Leu Lys Asn Leu Leu
 20 25 30

Ser Ser Ser Asp Ser Arg Arg Asn Ser Gln Asp Glu Asp Ser Leu Pro
 35 40 45

Asn Asn Thr Asn Leu Ile Lys Glu Ile Asp Trp Gln Gly Glu Lys Val
 50 55 60

Lys Thr Tyr Pro Leu Asn Tyr Gln Thr Val Pro Leu Val Lys Leu Gln
 65 70 75 80

Val Ile Ala Cys Leu Ile Met Phe Val Val Phe Gly Met Asn Asp Gln
 85 90 95

Thr Val Gly Ala Leu Leu Pro Thr Leu Ile Glu Tyr Tyr His Ile Ser
 100 105 110

Arg Val Asp Val Ser Asn Val Phe Ile Val Gln Leu Cys Gly Tyr Val
 115 120 125

Met Ala Ser Leu Ser Lys Glu Arg Leu Asn Lys His Phe Gly Met Arg
 130 135 140

Gly 145 Gly Met Leu Leu Ala 150 Ala Gly Leu Cys Ile 155 Val Phe Leu Ile Ile 160
 Leu Ala Thr Ala Pro 165 Ser Ser Phe Tyr Val 170 Cys Met Phe Cys Gly 175 Leu
 Pro Leu Gly Leu 180 Gly Ile Gly Ile Leu 185 Asp Ser Thr Gly Asn Val 190 Leu
 Met Gly Ser 195 Leu Leu Val His Lys 200 Asn Glu Leu Met Gly 205 Ile Met His
 Gly Leu Tyr Gly Ala Ala Ala 215 Met Val Thr Pro Pro 220 Leu Val Ser Tyr
 Phe Val Glu Trp Gly His 230 Trp Ser Leu Phe Phe 235 Leu Ile Pro Leu Phe 240
 Phe Ser Ile Ile Gly 245 Met Ile Val Ile Phe 250 Pro Ala Phe Lys Phe 255 Glu
 Thr Ala Ser Lys 260 Tyr Asp Tyr Leu Cys 265 Ser Val Glu Asn Lys 270 Glu Ser
 Asn Asn Asp Val Glu Glu Ala Gly 280 Asp Asn Ser Leu Met 285 Glu Ser Thr
 Lys Ala Ser Pro Gly Phe Phe 295 Glu Leu Leu Arg Asn 300 Pro Ala Ile Phe
 Leu Tyr Ser Leu Tyr Leu Phe Leu Tyr Leu Gly 315 Ala Glu Ile Thr Thr 320
 Gly Ser Trp Phe Phe 325 Ser Tyr Leu Leu Glu 330 Thr Lys Ser Ser Asn Lys 335
 Val Ala Met Ser 340 Tyr Ile Ala Ala Ser 345 Phe Trp Thr Gly Leu Thr Val 350
 Gly Arg Leu 355 Cys Leu Gly Phe Val 360 Thr Glu Arg Phe Phe 365 Glu Asn Glu
 Tyr Lys Ala Ser Lys Ala Tyr 375 Ala Phe Leu Thr Leu 380 Ser Ser Tyr Thr
 Leu Phe Val Leu Val Gly 390 Leu Ile Asn Ser Ser 395 Ser Val Phe Tyr Phe 400
 Val Val Leu Phe Phe 405 Val Val Phe Cys Cys 410 Gly Thr Phe Ile Gly 415 Pro

Leu Phe Pro Asn Ala Ser Ile Val Ala Leu Gln Val Leu Pro Lys Arg
 420 425 430

Leu His Val Ser Gly Val Gly Val Ala Val Ala Val Gly Gly Cys Gly
 435 440 445

Gly Ala Ala Ile Pro Tyr Leu Ala Gly Val Ile Ala His Thr Val Gly
 450 455 460

Ile Gln Tyr Ile Pro Leu Leu Cys Trp Ile Met Val Ala Leu Phe Thr
 465 470 475 480

Leu Glu Trp Thr Leu Tyr Pro Lys Phe Ile Lys Gly His Glu Glu Tyr
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Phe

<210> 149
 <211> 3117
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 aactcaaaac ctaatttact tcccgtcta ggacattctg ttaccattct gttgaaaatt 540
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 gtatcaatcc ttttaactag atgtgaaaat tctttaaata attgtgagaa agtgtttggt 1080
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acagtaaatt	tcgaaaactt	ggaaagtacg	aatgctctga	ttgctttacc	aagattatca	1440
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gaagcggtag	ttgaacaaat	aatatattgt	tgtattcagg	ttgttccagt	ggagaaaata	3060
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<210> 150
<211> 1038

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 150

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

Phe Ser Leu Asp Ile Lys Val Asn Lys Leu Thr Asp Ile Arg Glu Leu
 260 265 270

Ser Asp Thr Lys Leu Lys His Glu Ile Asn Gln Ser Phe Met Phe Asn
 275 280 285

Gly Pro Ile Val Leu Leu Arg Thr Asp Gly Lys Thr His Arg Asp Thr
 290 295 300

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

Phe Ile Pro Lys Leu Leu Lys Arg Asn Asn Glu Ser Ile Asp Glu Ala
 325 330 335

Leu Ala Thr Phe Val Ser Ile Leu Leu Thr Arg Cys Glu Asn Ser Leu
 340 345 350

Asn Asn Cys Glu Lys Val Leu Val Ser Thr Leu Val His Leu Glu Arg
 355 360 365

Asp Pro Met Ser Lys Leu Pro Ser His Leu Val Lys Leu Lys Glu Val
 370 375 380

Val Asn Glu Asp Leu His Lys Leu Ser Asp Ile Ile Arg Phe Glu Asn
 385 390 395 400

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

Asn Asn Glu Arg Asp Thr Met Ile Asn Glu Val Val Arg Cys Leu Phe
 420 425 430

Glu Ser Leu Asn Glu Ser Ile Glu Pro Pro Ser Leu Ile Asn His Lys
 435 440 445

Glu Arg Ile Ile Glu Gln Ser Ser Gln Leu Thr Thr Thr Val Asn Phe
 450 455 460

Glu Asn Leu Glu Ser Thr Asn Ala Leu Ile Ala Leu Pro Arg Leu Ser
 465 470 475 480

Glu Asp Met Ser Leu Lys Leu Lys Lys Phe Thr Tyr His Met Gly Ser
 485 490 495

Leu Leu Leu Glu Arg His Ile Leu Asn Asp Val Val Thr Glu Leu Ile
 500 505 510

Ser Glu Gln Val Asp Ser Pro Arg Thr Gln Lys Ile Val Ala Leu Trp
 515 520 525

Leu Ser Thr Asn Phe Ile Lys Ala Met Glu Lys Gln Pro Lys Glu Glu

530

535

540

Glu Val Tyr Leu Gln Phe Glu Ser Asp Ala Asn Tyr Ser Ser Ser Met
 545 550 555 560

Val Glu Glu Val Cys Leu Ile Val Leu Glu Phe Cys Asn Glu Leu Ser
 565 570 575

Gln Asp Ile Ser Met Glu Ile Glu Gly Lys Gly Ile Lys Lys Ser Asp
 580 585 590

Glu Phe Ala Val Cys Thr Val Leu Phe Ser Ile Glu Thr Ile Cys Ala
 595 600 605

Val Met Arg Glu Glu Phe Gln Pro Glu Leu Ile Asp Tyr Ile Tyr Thr
 610 615 620

Val Val Asp Ala Leu Ala Ser Pro Ser Glu Ala Ile Arg Tyr Val Ser
 625 630 635 640

Gln Ser Cys Ala Leu Arg Ile Ala Asp Thr Leu Tyr His Gly Ser Ile
 645 650 655

Pro Asn Met Ile Leu Ser Asn Val Asp Tyr Leu Val Glu Ser Ile Ser
 660 665 670

Ser Arg Leu Asn Ser Gly Met Thr Glu Arg Val Ser Gln Ile Leu Met
 675 680 685

Val Ile Cys Gln Leu Ala Gly Tyr Glu Thr Ile Glu Asn Phe Lys Asp
 690 695 700

Val Ile Glu Thr Ile Phe Lys Leu Leu Asp Tyr Tyr His Gly Tyr Ser
 705 710 715 720

Asp Leu Cys Leu Gln Phe Phe Gln Leu Phe Lys Ile Ile Ile Leu Glu
 725 730 735

Met Lys Lys Lys Tyr Ile Asn Asp Asp Glu Met Ile Leu Lys Ile Ala
 740 745 750

Asn Gln His Ile Ser Gln Ser Thr Phe Ser Pro Trp Gly Met Thr Asp
 755 760 765

Phe Gln Gln Val Leu Asn Ile Leu Asp Lys Glu Thr Gln Val Lys Asp
 770 775 780

Asp Ile Thr Asp Glu Asn Asp Val Asp Phe Leu Lys Asp Asp Asn Glu
 785 790 795 800

Pro Ser Asn Phe Gln Glu Tyr Phe Asp Ser Lys Leu Arg Glu Pro Asp
 805 810 815

Ser Asp Asp Asp Glu Glu Glu Arg Glu Glu Glu Val Glu Gly Ser Ser
 820 825 830
 Lys Glu Tyr Thr Asp Gln Trp Thr Ser Pro Ile Pro Ser Asp Ser Tyr
 835 840 845
 Lys Ile Leu Leu Gln Ile Leu Gly Tyr Gly Glu Arg Leu Leu Thr His
 850 855 860
 Pro Ser Lys Arg Leu Arg Val Gln Ile Leu Ile Val Met Arg Leu Ile
 865 870 875 880
 Phe Pro Leu Leu Ser Thr Gln His Asn Leu Leu Ile Arg Glu Val Ala
 885 890 895
 Ser Thr Trp Asp Ser Ile Ile Gln Cys Val Leu Cys Ser Asp Tyr Ser
 900 905 910
 Ile Val Gln Pro Ala Cys Ser Cys Val Glu Gln Met Ile Lys Tyr Ser
 915 920 925
 Gly Asp Phe Val Ala Lys Arg Phe Ile Glu Leu Trp Gln Lys Leu Cys
 930 935 940
 Gln Asp Ser Phe Ile Leu Lys Glu Leu Arg Ile Asp Pro Thr Val His
 945 950 955 960
 Asn His Glu Lys Lys Ser Ile Ser Lys His Val Lys Phe Pro Pro Val
 965 970 975
 Thr Glu Asn Ala Leu Val Ser Met Val His Met Val Leu Glu Gly Val
 980 985 990
 Lys Ile Thr Glu Tyr Leu Ile Ser Glu Ala Val Leu Glu Gln Ile Ile
 995 1000 1005
 Tyr Cys Cys Ile Gln Val Val Pro Val Glu Lys Ile Ser Ser Met
 1010 1015 1020
 Ser Leu Ile Val Gly Asp Ile Val Trp Lys Ile Arg Asn Ile Asn
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<210> 151
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 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 taccaggatt cttcaaagaa gtcattgaaa ttctggcaaa aatcaactga aataattaaa 180
 Seite 165

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ccgtatccaa atgaagataa tgtcatattht tggatggact cttctgccgt aaacgaatgt 360
caatggctaa atatgcaatg tccacaacag cttttggatt atttgggagg aaaatttgta 420
cccgaaatgg gcgtccccaattgaagtac ttttttagatg aatactctca tttacgagac 480
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gaatggaaca ttgaaggact tttgggaaga gaaaatctta atggatatagg caatgatgga 600
gaggtatctg gctggtcatt ttcattttac aaaaacatta taaatttacc atctaattga 660
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<210> 152
 <211> 542
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 152

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Met Ala Gln Glu Pro Val Pro Tyr Tyr Gln Asp Ser Ser Lys Lys Ser
 35 40 45

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

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Cys Ala Arg Lys Ile Leu Lys Asp Gly Ala Asp Ile Tyr Gln Val Leu
325 330 335

Glu Gln Thr Ile Arg Asp Ile Glu Lys Asn Asn Gly Leu Ser Ile His
340 345 350

Ile Leu Thr Lys Asp Met Phe Phe Tyr Gly Asp Tyr Glu Gly Asn Arg
355 360 365

Thr Pro Phe Ala Asp Pro Arg Ile Lys Gly Ser Phe Ile Gly Glu Ser
370 375 380

Thr Asp Thr Ser Met Leu Asn Leu Thr Tyr Lys Tyr Ile Cys Ile Leu
385 390 395 400

Glu Phe Leu Ser Phe Gln Thr Lys Leu Ile Ile Asp Thr Phe Gln Asn
405 410 415

Glu Asn Ser Asn Ile His Ile Lys Glu Leu Arg Ile Ser Gly Ser Gln
420 425 430

Ala Lys Asn Glu Arg Leu Leu Ser Leu Ile Ser Leu Val Asn Asn Gly
435 440 445

Val Ala Ile Ile Lys Pro Lys Glu Asn Val Asp Met Met Gly Ile Lys
450 455 460

Gly Ala Tyr Val Leu Ala Lys Ser Ala Lys Glu Lys Lys Gln Leu Ala
465 470 475 480

Asp Val Ile Thr Glu Arg Asp Ile Ser Asn Asp Ser Glu Lys Phe Glu
485 490 495

Ser Leu Ala Glu Tyr Arg Leu Gly Asn Asp Ser Ile Leu Leu Arg Lys
500 505 510

Leu Leu Cys Val Lys Tyr His Ile His Leu Asp Met Ala Lys Gln Gln
515 520 525

Lys Arg Tyr His Lys Leu Val Asp Glu Val Phe Gln His Leu
530 535 540

<210> 153
<211> 1035
<212> DNA
<213> Saccharomyces cerevisiae

<400> 153
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ccattgacat aactggcaa aaaatttcac ccaacacatc aaatcatcga aactaagcca 120
tcgacactat acagacaaga atgggggttg aaatccgcta ttccttcgaa aattaaatct 180

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cgatatttgg tgtacaacga tttggatacg ttggaaagaa ttaccacatt cgaacctaga 240
 ggcggtacgc aatggaatag gctaagattt caagaaatgg gagtaccat tgtgtctaat 300
 ataggcagac aaaatccatt tttcaagtac atatctcgtc ctgaggatga gtctcatgct 360
 aaattgtcct tattcaaaga aatgaaagga gatacagata tttcgctgc tgctatgaag 420
 aagcgtttga agaagataac agcactaatt agatcgtttc aagatgaatt taaagagtgg 480
 ctgggtgaaa atcatccgga tgaattgaaa ttgaattcta ataagctgga agactatgta 540
 gtgaagtttc taaacaaaaa gttggaaaca aaaacgaata aaaaatttaa cactgaaatc 600
 attggtacag gtggattatc atacagcttg ccaggaaagc taaaaaactc accaaatggt 660
 gtcattcaaa ggactgtagt acccggtaga atcttgaacg ttgttaagga gaacaacgac 720
 aataaatggc tggcagctat tgggtgggtt gtggccgatg tggatTTTTT ccaatcacca 780
 cctagttcct ttaactccat gggagatttc atcagaatga aaacgttctt gttcgagatc 840
 ttggaggcat ctatggagaa aaatggttct gtttcgatgc acgctagatt actcgaacca 900
 caaaatgaca agaccagaga atttttcaat aagagaccaa tttataaacc attgacctct 960
 agaagggcac gtcgaccatc agtgggaaac attcaagagg ccaataacct tttgaatata 1020
 atcaaggga attga 1035

<210> 154
 <211> 344
 <212> PRT
 <213> Saccharomyces cerevisiae
 <400> 154

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

Asn Asn His Lys Pro Leu Thr Tyr Thr Gly Lys Lys Phe His Pro Thr
20 25 30

His Gln Ile Ile Glu Thr Lys Pro Ser Thr Leu Tyr Arg Gln Glu Trp
35 40 45

Gly Leu Lys Ser Ala Ile Pro Ser Lys Ile Lys Ser Arg Tyr Leu Val
50 55 60

Tyr Asn Asp Leu Asp Thr Leu Glu Arg Ile Thr Thr Phe Glu Pro Arg
65 70 75 80

Gly Gly Thr Gln Trp Asn Arg Leu Arg Phe Gln Glu Met Gly Val Pro
85 90 95

Ile Val Ser Asn Ile Gly Arg Gln Asn Pro Phe Phe Lys Tyr Ile Ser
100 105 110

Arg Pro Glu Asp Glu Ser His Ala Lys Leu Ser Leu Phe Lys Glu Met
115 120 125

Lys Gly Asp Thr Asp Ile Ser Pro Ala Ala Met Lys Lys Arg Leu Lys
 130 135 140

Lys Ile Thr Ala Leu Ile Arg Ser Phe Gln Asp Glu Phe Lys Glu Trp
 145 150 155 160

Leu Val Glu Asn His Pro Asp Glu Leu Lys Leu Asn Ser Asn Lys Leu
 165 170 175

Glu Asp Tyr Val Val Lys Phe Leu Asn Lys Lys Leu Glu Thr Lys Thr
 180 185 190

Asn Lys Lys Phe Asn Thr Glu Ile Ile Gly Thr Gly Gly Leu Ser Tyr
 195 200 205

Ser Leu Pro Gly Lys Leu Lys Asn Ser Pro Asn Gly Val Ile Gln Arg
 210 215 220

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

Asn Lys Trp Leu Ala Ala Ile Gly Gly Phe Val Ala Asp Val Val Phe
 245 250 255

Phe Gln Ser Pro Pro Ser Ser Phe Asn Ser Met Gly Asp Phe Ile Arg
 260 265 270

Met Lys Thr Phe Leu Phe Glu Ile Leu Glu Ala Ser Met Glu Lys Asn
 275 280 285

Gly Ser Val Ser Met His Ala Arg Leu Leu Glu Pro Gln Asn Asp Lys
 290 295 300

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

Arg Arg Ala Arg Arg Pro Ser Val Gly Asn Ile Gln Glu Ala Asn Asn
 325 330 335

Leu Leu Asn Ile Ile Lys Gly Asn
 340

<210> 155
 <211> 1008
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 155
 atgttgaggt tatctttact gagatcaaca gctactttgc cagtgaaatg ccaacgtcgt 60
 gggctaatat tacctgcggc ggcaatgtac acctaggct cattaatatt tggttaaggaa 120
 gcaaggttgg cggatgccat ggaacgtggt gagttacata acaagaacgt tgattatgcg 180

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aaagaagctg aagagcgtac cgagttacgt attagggccc tggctaatac tcggccaatg 240
 gaacctcggg acaacggcca tgttcccctt catcgggtacg agaaattgct gctgtttgca 300
 atttccgggt ggaattcatt tttccatcct gaagatgggt ataatattgt acaattgggt 360
 gaggcaactg cattgccggg cttcttggag aatttgaagc aaacaatgtt aagtgattcc 420
 tctggggaggc gcattttgaa ggaacaaccc aatatcaca cagagatttt gcatatggac 480
 aaactagcta aattgccaca taacacgttt gggatatgtat attaccaatg gttgaaaaga 540
 gaaaacgttt ctccggacac tagagcacct gtcaaattta tcgacgatcc tatgcatgca 600
 tatatcttta agaggtatag acaatgccac gatttctatc acgctataac caacatgcct 660
 attatcattg agggggagat caccataaag gctcttgaag gtgccaacct gggcgtccca 720
 atggccattc tcggtgggtat cttgcacct ttacgtttga aaaaggtgca aagaaaaaga 780
 ttatataata tatatctccc ttgggctgtc agaacagggt taagctgcaa gccattgatc 840
 aacgtgtatt gggaggaaat gctggagaag gatgttactg ctttgaggaa agagctaaag 900
 ataacactcc ctccggatct aaggacaatg aggaaggagc gtgcagccct taggaaggag 960
 attgacgcaa aatacaactc acagaaacga gccacgactc cagcatga 1008

<210> 156
 <211> 335
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 156

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

Cys Gln Arg Arg Gly Leu Ile Leu Pro Ala Ala Ala Met Tyr Thr Leu
 20 25 30

Gly Ser Leu Ile Phe Gly Lys Glu Ala Arg Leu Ala Asp Ala Met Glu
 35 40 45

Arg Gly Glu Leu His Asn Lys Asn Val Asp Tyr Ala Lys Glu Ala Glu
 50 55 60

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

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

Leu Leu Phe Ala Ile Ser Gly Trp Asn Ser Phe Phe His Pro Glu Asp
 100 105 110

Gly Tyr Asn Ile Val Gln Leu Gly Glu Ala Thr Ala Leu Pro Val Phe
 115 120 125

Leu Glu Asn Leu Lys Gln Thr Met Leu Ser Asp Ser Ser Gly Arg Arg

130

135

140

Ile Leu Lys Glu Gln Pro Asn Ile Thr Thr Glu Ile Leu His Met Asp
 145 150 155 160

Lys Leu Ala Lys Leu Pro His Asn Thr Phe Gly Tyr Val Tyr Tyr Gln
 165 170 175

Trp Leu Lys Arg Glu Asn Val Ser Pro Asp Thr Arg Ala Pro Val Lys
 180 185 190

Phe Ile Asp Asp Pro Met His Ala Tyr Ile Phe Lys Arg Tyr Arg Gln
 195 200 205

Cys His Asp Phe Tyr His Ala Ile Thr Asn Met Pro Ile Ile Ile Glu
 210 215 220

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

Met Ala Ile Leu Gly Gly Ile Leu Ala Pro Leu Arg Leu Lys Lys Val
 245 250 255

Gln Arg Lys Arg Leu Tyr Asn Ile Tyr Leu Pro Trp Ala Val Arg Thr
 260 265 270

Gly Leu Ser Cys Lys Pro Leu Ile Asn Val Tyr Trp Glu Glu Met Leu
 275 280 285

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

Pro Asp Leu Arg Thr Met Arg Lys Glu Arg Ala Ala Leu Arg Lys Glu
 305 310 315 320

Ile Asp Ala Lys Tyr Asn Ser Gln Lys Arg Ala Thr Thr Pro Ala
 325 330 335

<210> 157
 <211> 2142
 <212> DNA
 <213> Escherichia coli

<400> 157
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 gaactggagt cggcgctggt ggcgcaaggc tttagatta tctggccaca aaacagcggtt 120
 gatttgctga aatttatcga gcataaccct cgaatttgcg gcgtgatttt tgactgggat 180
 gagtacagtc tcgatttatg tagcgatatc aatcagctta atgaatatct cccgctttat 240
 gccttcatca acaccactc gacgatggat gtcagcgtgc aggatatgcg gatggcgctc 300
 tggttttttg aatatgcgct ggggcaggcg gaagatatcg ccattcgtat gcgtcagtag 360

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accgacgaat atcttgataa cattacaccg ccgttcacga aagccttggtt tacctacgtc	420
aaagagcggg agtacacctt ttgtacgccg gggcatatgg gcggcaccgc atatcaaaaa	480
agcccgggtt gctgtctggt ttatgatttt ttcggcgggg atactcttaa ggctgatgtc	540
tctatttcgg tcaccgagct tgggtcgttg ctcgaccaca ccgggccaca cctggaagcg	600
gaagagtaca tcgcgcggac ttttggcgcg gaacagagtt atatcgttac caacggaaca	660
tcgacgtcga acaaaattgt gggatatgtac gccgcgccat ccggcagtac gctgttgatc	720
gaccgcaatt gtcataaatc gctggcgcgt ctgttgatga tgaacgatgt agtgccagtc	780
tggctgaaac cgacgcgtaa tgcgttgggg attcttgggt ggatcccgcg ccgtgaattt	840
actcgcgaca gcatcgaaga gaaagtcgct gctaccacgc aagcacaatg gccggttcatt	900
gcggtgatca ccaactccac ctatgatggc ttgctctaca acaccgactg gatcaaacag	960
acgctggatg tcccgtcgat tcacttcgat tctgcctggg tgccgtacac ccattttcat	1020
ccgatctacc agggtaaaag tggatatgagc ggcgagcgtg ttgcgggaaa agtgatcttc	1080
gaaacgcaat cgaccacaaa aatgctggcg gcgttatcgc aggcttcgct gatccacatt	1140
aaaggcgagt atgacgaaga ggcctttaac gaagccttta tgatgcatac caccacctcg	1200
cccagttatc ccattgttgc ttcggttgag acggcggcgg cgatgctgcg tggtaatccg	1260
ggcaaacggc tgattaaccg ttcagtagaa cgagctctgc attttcgcaa agaggtccag	1320
cggctgcggg aagagtctga cggttggttt ttcgatatct ggcaaccgcc gcaggtggat	1380
gaagccgaat gctggcccg tgcgcctggc gaacagtggc acggctttaa cgatgcggat	1440
gccgatcata tgtttctcga tccggttaaa gtcactatct tgacaccggg gatggacgag	1500
cagggcaata tgagcgagga ggggatcccg gcggcgctgg tagcaaaatt cctcgacgaa	1560
cgtgggatcg tagtagagaa aaccggccct tataacctgc tgtttctctt tagtattggc	1620
atcgataaaa ccaaagcaat gggattattg cgtgggttga cggaattcaa acgctcttac	1680
gatctcaacc tgcggatcaa aaatatgcta cccgatctct atgcagaaga tcccgatttc	1740
taccgcaata tgcgtattca ggatctggca caagggatcc ataagctgat tcgtaaacac	1800
gatcttcccg gtttgatgtt gcgggcattc gatactttgc cggagatgat catgacgcca	1860
catcaggcat ggcaacgaca aattaaaggc gaagtagaaa ccattgcgct ggaacaactg	1920
gtcggtagag tatcggaata tatgatcctg ctttatccac cgggcgtacc gctgttgatg	1980
cctggagaaa tgctgaccaa agagagccgc acagtactcg attttctact gatgctttgt	2040
tccgtcgggc aacattaccc cggttttgaa acggatattc acggcgcgaa acaggacgaa	2100
gacggcgttt accgcgtacg agtcctaaaa atggcgggat aa	2142

<210> 158

<211> 713

<212> PRT

<213> Escherichia coli

<400> 158

Met Asn Ile Ile Ala Ile Met Gly Pro His Gly Val Phe Tyr Lys Asp

1 5 10 15
 Glu Pro Ile Lys₂₀ Glu Leu Glu Ser Ala₂₅ Leu Val Ala Gln Gly₃₀ Phe Gln
 Ile Ile Trp₃₅ Pro Gln Asn Ser Val₄₀ Asp Leu Leu Lys Phe₄₅ Ile Glu His
 Asn Pro₅₀ Arg Ile Cys Gly Val₅₅ Ile Phe Asp Trp Asp₆₀ Glu Tyr Ser Leu
 Asp₆₅ Leu Cys Ser Asp Ile₇₀ Asn Gln Leu Asn Glu₇₅ Tyr Leu Pro Leu Tyr₈₀
 Ala Phe Ile Asn Thr₈₅ His Ser Thr Met Asp₉₀ Val Ser Val Gln Asp₉₅ Met
 Arg Met Ala₁₀₀ Leu Trp Phe Phe Glu Tyr₁₀₅ Ala Leu Gly Gln Ala₁₁₀ Glu Asp
 Ile Ala Ile₁₁₅ Arg Met Arg Gln Tyr₁₂₀ Thr Asp Glu Tyr Leu₁₂₅ Asp Asn Ile
 Thr Pro₁₃₀ Pro Phe Thr Lys Ala₁₃₅ Leu Phe Thr Tyr Val₁₄₀ Lys Glu Arg Lys
 Tyr₁₄₅ Thr Phe Cys Thr Pro₁₅₀ Gly His Met Gly Gly₁₅₅ Thr Ala Tyr Gln Lys₁₆₀
 Ser Pro Val Gly Cys₁₆₅ Leu Phe Tyr Asp Phe₁₇₀ Phe Gly Gly Asn Thr₁₇₅ Leu
 Lys Ala Asp Val₁₈₀ Ser Ile Ser Val Thr₁₈₅ Glu Leu Gly Ser Leu₁₉₀ Leu Asp
 His Thr Gly₁₉₅ Pro His Leu Glu Ala₂₀₀ Glu Glu Tyr Ile Ala₂₀₅ Arg Thr Phe
 Gly Ala Glu Gln Ser Tyr Ile₂₁₅ Val Thr Asn Gly Thr₂₂₀ Ser Thr Ser Asn
 Lys₂₂₅ Ile Val Gly Met Tyr₂₃₀ Ala Ala Pro Ser Gly₂₃₅ Ser Thr Leu Leu Ile₂₄₀
 Asp Arg Asn Cys His₂₄₅ Lys Ser Leu Ala His₂₅₀ Leu Leu Met Met Asn₂₅₅ Asp
 Val Val Pro Val₂₆₀ Trp Leu Lys Pro Thr₂₆₅ Arg Asn Ala Leu Gly₂₇₀ Ile Leu
 Gly Gly Ile₂₇₅ Pro Arg Arg Glu Phe₂₈₀ Thr Arg Asp Ser Ile₂₈₅ Glu Glu Lys

Val Ala Ala Thr Thr Gln Ala Gln Trp Pro Val His Ala Val Ile Thr
 290 295 300
 Asn Ser Thr Tyr Asp Gly Leu Leu Tyr Asn Thr Asp Trp Ile Lys Gln
 305 310 315 320
 Thr Leu Asp Val Pro Ser Ile His Phe Asp Ser Ala Trp Val Pro Tyr
 325 330 335
 Thr His Phe His Pro Ile Tyr Gln Gly Lys Ser Gly Met Ser Gly Glu
 340 345 350
 Arg Val Ala Gly Lys Val Ile Phe Glu Thr Gln Ser Thr His Lys Met
 355 360 365
 Leu Ala Ala Leu Ser Gln Ala Ser Leu Ile His Ile Lys Gly Glu Tyr
 370 375 380
 Asp Glu Glu Ala Phe Asn Glu Ala Phe Met Met His Thr Thr Thr Ser
 385 390 395 400
 Pro Ser Tyr Pro Ile Val Ala Ser Val Glu Thr Ala Ala Ala Met Leu
 405 410 415
 Arg Gly Asn Pro Gly Lys Arg Leu Ile Asn Arg Ser Val Glu Arg Ala
 420 425 430
 Leu His Phe Arg Lys Glu Val Gln Arg Leu Arg Glu Glu Ser Asp Gly
 435 440 445
 Trp Phe Phe Asp Ile Trp Gln Pro Pro Gln Val Asp Glu Ala Glu Cys
 450 455 460
 Trp Pro Val Ala Pro Gly Glu Gln Trp His Gly Phe Asn Asp Ala Asp
 465 470 475 480
 Ala Asp His Met Phe Leu Asp Pro Val Lys Val Thr Ile Leu Thr Pro
 485 490 495
 Gly Met Asp Glu Gln Gly Asn Met Ser Glu Glu Gly Ile Pro Ala Ala
 500 505 510
 Leu Val Ala Lys Phe Leu Asp Glu Arg Gly Ile Val Val Glu Lys Thr
 515 520 525
 Gly Pro Tyr Asn Leu Leu Phe Leu Phe Ser Ile Gly Ile Asp Lys Thr
 530 535 540
 Lys Ala Met Gly Leu Leu Arg Gly Leu Thr Glu Phe Lys Arg Ser Tyr
 545 550 555 560

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Asp Leu Asn Leu Arg Ile Lys Asn Met Leu Pro Asp Leu Tyr Ala Glu
565 570 575

Asp Pro Asp Phe Tyr Arg Asn Met Arg Ile Gln Asp Leu Ala Gln Gly
580 585 590

Ile His Lys Leu Ile Arg Lys His Asp Leu Pro Gly Leu Met Leu Arg
595 600 605

Ala Phe Asp Thr Leu Pro Glu Met Ile Met Thr Pro His Gln Ala Trp
610 615 620

Gln Arg Gln Ile Lys Gly Glu Val Glu Thr Ile Ala Leu Glu Gln Leu
625 630 635 640

Val Gly Arg Val Ser Ala Asn Met Ile Leu Pro Tyr Pro Pro Gly Val
645 650 655

Pro Leu Leu Met Pro Gly Glu Met Leu Thr Lys Glu Ser Arg Thr Val
660 665 670

Leu Asp Phe Leu Leu Met Leu Cys Ser Val Gly Gln His Tyr Pro Gly
675 680 685

Phe Glu Thr Asp Ile His Gly Ala Lys Gln Asp Glu Asp Gly Val Tyr
690 695 700

Arg Val Arg Val Leu Lys Met Ala Gly
705 710

<210> 159
<211> 1590
<212> DNA
<213> Escherichia coli

<400> 159
atgaacaata acgatctggt cgcaagctg tggaagctgt gcgacaacct gcgcgatggc 60
ggcgttttcct atcaaaacta cgtcaatgaa ctcgcctcgc tgctgttttt gaaaatgtgt 120
aaagagaccg gtcaggaagc ggaatacctg ccggaagggt accgctggga tgacctgaaa 180
tcccgcacg gccaggagca gttgcagttc taccgaaaaa tgctcgtgca tttaggcgaa 240
gatgacaaaa agctggtaca ggcagttttt cataatgtta gtaccaccat caccgagccg 300
aaacaaataa ccgcactggt cagcaatatg gattcgcctgg actggtacaa cggcgcgcac 360
ggtaagtcgc gcgatgactt cggcgatatg tacgaagggc tgttgcagaa gaacgcgaat 420
gaaaccaagt ctggtgcagg ccagtacttc acccgcgctc cgctgattaa aaccattatt 480
catctgctga aaccgcagcc gcgtgaagtg gtgcaggacc cggcggcagg tacggcgggc 540
tttttgattg aagccgaccg ctatgttaag tcgcaaacca atgatctgga cgaccttgat 600
ggcgacacgc aggatttcca gatccaccgc gcgtttatcg gcctcgaact ggtgcccggc 660

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acccgtcgtc tggcactgat gaactgcctg ctgcacgata ttgaaggcaa cctcgaccac 720
 ggcggcgcaa tccgtctggg caacactctg ggtagcgacg gtgaaaacct gccgaaggcg 780
 catattgtcg ccactaacc gccgtttggc agcgccgcag gcaccaacat taccgcgacc 840
 tttgttcacc cgaccagcaa caaacagttg tgctttatgc agcatattat cgaaacgctg 900
 catccccggcg gtcgtgcggc ggtggtggtg ccggataacg tgctgtttga aggcggcaaa 960
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 ccgaccggta ttttttacgc tcagggcgctg aagaccaacg tgctgttctt taccaaaggg 1080
 acggtggcga acccgaatca ggataagaac tgtaccgatg atgtgtgggt gtatgacctg 1140
 cgtaccaata tgccgagttt cggcaagcgc acaccgttta ccgacgagca tttgcagccg 1200
 tttgagcgcg tgtatggcga agaccgcac ggtttaagcc cgcgcactga aggtgaatgg 1260
 agttttaacg ccgaagagac ggaagttgcc gacagcgaag agaacaaaaa caccgaccag 1320
 catcttgcta ccagccgctg gcgcaagttc agccgtgagt ggatccgcac cgcaaaatcc 1380
 gattcgctgg atatctcctg gctgaaagat aaagacagta ttgatgccga cagcctgccg 1440
 gagccggatg tattagcggc agaagcgatg ggcgaactgg tacaggcgct gtctgaactg 1500
 gatgcgctga tgcgtgaact gggggcgagc gatgaggccg atttgcagcg tcagttgctg 1560
 gaagaagcgt ttggtggggg gaaggaataa 1590

<210> 160
 <211> 529
 <212> PRT
 <213> Escherichia coli

<400> 160

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

Leu Arg Asp Gly Gly Val Ser Tyr Gln Asn Tyr Val Asn Glu Leu Ala
 20 25 30

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

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

Gln Glu Gln Leu Gln Phe Tyr Arg Lys Met Leu Val His Leu Gly Glu
 65 70 75 80

Asp Asp Lys Lys Leu Val Gln Ala Val Phe His Asn Val Ser Thr Thr
 85 90 95

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

Leu Asp Trp Tyr Asn Gly Ala His Gly Lys Ser Arg Asp Asp Phe Gly
 Seite 177

115

120

125

Asp Met Tyr Glu Gly Leu Leu Gln Lys Asn Ala Asn Glu Thr Lys Ser
 130 135 140

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

His Leu Leu Lys Pro Gln Pro Arg Glu Val Val Gln Asp Pro Ala Ala
 165 170 175

Gly Thr Ala Gly Phe Leu Ile Glu Ala Asp Arg Tyr Val Lys Ser Gln
 180 185 190

Thr Asn Asp Leu Asp Asp Leu Asp Gly Asp Thr Gln Asp Phe Gln Ile
 195 200 205

His Arg Ala Phe Ile Gly Leu Glu Leu Val Pro Gly Thr Arg Arg Leu
 210 215 220

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

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

Leu Pro Lys Ala His Ile Val Ala Thr Asn Pro Pro Phe Gly Ser Ala
 260 265 270

Ala Gly Thr Asn Ile Thr Arg Thr Phe Val His Pro Thr Ser Asn Lys
 275 280 285

Gln Leu Cys Phe Met Gln His Ile Ile Glu Thr Leu His Pro Gly Gly
 290 295 300

Arg Ala Ala Val Val Val Pro Asp Asn Val Leu Phe Glu Gly Gly Lys
 305 310 315 320

Gly Thr Asp Ile Arg Arg Asp Leu Met Asp Lys Cys His Leu His Thr
 325 330 335

Ile Leu Arg Leu Pro Thr Gly Ile Phe Tyr Ala Gln Gly Val Lys Thr
 340 345 350

Asn Val Leu Phe Phe Thr Lys Gly Thr Val Ala Asn Pro Asn Gln Asp
 355 360 365

Lys Asn Cys Thr Asp Asp Val Trp Val Tyr Asp Leu Arg Thr Asn Met
 370 375 380

Pro Ser Phe Gly Lys Arg Thr Pro Phe Thr Asp Glu His Leu Gln Pro
 385 390 395 400

Phe Glu Arg Val Tyr Gly Glu Asp Pro His Gly Leu Ser Pro Arg Thr
 405 410 415

Glu Gly Glu Trp Ser Phe Asn Ala Glu Glu Thr Glu Val Ala Asp Ser
 420 425 430

Glu Glu Asn Lys Asn Thr Asp Gln His Leu Ala Thr Ser Arg Trp Arg
 435 440 445

Lys Phe Ser Arg Glu Trp Ile Arg Thr Ala Lys Ser Asp Ser Leu Asp
 450 455 460

Ile Ser Trp Leu Lys Asp Lys Asp Ser Ile Asp Ala Asp Ser Leu Pro
 465 470 475 480

Glu Pro Asp Val Leu Ala Ala Glu Ala Met Gly Glu Leu Val Gln Ala
 485 490 495

Leu Ser Glu Leu Asp Ala Leu Met Arg Glu Leu Gly Ala Ser Asp Glu
 500 505 510

Ala Asp Leu Gln Arg Gln Leu Leu Glu Glu Ala Phe Gly Gly Val Lys
 515 520 525

Glu

<210> 161
 <211> 918
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 161
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 atcgtgattg tacctgaatt caaaacctca ttccagttgg attctgcgct aggggaagatg 180
 tacagtatta ccagggatgt ccttttgggc tatggaatga tcaacagcgg aatcaacatc 240
 atattcaaca atattcattt cgtcgagagt aatttgcaat ggaaagtggg tttattgccca 300
 caggaatcca cttttgaaac ttggaagcta gagttgggac aaggacaata ccatagtata 360
 gaacattatg cattacacga taatataatg gaagagatag aagggtccca agatgctaac 420
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 35 40 45

Thr Ser Phe Gln Leu Asp Ser Ala Leu Gly Lys Met Tyr Ser Ile Thr
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Arg Asp Val Leu Leu Gly Tyr Gly Met Ile Asn Ser Gly Ile Asn Ile
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Ile Phe Asn Asn Ile His Phe Val Glu Ser Asn Leu Gln Trp Lys Val
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Val Leu Leu Pro Gln Glu Ser Thr Phe Glu Thr Trp Lys Leu Glu Leu
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Gly Gln Gly Gln Tyr His Ser Ile Glu His Tyr Ala Leu His Asp Asn
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Ile Met Glu Glu Ile Glu Gly Pro Lys Asp Ala Asn Lys Phe His Val
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Thr Ala Leu Gly Gly Thr Phe Asp His Ile His Asp Gly His Lys Ile
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Leu Leu Ser Val Ser Thr Phe Ile Thr Ser Gln Arg Leu Ile Cys Gly
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Ile Thr Cys Asp Glu Leu Leu Gln Asn Lys Lys Tyr Lys Glu Leu Ile
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Glu Pro Tyr Asp Thr Arg Cys Arg His Val His Gln Phe Ile Lys Leu
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Leu Lys Pro Asp Leu Ser Val Glu Leu Val Pro Leu Arg Asp Val Cys
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Gly Pro Thr Gly Lys Val Pro Glu Ile Glu Cys Leu Val Val Ser Arg
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Glu Thr Val Ser Gly Ala Glu Thr Val Asn Lys Thr Arg Ile Glu Lys
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Gly Met Ser Pro Leu Ala Val His Val Val Asn Val Leu Gly Gly Arg
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Glu Glu Asp Gly Trp Ser Glu Lys Leu Ser Ser Thr Glu Ile Arg Arg
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Leu Leu Lys Ser Ser Ala Ser Pro Thr Cys Thr Pro Gln Asn Pro Cys
 290 295 300

Val
 305