

**SEQ ID NO: 1**

<211> 780

<212> DNA

<213> Escherichia coli

<400> 1

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atgactgatac tgaagcaag cagcctgcgt gcactgaaat tgatggacct gaccacctg   60
aatgacgacg acaccgacga gaaagtgate gccctgtgtc atcaggccaa aactccggtc   120
ggcaataaccg ccgtatctg tatctatcct cgtttatcc cgattgctcg caaaactctg   180
aaagagcagg gcaccccgga aatccgtatc gctacggtaa ccaactccc acacggtaac   240
gacgacatcg acatgcgct ggcagaaacc cgtgcggcaa tcgcctacgg tgctgatgaa   300
gttgacgttg tgtcccgta ccgcgcgctg atggcgggta acgagcaggt tggttttgac   360
ctggtgaaag cctgtaaaga ggcttgcgcg gcagcgaatg tactgctgaa agtgatcatc   420
gaaaccggcg aactgaaaga cgaagcgtg atccgtaaag cgtctgaaat ctccatcaaa   480
gcgggtgcgg acttcatcaa aacctctacc ggtaaagtgg ctgtgaacgc gacgccggaa   540
agcgcgcgca tcgatgga agtgatccgt gatatggcg tagaaaaaac cgttggttc   600
aaaccggcgg gcggcgtgcg tactgcggaa gatgcgcaga aatatctgc cattgcagat   660
gaactgttcg gtgctgactg ggcagatgcg cgtcactacc gctttggcgc ttccagcctg   720
ctggcaagcc tctgaaagc gctgggtcac ggcgacggta agagcgccag cagctactaa   780
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**SEQ ID NO: 2**

<211> 259

<212> PRT

<213> Escherichia coli

<400> 2

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Met Thr Asp Leu Lys Ala Ser Ser Leu Arg Ala Leu Lys Leu Met Asp
1         5         10        15
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```
Leu Thr Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ile Ala Leu
20        25        30
```

```
Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile
35        40        45
```

Tyr Pro Arg Phe Ile Pro Ile Ala Arg Lys Thr Leu Lys Glu Gln Gly  
50 55 60

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

Asp Asp Ile Asp Ile Ala Leu Ala Glu Thr Arg Ala Ala Ile Ala Tyr  
85 90 95

Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala  
100 105 110

Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala  
115 120 125

Cys Ala Ala Ala Asn Val Leu Leu Lys Val Ile Ile Glu Thr Gly Glu  
130 135 140

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

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

Ala Thr Pro Glu Ser Ala Arg Ile Met Met Glu Val Ile Arg Asp Met  
180 185 190

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

Ala Glu Asp Ala Gln Lys Tyr Leu Ala Ile Ala Asp Glu Leu Phe Gly  
210 215 220

Ala Asp Trp Ala Asp Ala Arg His Tyr Arg Phe Gly Ala Ser Ser Leu  
225 230 235 240

Leu Ala Ser Leu Leu Lys Ala Leu Gly His Gly Asp Gly Lys Ser Ala  
245 250 255

Ser Ser Tyr

**SEQ ID NO: 3**

<211> 663

<212> DNA

<213> Unknown

<220>

<223> "Cloned"

<400> 3

atgaatatcg cgaaatgat cgatcatacg ctgctcaaac cggaagcgac agaacaacaa 60

atcgtgcaac tgtgcacgga agcaaagcaa tacggctttg ctgccgtgtg cgtcaacca 120

acgtgggtga aaacggcggc gcgcgagctt tccggcacgg atgtccgctg ctgcacggtc 180

atcggctttc cacttggggc aacgacgccg gaaacaaagg cgtttgaaac aacgaacgcc 240

atcgaaaacg gcgctcgca agtcgacatg gtgatcaaca tcggcgcggt aaaaagcggg 300

caagacgagc ttgtcagcg cgacattcgt gcggtgtcg aagcggcggc tggcagggcg 360

cttgtcaaag tgatcgtga aacggcgctt ttgaccgatg aggaaaaagt gcgcgcctgc 420

cagctcgag tgaaagccgg cgctgattat gtgaaaacgt cgaccgggtt ttccggcgga 480

ggtgcgacgg tggaggatgt ggcgctgatg cggaaaacgg tcggcgacag agcaggcgtc 540

aaagcatcag gcggcgctcg tgactggaaa accgctgagg cgatgatcaa cgccggcgcg 600

acgcgcatcg gcacaagctc tggggtggcg atcgtcaccg gcgggacggg ccgcgctgac 660

tac

663

**SEQ ID NO: 4**

<211> 663

<212> DNA

<213> Unknown

<220>

<223> "Cloned"

<400> 4  
atgaacatcg cgaatatgat cgtacacacc ctgctgaaac cggaagcgac cgaacagcag 60  
attgttcagc tgtgcaccga agcgaaacag tatggttttg cggcgggtgtg tgtaaatccg 120  
acctggggtta aaaccgcggc gcgtgaactg agcggcaccg atgttcgtgt gtcgaccgtg 180  
attggttttc cgctgggtgc gaccaccccg gaaaccaaag cgtttgaaac caccaacgcg 240  
attgaaaatg gtgcgcgcga agtggatatg gtgattaaca tcggcgcgct gaaaagcgg 300  
caggatgaac tggttgaacg cgtatctgt gcggtgttg aagcggcggc gggtcgcgcg 360  
ctggttaaag tgattgtgga aaccgcgctg ctgaccgatg aagaaaaagt gcgtgcctgt 420  
cagctggcgg ttaaagcggg tgcggattac gttaaaacca gcaccgggtt tagcgggtgt 480  
ggcgcgaccg ttgaagatgt tgcgctgatg cgtaaaaccg ttggtgatcg tgcgggtgtg 540  
aaagcgagcg gtggtgttcg cgattggaaa accgcggaag cgtatgattaa tgcgggcgcg 600  
accgtattg gcaccagcag cgggtgtgcg attgttaccg gtggcaccgg tcgtgcggat 660  
tat 663

**SEQ ID NO: 5**  
<211> 221  
<212> PRT  
<213> Unknown

<220>  
<223> testek

<400> 5

Met Asn Ile Ala Lys Met Ile Asp His Thr Leu Leu Lys Pro Glu Ala  
1 5 10 15

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

Phe Ala Ala Val Cys Val Asn Pro Thr Trp Val Lys Thr Ala Ala Arg  
35 40 45

Glu Leu Ser Gly Thr Asp Val Arg Val Cys Thr Val Ile Gly Phe Pro  
50 55 60

Leu Gly Ala Thr Thr Pro Glu Thr Lys Ala Phe Glu Thr Thr Asn Ala  
65                70                75                80

Ile Glu Asn Gly Ala Arg Glu Val Asp Met Val Ile Asn Ile Gly Ala  
                  85                90                95

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

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

Ala Leu Leu Thr Asp Glu Glu Lys Val Arg Ala Cys Gln Leu Ala Val  
                  130                135                140

Lys Ala Gly Ala Asp Tyr Val Lys Thr Ser Thr Gly Phe Ser Gly Gly  
145                150                155                160

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

Arg Ala Gly Val Lys Ala Ser Gly Gly Val Arg Asp Trp Lys Thr Ala  
                  180                185                190

Glu Ala Met Ile Asn Ala Gly Ala Thr Arg Ile Gly Thr Ser Ser Gly  
                  195                200                205

Val Ala Ile Val Thr Gly Gly Thr Gly Arg Ala Asp Tyr  
                  210                215                220

**SEQ ID NO: 6**

<211> 666

<212> DNA

<213> *Oceanobacillus iheyensis*

<400> 6

atggatttag ctaaatatat tgatcatact caattaaaac cagatactac aaaacaaagt 60

attgtaaaaa ttgtggaaga ggcaaaacaa catgaattg cttcagtatg tgttaatcca 120  
 cactggggtt cttactgtta taatgaatta aaagatacac cagttaaagt ttgtacagta 180  
 attgattcc cattaggagc cacttctact gaaacgaaaa ttttgaaac caatcaggct 240  
 attgctgatg gtgctacaga agtagacatg gtaattaatg tcggtgaatt aaaatcgaat 300  
 aatgatgctt ttgtgaaaa agacatccgt gctgttggtg aagcagcaaa aggtaaagct 360  
 ttaacaaaag tgataattga aacaagtctt ttaacagaag atgaaaaagt acgtgcttgt 420  
 aaattagcaa aaaatgcaga ggctgactat gtaaaaactt ctactgggtt ctctggtggc 480  
 ggcgcaactg ttgaggatat tcgcttaatg cgagagacag taggacctga aatgggagtg 540  
 aaagcatctg gtggtgttcg tgatttagag caaacagaag caatgattga agctggagca 600  
 actagaattg gagctagttc tggggtagcg attgtctcag gagaacaagg tacatcagat 660  
 tactaa 666

**SEQ ID NO: 7**

<211> 221

<212> PRT

<213> *Oceanobacillus iheyensis*

<400> 7

Met Asp Leu Ala Lys Tyr Ile Asp His Thr Gln Leu Lys Pro Asp Thr  
 1 5 10 15

Thr Lys Gln Ser Ile Val Lys Ile Val Glu Glu Ala Lys Gln His Glu  
 20 25 30

Phe Ala Ser Val Cys Val Asn Pro His Trp Val Ser Tyr Cys Tyr Asn  
 35 40 45

Glu Leu Lys Asp Thr Pro Val Lys Val Cys Thr Val Ile Gly Phe Pro  
 50 55 60

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

Ile Ala Asp Gly Ala Thr Glu Val Asp Met Val Ile Asn Val Gly Glu  
85 90 95

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

Val Glu Ala Ala Lys Gly Lys Ala Leu Thr Lys Val Ile Ile Glu Thr  
115 120 125

Ser Leu Leu Thr Glu Asp Glu Lys Val Arg Ala Cys Lys Leu Ala Lys  
130 135 140

Asn Ala Glu Ala Asp Tyr Val Lys Thr Ser Thr Gly Phe Ser Gly Gly  
145 150 155 160

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

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

Glu Ala Met Ile Glu Ala Gly Ala Thr Arg Ile Gly Ala Ser Ser Gly  
195 200 205

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

**SEQ ID NO: 8**

<211> 663

<212> DNA

<213> Deinococcus radiodurans

<400> 8

atgtcactcg cctcctacat cgaccacacg ctgcttaagg ccaccgccac gctcgccgac 60

atccgcacgc tgtgtgagga agcccgcgag cactcgttct acgcggtgtg catcaaccg 120

gtctttattc cccacgcccg cgcttggtc gaaggcagcg acgtgaaggt cgccaccgtc 180

tgcggctttc ccctcggcgc catcagctcc gagcagaaag ctctggaagc ccgcctgagc 240

gccgaaacgg gcgccgacga aatcgatatg gtcattccaca tcggctcggc gcttgccggc 300  
 gactgggacg cgggtgaagc cgactgcgg gcagtgcgcc gcgcggtgcc cgagcaggtg 360  
 ctcaaggtga ttatcgaac ctgctacctg accgacgagc aaaagcgctt ggcgactgag 420  
 gtcgccgtac agggcggcgc cgacttcgtg aagacgagca caggcttcgg caccggcggc 480  
 gccaccgtgg acgacgtgcg cctgatggcg gaagtgatcg ggggccgcgc cggactcaag 540  
 gcggcgggcg gcgtccgcac tcctgccgac gcgcaagcca tgatcgaggc gggcgcgacc 600  
 cggctgggca cctcggggcg cgtaggtctg gtgtcgggcg gcgaaaacgg agccggctac 660  
 tga 663

**SEQ ID NO: 9**

<211> 220

<212> PRT

<213> *Deinococcus radiodurans*

<400> 9

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

Thr Leu Ala Asp Ile Arg Thr Leu Cys Glu Glu Ala Arg Glu His Ser  
 20 25 30

Phe Tyr Ala Val Cys Ile Asn Pro Val Phe Ile Pro His Ala Arg Ala  
 35 40 45

Trp Leu Glu Gly Ser Asp Val Lys Val Ala Thr Val Cys Gly Phe Pro  
 50 55 60

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

Ala Glu Thr Gly Ala Asp Glu Ile Asp Met Val Ile His Ile Gly Ser  
 85 90 95

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



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

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

Gly Gly Ala Asp Phe Val Lys Thr Ser Thr Gly Phe Gly Thr Gly Gly  
145 150 155 160

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

Ala Gly Leu Lys Ala Ala Gly Gly Val Arg Thr Pro Ala Asp Ala Gln  
180 185 190

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

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

**SEQ ID NO: 10**

<211> 675

<212> DNA

<213> *Propionibacterium acnes*

<400> 10

atgtctctg cccactgtc tgccaccgag ttggccggca tgatcatca caccctgctg 60

accctgagg ccaccacaa cgacgtgcc aagctggtcg ccgatgcaa aaaatatggg 120

acgtggtcgg tgtgcgtatc gccatcatg ctgccgttga acctcgacat gggtgacgtg 180

catctggccg tcgtgtcgg gtttccgtca ggcaagcaca ccagcgcagt aaaggctgct 240

gaggctcgtg aggccatcgc cgcaggggcc gaggaggtcg acatggtgat caaccttggg 300

ctggtaaagg agggacgtg ggaggacgtc accgccgata tcgtgccgt caagcaggcc 360

gtcccgatc cgaagatcct taaggtcatt atcgatcgg cgggtgctgac cgacgacgag 420

atcgtgcggg catgccaggc tgccgagaag gccggcgccg acttcgtcaa gacgtcgacg 480  
ggattccacc cacgtggcgg cgcaagcgtc gaggccgtca aggtcatggc tgacactgtt 540  
ggtggacgtc tgggcgtcaa agcgtccggc ggcattccgc actaccagac ggcattgcgcg 600  
atggtcgagg ccggggcgac gcgtctagga gtttcctcga ccgccaagat ccttgccgga 660  
gctccacagg agtga 675

**SEQ ID NO: 11**

<211> 224

<212> PRT

<213> Propionibacterium acnes

<400> 11

Met Ser Ser Ala Pro Leu Ser Ala Thr Glu Leu Ala Gly Met Ile Asp  
1 5 10 15

His Thr Leu Leu Thr Pro Glu Ala Thr His Asn Asp Val Ala Lys Leu  
20 25 30

Val Ala Asp Ala Lys Lys Tyr Gly Thr Trp Ser Val Cys Val Ser Pro  
35 40 45

Ser Met Leu Pro Leu Asn Leu Asp Met Gly Asp Val His Leu Ala Val  
50 55 60

Val Cys Gly Phe Pro Ser Gly Lys His Thr Ser Ala Val Lys Ala Ala  
65 70 75 80

Glu Ala Arg Glu Ala Ile Ala Ala Gly Ala Glu Glu Val Asp Met Val  
85 90 95

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

Asp Ile Ala Ala Val Lys Gln Ala Val Pro Asp Pro Lys Ile Leu Lys  
115 120 125

Val Ile Ile Glu Ser Ala Val Leu Thr Asp Asp Glu Ile Val Arg Ala  
130 135 140

Cys Gln Ala Ala Glu Lys Ala Gly Ala Asp Phe Val Lys Thr Ser Thr  
145 150 155 160

Gly Phe His Pro Arg Gly Gly Ala Ser Val Glu Ala Val Lys Val Met  
165 170 175

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

Arg Asp Tyr Gln Thr Ala Cys Ala Met Val Glu Ala Gly Ala Thr Arg  
195 200 205

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

**SEQ ID NO: 12**

<211> 768

<212> DNA

<213> *Chromobacterium violaceum*

<400> 12

atgtctgcac tgattgaage cgcgcgccgc gcgctgtccc tgatggacct gaccaccctc 60

aacgacgacg ataccgacga gaaggtggcc gcgctgtgcc gcaaggccaa gagcccgac 120

ggcaccgtgg cggcgggtatg cgtgtttccc cgcttcgtgc ccatcgccaa gaagacgtg 180

cgcgaagcgg gttgtccgga ggtgcagggtg gccaccgtca ccaactccc gcacggcaat 240

gacgacgtct ccatcgcggt ggccgaaacc cgcgccgcca tcgcctacgg cgccgacgaa 300

gtggacgtgg tgttcccgtg ccgcgcgctg atggccggca accgcgacat cggcttcgag 360

ctggtcaagg cctgcaagga agcctgcggc ggcaagctct taaaagtgat catcgagagc 420

ggcgaactga aggacgcggc gctgatccgc gaagccagcg agatttccat ccgcgccggg 480

gccgacttca tcaagacttc caccggcaag gtgccggtea acgccacctt gcccgccggc 540

gagaccatgc tggccgtgat caaggagcag ggcggccagt gcggcttcaa ggccgccggc 600

ggcgtcaaga ggcgccaccga ggcggccgaa tacctggccc tggccgcgcg cctgctgggc 660

gaagattggg tgagcgcccg ccacttcgc ttcggcgcgt ccagcctgct ggccaatctg 720

cagatcgaga tcgccggcgg cgtcgccaag ccgagcagcg gctactga 768

**SEQ ID NO: 13**

<211> 255

<212> PRT

<213> Chromobacterium violaceum

<400> 13

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

Leu Thr Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ala Ala Leu  
20 25 30

Cys Arg Lys Ala Lys Ser Pro Asp Gly Thr Val Ala Ala Val Cys Val  
35 40 45

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

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

Asp Asp Val Ser Ile Ala Val Ala Glu Thr Arg Ala Ala Ile Ala Tyr  
85 90 95

Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala  
100 105 110

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

Cys Gly Gly Lys Leu Leu Lys Val Ile Ile Glu Ser Gly Glu Leu Lys  
130 135 140

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

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

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

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

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

Ser Ala Arg His Phe Arg Phe Gly Ala Ser Ser Leu Leu Ala Asn Leu  
225                    230                    235                    240

Gln Ile Glu Ile Ala Gly Gly Val Ala Lys Pro Ser Ser Gly Tyr  
                  245                    250                    255

**SEQ ID NO: 14**

<211> 780

<212> DNA

<213> Agrobacterium tumefaciens

<400> 14

gtgaccatgg aactccagcg tccgcgcgaa gcggctgccc tcaattgtc cttgctggac    60  
ctgaccaatc ttagggaaga ctgcacgccg cagcagatcg caaccctctg ccagcgggcg    120  
catacggagt ttggcaacac cgctgccatt tgcatttggc cgcgtttcgt cgcgcaggcc    180  
cgagcggcgt tcggaaaaga ccacacgatt cgcacgcgaa cggtcgtgaa ttcccctcc    240  
ggcgaatcgc atgtcgcgac cgtggttgcg gaaacggaag ctgcaatcgg cgatggcgcc    300  
gacgaaatcg atctggtcat tccctatcgt aaattcatgg caggcgatga atcggcggtg    360  
gccgaaatga tcgcggccgt gcgtaaggct tgcgcggcac ctgtgttgct caaggtcatt    420  
cttgagaccg gtgagctgaa ggacaaggcc ctgatccgcc gtgcctcgga aatcgccatt    480

gccgaagggg cggatttcac caagacctcg accggcaagg tcgccgtcaa tgccacgctg 540  
 gaagcggccg atatcatgct gcaggcgatc cgggacagca aaaagaaggt gggcttcaag 600  
 ccggccggcg gcatcggcac ggtggaggac gcgacactat acctcgggct ggcggaaacc 660  
 atcatggcgc ccaactgggc catgccgtcg accttccgtt tcggtgcctc gggcgtcctc 720  
 gatgatgtgc tgaacgtgct ggccggcggc gaaccggcca aggccgccag cgggtattga 780

**SEQ ID NO: 15**

<211> 259

<212> PRT

<213> Agrobacterium tumefaciens

<400> 15

Met Thr Met Glu Leu Gln Arg Pro Arg Glu Ala Ala Ala Leu Thr Leu  
 1 5 10 15

Ser Leu Leu Asp Leu Thr Asn Leu Arg Glu Asp Cys Thr Pro Gln Gln  
 20 25 30

Ile Ala Thr Leu Cys Gln Arg Ala His Thr Glu Phe Gly Asn Thr Ala  
 35 40 45

Ala Ile Cys Ile Trp Pro Arg Phe Val Ala Gln Ala Arg Ala Ala Phe  
 50 55 60

Gly Lys Asp His Thr Ile Arg Ile Ala Thr Val Val Asn Phe Pro Ser  
 65 70 75 80

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

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

Met Ala Gly Asp Glu Ser Ala Val Ala Glu Met Ile Ala Ala Val Arg  
 115 120 125

Lys Ala Cys Ala Ala Pro Val Leu Leu Lys Val Ile Leu Glu Thr Gly  
130 135 140

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

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

Asn Ala Thr Leu Glu Ala Ala Asp Ile Met Leu Gln Ala Ile Arg Asp  
180 185 190

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

Glu Asp Ala Thr Leu Tyr Leu Arg Leu Ala Glu Thr Ile Met Ala Pro  
210 215 220

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

Asp Asp Val Leu Asn Val Leu Ala Gly Gly Glu Pro Ala Lys Ala Ala  
245 250 255

Ser Gly Tyr

**SEQ ID NO:** 16

<211> 681

<212> DNA

<213> *Anabaena variabilis*

<400> 16

atggcagcag actatccgaa cattgatatt gcgccattta tcgatcacgc cctgttaacg 60

ccaacgggcta ctccagagca ggttgaccaa tgggtggaac aagcagacag atataatttt 120

gcgtcgggtt gtttgatcc tacttatgta aaacaagcag cagaatttct ccacggcaag 180

aaacctaagg ttgtacggt aattggttt cctactgggg ctacgactcg ctacgtcaag 240

ttgtatgagg cactggaagc ggtggagaat ggagccacag agctagatgt agtcatcaat 300  
 ttgggctgct tgaatctgg taatacggaa gcagtacacc gggaaattgc cgaaatttgc 360  
 gaagagactg gacaagtagt taaagtaatt ttggaacaa acttactgac ggatgcagaa 420  
 aaaaaaatcg cggccgatat agcaatggat gcaggagcca cattcttaa aaccaataca 480  
 ggttggaatg gcggtgctac agtggcagat gtgcggcttt taaaagaaat cacacgggaa 540  
 aggggtgggta taaaggcatc tgggtgggatt cgcaccctca atcaagcctt agacttaata 600  
 ttagcgggtg cgactagatt aggtacgtct cgtggtatcg atttaatcca ccagcgagat 660  
 aaccgggaaa aagttgaata g 681

**SEQ ID NO: 17**

<211> 226

<212> PRT

<213> *Anabaena variabilis*

<400> 17

Met Ala Ala Asp Tyr Pro Asn Ile Asp Ile Ala Pro Phe Ile Asp His  
 1 5 10 15

Ala Leu Leu Thr Pro Thr Ala Thr Pro Glu Gln Val Asp Gln Trp Cys  
 20 25 30

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

Tyr Val Lys Gln Ala Ala Glu Phe Leu His Gly Lys Lys Pro Lys Val  
 50 55 60

Cys Thr Val Ile Gly Phe Pro Thr Gly Ala Thr Thr Arg Ser Val Lys  
 65 70 75 80

Leu Tyr Glu Ala Leu Glu Ala Val Glu Asn Gly Ala Thr Glu Leu Asp  
 85 90 95

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



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

Val Ile Leu Glu Thr Asn Leu Leu Thr Asp Ala Glu Lys Lys Ile Ala  
130 135 140

Ala Asp Ile Ala Met Asp Ala Gly Ala Thr Phe Leu Lys Thr Asn Thr  
145 150 155 160

Gly Trp Asn Gly Gly Ala Thr Val Ala Asp Val Arg Leu Leu Lys Glu  
165 170 175

Ile Thr Arg Glu Arg Val Gly Ile Lys Ala Ser Gly Gly Ile Arg Thr  
180 185 190

Leu Asn Gln Ala Leu Asp Leu Ile Leu Ala Gly Ala Thr Arg Leu Gly  
195 200 205

Thr Ser Arg Gly Ile Asp Leu Ile His Gln Arg Asp Asn Pro Glu Lys  
210 215 220

Val Glu  
225

**SEQ ID NO: 18**

<211> 681

<212> DNA

<213> *Pseudomonas syringae*

<400> 18

atgaattcgc tcgaaccgcg tgcactggcc caggccatcg atcacacctt gttggcggcg 60

gatgccagcc gagagcagat tgccacgctt tgcgcagaag cccgggaaca cggtctctac 120

tcggtgtgcg tgaactccag ccaggtgcct ttgccgccc gacaactggc cgggtctgcc 180

gtgaaggtct gtgcggtggt gggctttccg ctgggcgccg ggctgagtc cagcaaggcg 240

tcggaagcag ccctgacgat cgccgccggg gctcaggaaa tcgacatggt gctgaacatc 300

ggctggctca aggacggtct gttcgatgag gtccgcgacg atatcgccgc ggtgctgcaa 360  
 gcctgtggca aggtgccgct caaggtgac ctggaaacct gcctgctcga tgaggcgag 420  
 aaggtgcgcg cctgcgagat ctgccgcgag ctgggcgtgg cattcgtcaa gacctcact 480  
 ggcttcagcc gcagcggcgc gacgctcgag gatgtggcgc tgatgcgccg tgtggtaggc 540  
 cctgacatcg gcgtcaaggc gtctggcggg gtgcgtgacg tggccacggc cagagcgatg 600  
 atcgaagctg gcgcaacgcg cctgggcacc agttccggga ttgcgatcgt gaccggcgca 660  
 ggtacggggg cgggttattg a 681

**SEQ ID NO: 19**

<211> 226

<212> PRT

<213> *Pseudomonas syringae*

<400> 19

Met Asn Ser Leu Glu Pro Ala Ala Leu Ala Gln Ala Ile Asp His Thr  
 1 5 10 15

Leu Leu Ala Ala Asp Ala Ser Arg Glu Gln Ile Ala Thr Leu Cys Ala  
 20 25 30

Glu Ala Arg Glu His Gly Phe Tyr Ser Val Cys Val Asn Ser Ser Gln  
 35 40 45

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

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

Ser Glu Ala Ala Leu Thr Ile Ala Ala Gly Ala Gln Glu Ile Asp Met  
 85 90 95

Val Leu Asn Ile Gly Trp Leu Lys Asp Gly Leu Phe Asp Glu Val Arg  
 100 105 110

Asp Asp Ile Ala Ala Val Leu Gln Ala Cys Gly Lys Val Pro Leu Lys  
115 120 125

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

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

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

Arg Val Val Gly Pro Asp Ile Gly Val Lys Ala Ser Gly Gly Val Arg  
180 185 190

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

Gly Thr Ser Ser Gly Ile Ala Ile Val Thr Gly Ala Gly Thr Gly Ala  
210 215 220

Gly Tyr  
225

**SEQ ID NO:** 20

<211> 669

<212> DNA

<213> *Erwinia carotovora*

<400> 20

atgactgact acgcacgcta tategaccac accctgctgg cagcaaatgc caccgaacag 60

caaatcgta cgctgtgcga tgaagcgata gcgcaccatt ttatgccgt ctgtgttaat 120

tccggctacg ttcccttagt agctgaaaaa ttgaaaggtt cagcgggtaca ggtgtgctcg 180

gttattggat ttctctcgg tgcaggcctg actccagca aagcatttga agcgaaagcc 240

gcgattgatg ccggtgcaca ggaaatcgac atggtgatta acgtcggctg gctgaaaagc 300

gggaagattg atgccgtcaa agcggatatt caggccgtgc gtgggggttg cgccgctata 360

ccgttgaagg taatattgga aacctgtctg cttgatgacg aacagattgt gctggtgtgt 420  
gaaatgtgtc gtcagttgga tgtcgcgttc gtcaaaacgt ctaccggttt cagcaccgac 480  
ggcgcacgcg aagaacacgt tcgactgatg cgtagcactg tcggcagcga gatgggtgta 540  
aaagcctccg gcgcgggttc cgatcgcgaa acggcacaac gaatgattga agcaggcgcc 600  
acgcgtattg gcaccagttc aggcgttgc atcgtttctg atgacgctgc cgcagcaggg 660  
aactactaa 669

**SEQ ID NO: 21**

<211> 222

<212> PRT

<213> Erwinia carotovora

<400> 21

Met Thr Asp Tyr Ala Arg Tyr Ile Asp His Thr Leu Leu Ala Ala Asn  
1 5 10 15

Ala Thr Glu Gln Gln Ile Val Thr Leu Cys Asp Glu Ala Ile Ala His  
20 25 30

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

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

Pro Leu Gly Ala Gly Leu Thr Ser Ser Lys Ala Phe Glu Ala Lys Ala  
65 70 75 80

Ala Ile Asp Ala Gly Ala Gln Glu Ile Asp Met Val Ile Asn Val Gly  
85 90 95

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

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

Cys Leu Leu Asp Asp Glu Gln Ile Val Leu Val Cys Glu Met Cys Arg  
130 135 140

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

Gly Ala Arg Glu Glu His Val Arg Leu Met Arg Ser Thr Val Gly Ser  
165 170 175

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

Gln Arg Met Ile Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser Ser Gly  
195 200 205

Val Ala Ile Val Ser Asp Asp Ala Ala Ala Ala Gly Asn Tyr  
210 215 220

**SEQ ID NO: 22**

<211> 684

<212> DNA

<213> Desulfotalea psychrophila

<400> 22

atgaatacaa tcattagccc gaaagaaatt gccttgata ttgatcacac tctcctcaaa 60

cctgaggcaa gcctgcagc tattegtacc ctatgcgcag aagctcgtga gtactctttc 120

aagactgtat gcgtcaactc ttgctatgac cctctctgtg tggaagaact tcaagcttgc 180

cccgttgatg ttgctcggg ggtgggggtc ccacttgggg ctatgctgag ttcggcaaag 240

gcctacgagg caaaacttgc agtggcagcc ggggccgacg aaattgatat ggttatcaat 300

attggtctct tgaaggcagg agaactgaa gctgttcggg cagatattga aacagttttt 360

gccgcctgtg gagaggcaga ccttaagggtg atcattgaga caggcctgct cagcgatgcg 420

gagaaaaaaa gcgtctgtca gatatgcaag gaagttgggtg tcgcctttgt taagacctcc 480

acgggttttg gtcattggtg cgcaaccgtt gccgatgtag aacttatgcg tgctgtgttt 540

ggtgagagat gtaagggttaa ggcctctggc ggggtacgca accttgccga tgcccgcgcc 600

ctgatagcgg caggagccaa tagaattggg gcaagtgccg gtatcgcaat tgtcaatgga 660

gaagaggtcc ccccttctcg ttaa 684

**SEQ ID NO: 23**

<211> 227

<212> PRT

<213> Desulfotalea psychrophila

<400> 23

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

Thr Leu Leu Lys Pro Glu Ala Ser Pro Ala Ala Ile Arg Thr Leu Cys  
20 25 30

Ala Glu Ala Arg Glu Tyr Ser Phe Lys Thr Val Cys Val Asn Ser Cys  
35 40 45

Tyr Val Pro Leu Cys Val Glu Glu Leu Gln Ala Cys Pro Val Asp Val  
50 55 60

Cys Ser Val Val Gly Phe Pro Leu Gly Ala Met Leu Ser Ser Ala Lys  
65 70 75 80

Ala Tyr Glu Ala Lys Leu Ala Val Ala Ala Gly Ala Asp Glu Ile Asp  
85 90 95

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

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

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

Val Cys Gln Ile Cys Lys Glu Val Gly Val Ala Phe Val Lys Thr Ser  
145                    150                    155                    160

Thr Gly Phe Gly His Gly Gly Ala Thr Val Ala Asp Val Glu Leu Met  
                  165                    170                    175

Arg Ala Val Val Gly Glu Arg Cys Lys Val Lys Ala Ser Gly Gly Val  
                  180                    185                    190

Arg Asn Leu Ala Asp Ala Arg Ala Leu Ile Ala Ala Gly Ala Asn Arg  
                  195                    200                    205

Ile Gly Ala Ser Ala Gly Ile Ala Ile Val Asn Gly Glu Glu Val Pro  
                  210                    215                    220

Pro Ser Arg  
225

**SEQ ID NO: 24**

<211> 636

<212> DNA

<213> Bacillus subtilis

<400> 24

atgtcattag ccaacataat tgatcataca gctttgaaac cgcatacaca aaaagcggac    60

attctaaaac taattgaaga agcgaaaaca taaaatttg cttcagtatg tgtcaatccg    120

acatgggtgg agcttgctgc aaaagagctt aagggaactg gagtcgacgt ttgtacggtc    180

atcggttcc cgctcgggtc caatacaact gaaacaaaag cgttcgaaac aaaagacgcc    240

atttcaaaag gcgccactga agtggatatg gtcattaata ttgccgcttt aaaagacaag    300

gaagacgatg tggtggaagc tgatatccgc ggtgtagtgg aagctgtagc cggaagagcg    360

cttgtaaaag tcattatcga aacgtgcctt ctgactgatg aagaaaaaga acgtgcatgc    420

cgtttagcgg tgtctgcggg agcggatttc gtaaaaacat caacaggctt ttctacaggc    480

ggcgcaacga aggaagatat cgccttaatg cgcaaaacag tagggcctga tatcggcgtg    540

aaagcatctg gcggcgtcag aacgaaagaa gatgtagaca caatggtaga ggccggagca    600

agccgaattg cgccagcgca ggcgtttcta tcgtaa

636

**SEQ ID NO: 25**

<211> 211

<212> PRT

<213> Bacillus subtilis

<400> 25

Met Ser Leu Ala Asn Ile Ile Asp His Thr Ala Leu Lys Pro His Thr

1 5 10 15

Gln Lys Ala Asp Ile Leu Lys Leu Ile Glu Glu Ala Lys Thr Tyr Lys

20 25 30

Phe Ala Ser Val Cys Val Asn Pro Thr Trp Val Glu Leu Ala Ala Lys

35 40 45

Glu Leu Lys Gly Thr Gly Val Asp Val Cys Thr Val Ile Gly Phe Pro

50 55 60

Leu Gly Ala Asn Thr Thr Glu Thr Lys Ala Phe Glu Thr Lys Asp Ala

65 70 75 80

Ile Ser Lys Gly Ala Thr Glu Val Asp Met Val Ile Asn Ile Ala Ala

85 90 95

Leu Lys Asp Lys Glu Asp Asp Val Val Glu Ala Asp Ile Arg Gly Val

100 105 110

Val Glu Ala Val Ala Gly Lys Ala Leu Val Lys Val Ile Ile Glu Thr

115 120 125

Cys Leu Leu Thr Asp Glu Glu Lys Glu Arg Ala Cys Arg Leu Ala Val

130 135 140

Ser Ala Gly Ala Asp Phe Val Lys Thr Ser Thr Gly Phe Ser Thr Gly

145 150 155 160



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

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

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

Phe Leu Ser  
210

**SEQ ID NO: 26**

<211> 672

<212> DNA

<213> *Listeria innocua*

<400> 26

atgacaattg ccaaaatgat cgaccacact gctttaaacc cagacacaac gaaagaacaa 60

attttaacat taacaaaaga agcaagagaa tatggttttg cttccgtatg cgtgaatcca 120

acttggtgga aattatccgc tgaacagctt tcaggagcag aatccgttgt atgtacagtt 180

atcggtttcc cacttgagc aaatacacca gaagtaaaag cttttgaagt gaaaaatgcc 240

atcgaaaacg gcgctaaaga agtggatatg gttattaata tcggcgcatt aaaagacaaa 300

gacgatgaat tagtagaacg tgatattcgt gctgtagttg atgctgccaa agggaaagca 360

ttagtaaaag taattattga aacttgccta ttaacagacg aagaaaaagt tcgcgcatgt 420

gaaatcgctg taaaagcagg aacagacttc gttaaaacat cactggatt ctccacaggt 480

ggcgcaactg ccgaagatat tgccttaatg cgtaaaactg taggaccaa catcggcgta 540

aaagcatctg gcggagttcg tacaaaagaa gacgtagaaa aaatgattga agcaggtgca 600

actcgatatg gcgcaagtgc aggtgtcgca attgtttccg gcgaaaaacc agctaaacca 660

gataattact aa 672

**SEQ ID NO: 27**

<211> 223

<212> PRT

<213> Listeria innocua

<400> 27

Met Thr Ile Ala Lys Met Ile Asp His Thr Ala Leu Lys Pro Asp Thr  
1 5 10 15

Thr Lys Glu Gln Ile Leu Thr Leu Thr Lys Glu Ala Arg Glu Tyr Gly  
20 25 30

Phe Ala Ser Val Cys Val Asn Pro Thr Trp Val Lys Leu Ser Ala Glu  
35 40 45

Gln Leu Ser Gly Ala Glu Ser Val Val Cys Thr Val Ile Gly Phe Pro  
50 55 60

Leu Gly Ala Asn Thr Pro Glu Val Lys Ala Phe Glu Val Lys Asn Ala  
65 70 75 80

Ile Glu Asn Gly Ala Lys Glu Val Asp Met Val Ile Asn Ile Gly Ala  
85 90 95

Leu Lys Asp Lys Asp Asp Glu Leu Val Glu Arg Asp Ile Arg Ala Val  
100 105 110

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

Cys Leu Leu Thr Asp Glu Glu Lys Val Arg Ala Cys Glu Ile Ala Val  
130 135 140

Lys Ala Gly Thr Asp Phe Val Lys Thr Ser Thr Gly Phe Ser Thr Gly  
145 150 155 160

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

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

Glu Lys Met Ile Glu Ala Gly Ala Thr Arg Ile Gly Ala Ser Ala Gly  
195 200 205

Val Ala Ile Val Ser Gly Glu Lys Pro Ala Lys Pro Asp Asn Tyr  
210 215 220

**SEQ ID NO: 28**

<211> 648

<212> DNA

<213> Clostridium acetobutylicum

<400> 28

atgaatattg ctaaaattat agatcataca gcattaaagc cagatacaac aaaggagcag 60  
atactaaaac taatagaaga agctaaacaa aataactttg catcagtttg tgtaaatcca 120  
aagtgggtta aagaggcaag ctgtgcatta aaggacagca gtgttaaagt gtgtactgta 180  
atagggtttc ctcttgagc taatacaact gctacaaaag tatttgaaac acaagatgct 240  
attaaaaatg gtgcagaaga agtagatatg gttgtttcta taggagaatt aaaagataaa 300  
aatgatgatt atgtagaaaa agatatagaa gaagttgtta aggcagctag tggaaaggcc 360  
ttagttaaag taattattga aacttgtctt cttaccgaag aagagaagat aagagcgtgt 420  
aaactagcta aaaaagcagg tgcagatttt gttaaacaat caacagggtt ttcaacagga 480  
ggggctaagg cagaagatat taaattaatg agaaaaacag ttggagctgg tatgggagtt 540  
aaggcctcag gtggtattca tacaagagaa gaagcaatta aacttataga agctggagct 600  
acacgtattg gagctagtgc aagtatagat ataattcag aaaattaa 648

**SEQ ID NO: 29**

<211> 215

<212> PRT

<213> Clostridium acetobutylicum

<400> 29

Met Asn Ile Ala Lys Ile Ile Asp His Thr Ala Leu Lys Pro Asp Thr  
1 5 10 15

Thr Lys Glu Gln Ile Leu Lys Leu Ile Glu Glu Ala Lys Gln Asn Asn  
20 25 30

Phe Ala Ser Val Cys Val Asn Pro Lys Trp Val Lys Glu Ala Ser Cys  
35 40 45

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

Leu Gly Ala Asn Thr Thr Ala Thr Lys Val Phe Glu Thr Gln Asp Ala  
65 70 75 80

Ile Lys Asn Gly Ala Glu Glu Val Asp Met Val Val Ser Ile Gly Glu  
85 90 95

Leu Lys Asp Lys Asn Asp Asp Tyr Val Glu Lys Asp Ile Glu Glu Val  
100 105 110

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

Cys Leu Leu Thr Glu Glu Glu Lys Ile Arg Ala Cys Lys Leu Ala Lys  
130 135 140

Lys Ala Gly Ala Asp Phe Val Lys Thr Ser Thr Gly Phe Ser Thr Gly  
145 150 155 160

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

Gly Met Gly Val Lys Ala Ser Gly Gly Ile His Thr Arg Glu Glu Ala  
180 185 190

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

Ile Asp Ile Ile Ser Glu Asn  
210 215

**SEQ ID NO: 30**

<211> 822

<212> DNA

<213> *Geobacillus kaustophilus*

<400> 30

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atggagctca taaccagcc tagtgctgg gttttctg tcttttccg gagacaatac   60
ggatggctag ttttgcga gggagcatgg tatgatgga gacgtcagac ttccatctt  120
gacggaaatg gcagaaaggg gtttctcca atgacgatga atacgcgaa aatgatcgat  180
catacgctgc taaaccgga agcgacagaa caacaaatcg tgcaactgtg cacggaagca  240
aagcaatacg gctttgcttc cgtgtgcgtc aacccaacgt gggtgaaaac ggcggcgcgc  300
gagctttccg gcacggatgt ccgcgtctgc acggtcatcg gctttccact tggggcaacg  360
acgccggaac caaaggcgtt tgaacaacg aacgccatcg aaaacggcgc tcgcgaagtc  420
gacatggtga tcaacatcgg cgcgttaaaa agcgggcaag acgagcttgt cgagcgcgac  480
attcgtcggg ttgtcgaagc ggcggctggc agggcgcttg tcaaagtgat cgttgaaacg  540
gcgcttttga ccgatgagga aaaagtgcgc gcctgccagc tcgcagtga agccggcgct  600
gattatgtga aaacgtcgac cgggttttcc ggcggaggtg cgacggtgga ggatgtggcg  660
ttgatgcgga aaacggtcgg cgacagagca ggcgtcaaag catcaggcgg cgtccgtgac  720
tgaaaaccg ctgaggcgat gatcaacgcc ggcgcgacgc gcatcggcac aagctctggg  780
gtggcgatcg tcaccggcgg gacgggccgc gctgactact aa                    822
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**SEQ ID NO: 31**

<211> 273

<212> PRT

<213> *Geobacillus kaustophilus*

<400> 31

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Met Glu Leu Ile Thr Gln Pro Ser Cys Trp Val Phe Ser Val Phe Phe
1         5         10        15
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Arg Arg Gln Tyr Gly Trp Leu Val Phe Val Glu Gly Ala Trp Tyr Asp
20        25        30
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Gly Arg Arg Gln Thr Phe His Leu Asp Gly Asn Gly Arg Lys Gly Phe  
35 40 45

Leu Arg Met Thr Met Asn Ile Ala Lys Met Ile Asp His Thr Leu Leu  
50 55 60

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

Lys Gln Tyr Gly Phe Ala Ser Val Cys Val Asn Pro Thr Trp Val Lys  
85 90 95

Thr Ala Ala Arg Glu Leu Ser Gly Thr Asp Val Arg Val Cys Thr Val  
100 105 110

Ile Gly Phe Pro Leu Gly Ala Thr Thr Pro Glu Thr Lys Ala Phe Glu  
115 120 125

Thr Thr Asn Ala Ile Glu Asn Gly Ala Arg Glu Val Asp Met Val Ile  
130 135 140

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

Ile Arg Ala Val Val Glu Ala Ala Ala Gly Arg Ala Leu Val Lys Val  
165 170 175

Ile Val Glu Thr Ala Leu Leu Thr Asp Glu Glu Lys Val Arg Ala Cys  
180 185 190

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

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

Trp Lys Thr Ala Glu Ala Met Ile Asn Ala Gly Ala Thr Arg Ile Gly  
245 250 255

Thr Ser Ser Gly Val Ala Ile Val Thr Gly Gly Thr Gly Arg Ala Asp  
260 265 270

**SEQ ID NO: 32**

<211> 675

## <212> DNA

&lt;213&gt; Bacillus halodurans

&lt;400&gt; 32

atgtcacgtt cgattgcaca aatgattgat catacgtac ttaaaccaaa tacaacagaa 60

gaccaaattg taaagctctg tgaggaagca aaggaatatt catttgcac tgtttgtgtg 120

aatcctactt gggtcgctct tgctgcgcag ttgctaaaag atgcacctga tgtgaaagta 180

tgtagcagttg tgggctttcc gttagggggca acgactccgg aagtgaaagc gtttgaaacg 240

actaatgcc a ttgaaaatgg agcgacagaa gtggacatgg tcattaacat tggagcgtta 300

aaagataaac aatacgagct tgttgacgc gacattcaag cggttgttaa agcagcagaa 360

gggaaagcat taacgaaagt aatcattgaa acatcgttat taacggagga agagaagaag 420

gctgcgtgtg agcttgccgt aaaagcagga gccgactttg tcaaaacgtc gactggattc 480

tctggcggag gtgctacggc tgaggataac gcgctcatgc gaaaagtggc cggaccaaatt 540

ttaggagtca aagcttctgg aggtgttaga gatctgtccg acgcgaaagc gatgattgat 600

gctggtgcta ctcggattgg tgcgagtgct ggggtggcga ttgtaacggg ggagcgtagc 660

gaagggagtt attaa

675

**SEQ ID NO: 33**

 $\langle 211 \rangle$  224

&lt;212&gt; PRT

<213> Bacillus halodurans

<400> 33

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

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

Tyr Ser Phe Ala Ser Val Cys Val Asn Pro Thr Trp Val Ala Leu Ala  
35 40 45

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

Gly Phe Pro Leu Gly Ala Thr Thr Pro Glu Val Lys Ala Phe Glu Thr  
65 70 75 80

Thr Asn Ala Ile Glu Asn Gly Ala Thr Glu Val Asp Met Val Ile Asn  
85 90 95

Ile Gly Ala Leu Lys Asp Lys Gln Tyr Glu Leu Val Gly Arg Asp Ile  
100 105 110

Gln Ala Val Val Lys Ala Ala Glu Gly Lys Ala Leu Thr Lys Val Ile  
115 120 125

Ile Glu Thr Ser Leu Leu Thr Glu Glu Glu Lys Lys Ala Ala Cys Glu  
130 135 140

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

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

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



Ser Asp Ala Lys Ala Met Ile Asp Ala Gly Ala Thr Arg Ile Gly Ala  
195 200 205

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

**SEQ ID NO: 34**

<211> 672

<212> DNA

<213> Bacillus licheniformis

<400> 34

atgacaaaac aaattgcgcg aatgatcgat cacactgcat tgaagccaga taccgtcaaa 60  
tccgaaatcg aagcgctttg caaagaagcg cgtgtttacg gtttgcctc cgtttgtgtc 120  
aacccttgct ggggtgaagct ttgcgccgag cttcttaaag agtcagaggt gaaagtatgt 180  
acagttatcg gctttccttt aggtgcagcg tctccgaaa caaaagcctt tgaaccagg 240  
caggcaattg cagacggtgc cggatgaagt gatattgtga tcaacatcgg tgcactaaaa 300  
gaccgcgata cggaacagt ggaacatgac atcagggcgg tgacagacgc ggccgacggc 360  
aaagctcttg taaaagtcac catagagacg tcgcttttga cggatgaaga aaaaaggctg 420  
gcttgtgaac tggccgtaaa agcagggccc gactttgtca aaacatcgac cggtttttcc 480  
ggcggcggtg cgacagtccg ggatataaaa ctgatgcggg aagctgtcgg acctgatatc 540  
ggcggttaaag cttcaggtgg cgtccgcgat aaggaaagcg cacttgccat gattgaagcc 600  
ggagcgacga gaatcggagc gagcgccggc gtgtcgattg tcaaagggtt aacagcggat 660  
gaagactact aa 672

**SEQ ID NO: 35**

<211> 223

<212> PRT

<213> Bacillus licheniformis

<400> 35

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

Asp Thr Val Lys Ser Glu Ile Glu Ala Leu Cys Lys Glu Ala Arg Val  
20 25 30

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

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

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

Gln Ala Ile Ala Asp Gly Ala Gly Glu Val Asp Met Val Ile Asn Ile  
85 90 95

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

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

Glu Thr Ser Leu Leu Thr Asp Glu Glu Lys Arg Leu Ala Cys Glu Leu  
130 135 140

Ala Val Lys Ala Gly Ala Asp Phe Val Lys Thr Ser Thr Gly Phe Ser  
145 150 155 160

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

Gly Pro Asp Ile Gly Val Lys Ala Ser Gly Gly Val Arg Asp Lys Glu  
180 185 190

Ser Ala Leu Ala Met Ile Glu Ala Gly Ala Thr Arg Ile Gly Ala Ser  
195 200 205

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

**SEQ ID NO: 36**

<211> 663

<212> DNA

<213> Streptococcus mutans

<400> 36

atgaaaatca atcaatatat tgaccatact ttattaaaac cagaaagtag gcaagatcag 60  
attgataaac tgattcgaga agctaagaca tataattttg ccagtgtctg tatcaatcca 120  
acttggtttt cttatcgggc taaagctctt gaaggaacag acattaaagt ttgtactgtt 180  
attggttttc ctttaggagc aacgactagt gctgtaaaag cctttgaaac caaggatgct 240  
attagtcatg gagctgacga agttgatatg gttatcaata ttgtcaagc taaatctggt 300  
cattttgctt ttgttgaaga agatatcgg gcagttgttg aagccagtgg tgacaaattg 360  
gtgaaagtta ttattgaaac ttgtctcctt acagataaag aaaaaattaa agcttgtcaa 420  
gctgcagtag cagcaggtgc tgatttcgtt aaaacatcaa ctggttttc aactgctgga 480  
gctaggttag atgatgttcg tcttatgcgt caaacggtag gacctgatgt tggagtaaag 540  
gcggcaggag gaacgcgac tttagaagat gcgcaagctt ttattgaagc aggtgcaaca 600  
cgtattggga catctgctgg agttactatt atggaaggaa agcaaacaaa cagtggttat 660  
tga 663

**SEQ ID NO: 37**

<211> 220

<212> PRT

<213> Streptococcus mutans

<400> 37

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

Arg Gln Asp Gln Ile Asp Lys Leu Ile Arg Glu Ala Lys Thr Tyr Asn  
20 25 30

Phe Ala Ser Val Cys Ile Asn Pro Thr Trp Val Ser Tyr Ala Ala Lys  
35 40 45

Ala Leu Glu Gly Thr Asp Ile Lys Val Cys Thr Val Ile Gly Phe Pro  
50 55 60

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

Ile Ser His Gly Ala Asp Glu Val Asp Met Val Ile Asn Ile Gly Gln  
85 90 95

Ala Lys Ser Gly His Phe Ala Phe Val Glu Glu Asp Ile Arg Ala Val  
100 105 110

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

Leu Leu Thr Asp Lys Glu Lys Ile Lys Ala Cys Gln Ala Ala Val Ala  
130 135 140

Ala Gly Ala Asp Phe Val Lys Thr Ser Thr Gly Phe Ser Thr Ala Gly  
145 150 155 160

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

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

Ala Phe Ile Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser Ala Gly Val  
195 200 205

Thr Ile Met Glu Gly Lys Gln Thr Asn Ser Gly Tyr  
210 215 220

**SEQ ID NO:** 38  
<211> 663

<212> DNA

<213> Staphylococcus epidermidis

<400> 38

atgaataaag caaaattgat agaccataca ttattaaaac ctgattcaac aaaggaacaa 60  
atagatacta ttataaatga agcaaaagca tatcagttta agtctgtatg tgtgaaccct 120  
acacatgtac aatatgcac tgaacaactt aaaggaacag acgttttagt gtgtactgtt 180  
attggatttc cactaggtgc aacaactaca gcggttaaatt cttatgaaac aaaagatgcg 240  
attaacaatg gtgccaaga gattgatatg gtgataaata ttggagcact taaggatggc 300  
cgttttgatg aagtcaaaa tgatatcgaa gccgtcgttc aagcagccaa tggtaaaaca 360  
gtaaggttaa ttattgagac tgttttatta actgagaaag agaagattaa agcatgtcaa 420  
ttatctgaag cggcaggtgc acattttgtt aaaacatcca caggttttgc tgggtgggggt 480  
gcaacagttg aagatgtaaa attaataaaa gatactgttg gtgatcggtt agaagtaaaa 540  
gcgtcaggcg gcgtgagaaa tctagaagat ttaataata tgattgaagc gggtgctaca 600  
cgtattggtg ctagtccggg tgtgcaaatt attcaaggac ttgaatcaaa tactgattac 660  
taa 663

**SEQ ID NO: 39**

<211> 220

<212> PRT

<213> Staphylococcus epidermidis

<400> 39

Met Asn Lys Ala Lys Leu Ile Asp His Thr Leu Leu Lys Pro Asp Ser  
1 5 10 15  
Thr Lys Glu Gln Ile Asp Thr Ile Ile Asn Glu Ala Lys Ala Tyr Gln  
20 25 30  
Phe Lys Ser Val Cys Val Asn Pro Thr His Val Gln Tyr Ala Ser Glu  
35 40 45  
Gln Leu Lys Gly Thr Asp Val Leu Val Cys Thr Val Ile Gly Phe Pro  
50 55 60

Leu Gly Ala Thr Thr Thr Ala Val Lys Ser Tyr Glu Thr Lys Asp Ala  
65                      70                      75                      80

Ile Asn Asn Gly Ala Gln Glu Ile Asp Met Val Ile Asn Ile Gly Ala  
                    85                      90                      95

Leu Lys Asp Gly Arg Phe Asp Glu Val Gln Asn Asp Ile Glu Ala Val  
                    100                      105                      110

Val Gln Ala Ala Asn Gly Lys Thr Val Lys Val Ile Ile Glu Thr Val  
                    115                      120                      125

Leu Leu Thr Glu Lys Glu Lys Ile Lys Ala Cys Gln Leu Ser Glu Ala  
                    130                      135                      140

Ala Gly Ala His Phe Val Lys Thr Ser Thr Gly Phe Ala Gly Gly Gly  
145                      150                      155                      160

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

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

Asn Met Ile Glu Ala Gly Ala Thr Arg Ile Gly Ala Ser Ala Gly Val  
                    195                      200                      205

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

**SEQ ID NO:** 40

<211> 648

<212> DNA

<213> Lactobacillus plantarum

<400> 40

atgaaattga atcggtattt agatcacacg ttattaaac cggaagcgac tgagcaacaa 60

attgatcagg tagtacggga ggcactcgaa aatcactttt attcagttat ggtcaatcca 120  
 tactgggtca agcacgtcca tgcgcaactt gctggttcgg atgttgcgac tgcattgcgtg 180  
 attggtttcc ctctggggcg gaatacaacc gccattaaag ttgcggaagc caaacaggca 240  
 attgctgacg gtgtggatga gctggatatg gtcattaata tcggcgaatt gaaaggcgac 300  
 cactatgatg cagttcaaca agacattgaa agtgttgtaa cagttggaca tacggctgat 360  
 aaggtcgtca aagtgattat tgaacggcg ctgttgacgg atggggaaat cgtaaggct 420  
 agtgaaattg ttccgatgc acacgctgat tttgtgaaga catcgactgg atttcaacc 480  
 cgtggtgctt cggttcatga tattagttg atgaagggtg ccgttcagga tcgaatcggg 540  
 gtcaaagcat ctgggggaat ccatacacgc gatgaagcat tagcgatgat tgatgctgga 600  
 gcaacgcgcc tcggtgtatc agcaagtatg gcaattattg gtaagtag 648

**SEQ ID NO:** 41

<211> 215

<212> PRT

<213> Lactobacillus plantarum

<400> 41

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

Thr Glu Gln Gln Ile Asp Gln Val Val Arg Glu Ala Leu Glu Asn His  
 20 25 30

Phe Tyr Ser Val Met Val Asn Pro Tyr Trp Val Lys His Val His Ala  
 35 40 45

Gln Leu Ala Gly Ser Asp Val Ala Thr Ala Cys Val Ile Gly Phe Pro  
 50 55 60

Leu Gly Ala Asn Thr Thr Ala Ile Lys Val Ala Glu Ala Lys Gln Ala  
 65 70 75 80

Ile Ala Asp Gly Val Asp Glu Leu Asp Met Val Ile Asn Ile Gly Glu  
 85 90 95

Leu Lys Gly Asp His Tyr Asp Ala Val Gln Gln Asp Ile Glu Ser Val  
100 105 110

Val Thr Val Gly His Thr Ala Asp Lys Val Val Lys Val Ile Ile Glu  
115 120 125

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

Ala Asp Ala His Ala Asp Phe Val Lys Thr Ser Thr Gly Phe Ser Thr  
145 150 155 160

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

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

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

Ser Met Ala Ile Ile Gly Lys  
210 215

**SEQ ID NO: 42**

<211> 728

<212> DNA

<213> Lactobacillus acidophilus

<400> 42

cagaggtaaa aattatgaaa tatacttttag acgactttgc acgtttaatt gatcacacta 60

acttacacgc tgatgcaact gaagccgata tgaagaagtt atgtgatgaa gcaaagaaat 120

atcattttaa aatggtagct attaatacaag ttcaatccaa gttttgctca gagcaattaa 180

agggaaacaga cattgatact ggtgctgcaa ttgcttttcc ttaggacaa caaactattg 240

aatccaaggt atttgatact agggatgcaa ttaagaatgg tgctaatagaa attgattatg 300



tgattaatat tactcaatta aaagctaaag actacgatta tataaagcaa gaaatgcaag 360  
 agatgggttaa tgcttgcat gaaaatcatg ttccatgtaa agtgattttt gaaaattgct 420  
 atttaaccaa agatgaaata aaaaaattag ctgagattgc taaagaagta aagcctgact 480  
 ttattaagac ttctactggc ttggtagtt caggcgctaa ggtagaagac gtaaagctaa 540  
 tgaaatcaat tgtggcgat gaagtaaaag taaaggctgc cgggtgtatt cgtaatagt 600  
 atgatttctt agccatggtg cgcgctggtg ctgatagaat tggttgttct gctggagtca 660  
 aaatttatca agctttaaag tgtagaatga aagacgacca tgtggatagt attgagattg 720  
 cacgttag 728

**SEQ ID NO:** 43

<211> 237

<212> PRT

<213> Lactobacillus acidophilus

<400> 43

Met Lys Tyr Thr Leu Asp Asp Phe Ala Arg Leu Ile Asp His Thr Asn  
 1 5 10 15

Leu His Ala Asp Ala Thr Glu Ala Asp Met Lys Lys Leu Cys Asp Glu  
 20 25 30

Ala Lys Lys Tyr His Phe Lys Met Val Ala Ile Asn Gln Val Gln Ser  
 35 40 45

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

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

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

Ile Asn Ile Thr Gln Leu Lys Ala Lys Asp Tyr Asp Tyr Ile Lys Gln  
 100 105 110

Glu Met Gln Glu Met Val Asn Ala Cys His Glu Asn His Val Pro Cys  
115 120 125

Lys Val Ile Phe Glu Asn Cys Tyr Leu Thr Lys Asp Glu Ile Lys Lys  
130 135 140

Leu Ala Glu Ile Ala Lys Glu Val Lys Pro Asp Phe Ile Lys Thr Ser  
145 150 155 160

Thr Gly Phe Gly Ser Ser Gly Ala Lys Val Glu Asp Val Lys Leu Met  
165 170 175

Lys Ser Ile Val Gly Asp Glu Val Lys Val Lys Ala Ala Gly Gly Ile  
180 185 190

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

Ile Gly Cys Ser Ala Gly Val Lys Ile Tyr Gln Ala Leu Lys Cys Arg  
210 215 220

Met Lys Asp Asp His Val Asp Ser Ile Glu Ile Ala Arg  
225 230 235

**SEQ ID NO: 44**

<211> 672

<212> DNA

<213> Streptococcus pyogenes

<400> 44

gtggaagtaa aagatat tttt aaaaacggta gaccatactt tgctagcaac aacagcaacg 60

tggccagaaa tccaaacaat ttagatgat gccatggctt atgaaacagc ttcagcatgt 120

attccagctt cttacgtcaa aaaagcagca gaatacgttt caggtaaatt agctatttgt 180

actgttattg ggttcccaaa tggtatatgt acaactgcgg cgaagggttt tgaatgtcaa 240

gatgctattc aaaatgggtgc tgatgaaatt gacatgggtca ttaatttgac agacgttaaa 300

aatggggatt ttgatactgt tgaagaagaa attcgtcaaa tcaaagctaa atgtcaagac 360  
catatcttaa aagttatcgt tgagacatgt caattaacta aagaagaact tategaactt 420  
tgtggagttg tcacacgttc aggtgcagac ttattaaaa cctctactgg ttttcgaca 480  
gcaggtgcta catttgaaga tgttgaagtg atggcaaaat atgtcggcga aggtgttaaa 540  
attaaggcag caggtggaat ctcacattg gaagatgcta aaacatttat tgcttagga 600  
gcttcacgt tgggtactag ccgtatcatc aagattgta agaacgaagc tacaaaaccc 660  
gatagctatt aa 672

**SEQ ID NO:** 45

<211> 223

<212> PRT

<213> Streptococcus pyogenes

<400> 45

Met Glu Val Lys Asp Ile Leu Lys Thr Val Asp His Thr Leu Leu Ala  
1 5 10 15

Thr Thr Ala Thr Trp Pro Glu Ile Gln Thr Ile Leu Asp Asp Ala Met  
20 25 30

Ala Tyr Glu Thr Ala Ser Ala Cys Ile Pro Ala Ser Tyr Val Lys Lys  
35 40 45

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

Phe Pro Asn Gly Tyr Ser Thr Thr Ala Ala Lys Val Phe Glu Cys Gln  
65 70 75 80

Asp Ala Ile Gln Asn Gly Ala Asp Glu Ile Asp Met Val Ile Asn Leu  
85 90 95

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

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

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

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

Ala Gly Ala Thr Phe Glu Asp Val Glu Val Met Ala Lys Tyr Val Gly  
165 170 175

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

Ala Lys Thr Phe Ile Ala Leu Gly Ala Ser Arg Leu Gly Thr Ser Arg  
195 200 205

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

**SEQ ID NO:** 46

<211> 783

<212> DNA

<213> Rhodopirellula baltica

<400> 46

ttgcgcgaca cccgacctcc tgccgcatcg ctatcgcttc acggaaacct gctcaccatg 60  
gctgactatc aatatcacga cgtctccaag atgattgacc actcgctgct tccaccaca 120  
ctgaccgaag cggacttgga ttccggcatc gatttggcaa tcgcttatga agtcgccagc 180  
gtttgtatct tgccctacta cttgaaacgt tgtgctgcga agctcgcggg caccggcgtg 240  
aaagcgtcaa ccacgatcgg ttttctcat ggtggtcaca ccaccgcgat caagaaagcc 300  
gaagccgaac aagccatcca agatggctgc gaagaactcg acttcgtcgt caacatctcg 360  
caagtctga gcggcggttg ggactacgtc caaatgaaa ttggcgaggt caccgaactg 420  
acccatgcgg ccggacaaaa gatcaaggtg atcttcgaga actgctacct gcaggacgaa 480

cacaagattc gtctgtgcga gatctgcacc gagctcaaag tggactgggt caaacatcg 540  
 actggttatg gaactggagg cgcgaccatg gacgacctgc gtctgatgcg acaacactca 600  
 ggcgaaaacg tccaagtcaa agctgccggt ggcgtccgag atctcgcgac actgctggag 660  
 gtccgagccc tcggagcatc ccgttgcggt gccagccgaa ccgccgagat gctgggcgaa 720  
 gcccgaaagc aacttggcat gcccgcgatt gaaatcacgc cgaccggcag ctccggctac 780  
 tga 783

**SEQ ID NO: 47**

<211> 260

<212> PRT

<213> Rhodopirellula baltica

<400> 47

Met Arg Asp Thr Arg Pro Pro Ala Ala Ser Leu Ser Leu His Gly Asn  
 1 5 10 15

Leu Leu Thr Met Ala Asp Tyr Gln Tyr His Asp Val Ser Lys Met Ile  
 20 25 30

Asp His Ser Leu Leu Pro Pro Thr Leu Thr Glu Ala Asp Leu Asp Ser  
 35 40 45

Gly Ile Asp Leu Ala Ile Ala Tyr Glu Val Ala Ser Val Cys Ile Leu  
 50 55 60

Pro Tyr Tyr Leu Lys Arg Cys Ala Ala Lys Leu Ala Gly Thr Gly Val  
 65 70 75 80

Lys Ala Ser Thr Thr Ile Gly Phe Pro His Gly Gly His Thr Thr Ala  
 85 90 95

Ile Lys Lys Ala Glu Ala Glu Gln Ala Ile Gln Asp Gly Cys Glu Glu  
 100 105 110

Leu Asp Phe Val Val Asn Ile Ser Gln Val Leu Ser Gly Gly Trp Asp  
 115 120 125

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

Gly Gln Lys Ile Lys Val Ile Phe Glu Asn Cys Tyr Leu Gln Asp Glu  
145 150 155 160

His Lys Ile Arg Leu Cys Glu Ile Cys Thr Glu Leu Lys Val Asp Trp  
165 170 175

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

Leu Arg Leu Met Arg Gln His Ser Gly Glu Asn Val Gln Val Lys Ala  
195 200 205

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

Gly Ala Ser Arg Cys Gly Ala Ser Arg Thr Ala Glu Met Leu Gly Glu  
225 230 235 240

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

Ser Ser Gly Tyr  
260

**SEQ ID NO: 48**

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 48

cgggatccac tgatctgaaa gcaagcagcc

**SEQ ID NO:** 49

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 49

gcaagcttgc tgctggcgct cttacc

26