

SGI1660-1WO\_ST25.txt  
SEQUENCE LISTING

<110> SYNTHETIC GENOMICS, INC.  
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GRIFFIN, Benjamin M.  
MARTIN, Kevin V.

<120> COMPOSITIONS AND METHODS FOR PRODUCING CHEMICALS AND DERIVATIVES  
THEREOF

<130> SGI1660-1WO

<140> PCT/US2013/061036  
<141> 2013-09-20

<150> US 61/704,408  
<151> 2012-09-21

<160> 72

<170> PatentIn version 3.5

<210> 1  
<211> 267  
<212> PRT  
<213> Agrobacterium tumefaciens

<400> 1

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Arg Val Met Arg Lys Arg Leu Ala Ser Met Ala Glu Ile Val Arg Leu  
20 25 30

Ala Asp Leu Ala Pro Leu Asp Pro Ala Gly Pro Asn Glu Glu Cys Met  
35 40 45

Gln Cys Asp Leu Ala Asp Ala Asp Ala Val Asp Ala Met Val Ala Gly  
50 55 60

Cys Asp Gly Ile Val His Leu Gly Gly Ile Ser Val Glu Lys Pro Phe  
65 70 75 80

Glu Gln Ile Leu Gln Gly Asn Ile Ile Gly Leu Tyr Asn Leu Tyr Glu  
85 90 95

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Ala Ala Arg Ala His Gly Gln Pro Arg Ile Ile Phe Ala Ser Ser Asn  
 100 105 110

His Thr Ile Gly Tyr Tyr Pro Gln Thr Glu Arg Leu Gly Pro Asp Val  
 115 120 125

Pro Phe Arg Pro Asp Gly Leu Tyr Gly Val Ser Lys Cys Phe Gly Glu  
 130 135 140

Ser Leu Ala Arg Met Tyr Phe Glu Lys Phe Gly Gln Glu Thr Ala Leu  
 145 150 155 160

Val Arg Ile Gly Ser Cys Thr Pro Glu Pro Leu Asn Tyr Arg Met Leu  
 165 170 175

Ser Thr Trp Phe Ser His Asp Asp Phe Val Ser Leu Ile Glu Ala Ala  
 180 185 190

Phe Arg Ala Pro Val Leu Gly Cys Pro Ile Val Trp Gly Ala Ser Ala  
 195 200 205

Asn Asp Ala Ser Trp Trp Asp Asn Ser His Leu Gly Phe Ile Gly Trp  
 210 215 220

Lys Pro Lys Asp Asn Ala Glu Ala Phe Arg Arg Lys Ile Ala Glu Thr  
 225 230 235 240

Thr Pro Gln Pro Asp Ala Arg Asp Pro Ile Val Arg Phe Gln Gly Gly  
 245 250 255

Val Phe Val Asp Asn Pro Ile Phe Lys Glu Thr  
 260 265

<210> 2

<211> 266

<212> PRT

<213> Rhizobium lupini

<400> 2

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

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

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

Asp Leu Ala Asp Ala Lys Ala Val His Ala Leu Val Glu Asp Cys Asp  
 50 55 60

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

Ile Val Ala Gly Asn Ile Val Gly Leu Tyr Asn Leu Tyr Glu Ala Ala  
 85 90 95

Arg Ala His Arg Met Pro Arg Ile Val Phe Ala Ser Ser Asn His Thr  
 100 105 110

Ile Gly Phe Tyr Pro Gln Thr Glu Arg Leu Ser Val Asp His Pro Tyr  
 115 120 125

Arg Pro Asp Gly Leu Tyr Gly Val Ser Lys Cys Phe Gly Glu Ser Leu  
 130 135 140

Ala His Met Tyr His Glu Lys Phe Gly Gln Glu Thr Ala Leu Val Arg  
 145 150 155 160

Ile Gly Ser Cys Val Thr Glu Pro Val Asn His Arg Met Leu Ser Thr  
 165 170 175

Trp Leu Ser Tyr Asp Asp Phe Val Ser Leu Ile Glu Ala Val Phe Arg  
 180 185 190

Ala Pro Lys Leu Gly Cys Pro Val Ile Trp Gly Ala Ser Asn Asn Asp  
 195 200 205

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Ala Gly Trp Trp Asp Asn Ser Ala Ala Gly Phe Leu Gly Trp Lys Pro  
210 215 220

Lys Asp Asn Ala Glu Ile Phe Arg Ser Lys Ile Glu Ala Ala Cys Glu  
225 230 235 240

Arg Pro Gly Ser Asp Asp Pro Ala Ala Arg Trp Gln Gly Gly Leu Phe  
245 250 255

Thr Gln Asp Pro Ile Phe Pro Glu Asp Glu  
260 265

<210> 3  
<211> 272  
<212> PRT  
<213> Pseudomonas sp.

<400> 3

Met Thr Thr Ala Tyr Thr Pro Phe Asn Arg Leu Leu Leu Thr Gly Ala  
1 5 10 15

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

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

Ala His Glu Glu Val Gln Val Cys Asp Leu Ala Asp Lys Ala Ala Val  
50 55 60

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

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

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

Ile Phe Ala Ser Ser Asn His Val Ile Gly Phe Tyr Lys Gln Asp Glu

115

120

125

Thr Ile Asp Ala Asn Cys Pro Arg Arg Pro Asp Ser Tyr Tyr Gly Leu  
 130 135 140

Ser Lys Ser Tyr Gly Glu Asp Met Ala Ser Phe Tyr Phe Asp Arg Tyr  
 145 150 155 160

Gly Ile Glu Thr Val Ser Ile Arg Ile Gly Ser Ser Phe Pro Glu Pro  
 165 170 175

His Asn Arg Arg Met Met Ser Thr Trp Leu Ser Phe Ala Asp Leu Thr  
 180 185 190

Gln Leu Leu Glu Arg Ala Leu Tyr Thr Pro Asn Val Gly His Thr Val  
 195 200 205

Val Tyr Gly Met Ser Ala Asn Lys Asn Val Trp Trp Asp Asn His Leu  
 210 215 220

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

Ala Gln Ile Asp Ala Gln Pro Met Pro Ala Ala Asp Asp Pro Ala Met  
 245 250 255

Val Phe Gln Gly Gly Ala Phe Val Ala Ala Gly Pro Phe Gly Asp Asp  
 260 265 270

&lt;210&gt; 4

&lt;211&gt; 804

&lt;212&gt; DNA

&lt;213&gt; Agrobacterium Tumefaciens

&lt;400&gt; 4

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aaacgccttg catcgatggc cgagatcggt cgccttgccg atctcgcccc gctcgatccg 120

gcaggcccga acgaggaatg catgcaatgc gaccttgccg atgcagacgc cgttgacgcc 180

atggttgccg gttgcgacgg catcggtcac ctcggcgcca tatcggtgga gaagcctttc 240

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|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaacaaatcc ttcagggcaa catcatcggg ctgtataatc tctatgaggc cgcccgcgcc  | 300 |
| cacggccagc cgcgcatcat cttcgccagt tcgaaccata cgatcggtta ttaccgcag   | 360 |
| acggagaggc ttggaccgga tgttcccttc cgcccggatg ggctttacgg cgtctccaaa  | 420 |
| tgtttcggcg agagccttgc ccgcatgtat ttcgagaaat tcggccagga gaccgcactt  | 480 |
| gtccgcatcg gtcctgcac gccggaaccc ctttaattacc gcatgctgtc cacctggttt  | 540 |
| tcgcatgacg atttcgtctc gctgatcgag gcggcgttcc gcgccccgt gctcggctgc   | 600 |
| cccatcgtct ggggggctgc ggccaacgat gcgagctggg gggacaattc gcatctcggc  | 660 |
| tttattggat ggaaaccgaa ggacaatgcc gaggccttcc gccggaagat tgccgaaacg  | 720 |
| acgccgcagc cggacgcgcg cgacccgatt gtccgctttc aggggtggcgt gtttgtcgac | 780 |
| aacccgatct tcaaggagac gtga                                         | 804 |

<210> 5  
 <211> 801  
 <212> DNA  
 <213> Rhizobium lupini

|                                                                              |     |
|------------------------------------------------------------------------------|-----|
| <400> 5<br>atgaagagac ttctgattac cggcgcagcg ggtgcactgg gccgcgtgat gcgggaaagg | 60  |
| ctcgcaccca tggcaacgat tctgcgcctt tccgatatcg ccccgattgg agcggcccg             | 120 |
| cagaacgagg aaatcgtcca gtgcgatctt gccgatgcca aagcagtgca tgctctggtc            | 180 |
| gaagattgcg acgggatcgt ccatctcggg ggcgtctcag tagagcgcaa gttctcgcag            | 240 |
| atcgctcgccg gcaacatcgt cggcctttac aatctctacg aagccgcacg cgcgcatcgg           | 300 |
| atgccgcgca tcgtctttgc aagttccaat cacaccatcg gcttttatcc gcaaaccgaa            | 360 |
| cggttgtcgg tggaccatcc ctatcgtccg gacgggctct acggcgtatc gaaatgtttc            | 420 |
| ggcgagtctc tggcgcatat gtaccatgag aagttcgggc aggagacggc actcgtgcgc            | 480 |
| atcgggtcct gcgtgaccga accggtcaac catcgcatgc tttccacctg gctttcctac            | 540 |
| gatgatttcg tctcgcttat cgaggccgta ttccgtgcgc cgaaactcgg ctgccccgtc            | 600 |
| atctggggcg cgtcgaacaa cgatgcagga tgggtgggaca attccgccgc cggctttctc           | 660 |
| ggctggaagc cgaaagacaa tgccgaaatc ttccgttcga agatcgaagc cgcttgcgaa            | 720 |

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cgccccggtt ctgatgatcc ggccgcccgc tggcaaggcg ggctcttcac gcaggaccgc 780  
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<210> 6  
<211> 819  
<212> DNA  
<213> Pseudomonas sp.

<400> 6  
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ggcaagggtcc tgcgcgaaag cctgcgacct tatgccaacg tcctgcgcgt ctccgacatc 120  
gcggcccatga gccctgccac aggcgccccat gaagaagtcc aggtctgcga cctcgccgat 180  
aaagcggcgg tccatcaact ggtcgaaggc gtcgacgcaa tcctgcactt cgggtggcgta 240  
tcggtggagc ggcccttcga ggaaatcctc ggggccaata tctgcggcgt gtttcatatc 300  
tatgaagcgg cgcgccggca tggcgtaaag cgggtgatct tcgccagctc caaccacgtc 360  
atcggttttt ataagcagga cgaaaccatc gacgccaaact gcccgcgccg ccccgacagc 420  
tactacggtc tgtccaagtc ctacggcgaa gacatggcca gcttctactt cgaccgctac 480  
ggcatcgaga ccgtgagcat ccgcatcggc tcctcgttcc ccgagccgca caatcgccgc 540  
atgatgagca cctgggtgag ctttgccgac ctgacgcagc tgctcgaacg cgcgctgtac 600  
acccccaacg tcggccacac cgtgggtctac ggcatgtccg ctaacaagaa cgtctggtgg 660  
gacaaccacc tggccgcgca cctgggcttc caaccgaagg acagctccga ggtgttccgt 720  
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ggcgcctttg tcgcagccgg gccgttcggc gacgactga 819

<210> 7  
<211> 274  
<212> PRT  
<213> Rhizobium sp.

<400> 7

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

Ser Leu Asp Thr Glu Gly Leu Arg Arg His Phe Leu Ala Gln Gly Leu

20

25

30

Phe Ala Glu Gly Glu Ile Arg Leu Ile Tyr Thr His Tyr Asp Arg Phe  
           35                          40                          45

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

Val Glu Glu Thr Lys Thr Pro Gly Phe Leu Asp Arg Arg Glu Met Gly  
   65                          70                          75                          80

Ile Val Asn Ile Gly Ala Glu Gly Ser Val His Ala Gly Asn Glu Ser  
                           85                          90                          95

Trp Ser Leu Asn Arg Gly Asp Val Leu Tyr Leu Gly Met Gly Ala Gly  
                           100                          105                          110

Pro Val Thr Phe Glu Gly Ala Gly Arg Phe Tyr Leu Val Ser Ala Pro  
           115                          120                          125

Ala His Arg Ser Leu Pro Asn Arg Leu Val Thr Pro Ala Asp Ser Lys  
       130                          135                          140

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

Gln Phe Ile His Pro Leu Val Met Glu Ser Cys Gln Leu Val Leu Gly  
                           165                          170                          175

Tyr Thr Thr Leu Glu Asp Gly Ser Val Trp Asn Thr Met Pro Ala His  
           180                          185                          190

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

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

Leu Phe Val Ala Asn Glu Glu Gly Ala Ile Ser Pro Pro Trp Ser Ile



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Asn Cys Ala Pro Ala His Thr Thr Tyr Pro Thr Lys Lys Val Thr Pro  
130 135 140

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

Arg Thr Ile Asn Lys Tyr Phe Val Pro Asp Val Leu Glu Thr Cys Gln  
165 170 175

Leu Ser Met Gly Leu Thr Glu Leu Ala Pro Gly Asn Leu Trp Asn Thr  
180 185 190

Met Pro Cys His Thr His Glu Arg Arg Met Glu Val Tyr Phe Tyr Phe  
195 200 205

Asn Met Asp Asp Asp Ala Cys Val Phe His Met Met Gly Gln Pro Gln  
210 215 220

Glu Thr Arg His Ile Val Met His Asn Glu Gln Ala Val Ile Ser Pro  
225 230 235 240

Ser Trp Ser Ile His Ser Gly Val Gly Thr Lys Ala Tyr Thr Phe Ile  
245 250 255

Trp Gly Met Val Gly Glu Asn Gln Val Phe Asp Asp Met Asp His Val  
260 265 270

Ala Val Lys Asp Leu Arg  
275

<210> 9  
<211> 278  
<212> PRT  
<213> Rhizobium sp.

<400> 9

Met Thr Met Lys Ile Leu Tyr Gly Ala Gly Pro Glu Asp Val Lys Gly  
1 5 10 15

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Tyr Asp Thr Gln Arg Leu Arg Asp Ala Phe Leu Leu Asp Asp Leu Phe  
20 25 30

Ala Asp Asp Arg Val Ser Phe Thr Tyr Thr His Val Asp Arg Leu Ile  
35 40 45

Leu Gly Gly Ala Val Pro Val Thr Thr Ser Leu Thr Phe Gly Ser Gly  
50 55 60

Thr Glu Ile Gly Thr Pro Tyr Leu Leu Ser Ala Arg Glu Met Gly Ile  
65 70 75 80

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

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

Met Thr Ala Ser Ser Leu Ser Ala Glu Arg Pro Ala Arg Phe Tyr Met  
115 120 125

Asn Ser Val Pro Ala Gly Ala Asp Phe Pro His Arg Leu Ile Thr Arg  
130 135 140

Gly Glu Ala Lys Pro Leu Asp Leu Gly Asp Ala Arg Arg Ser Asn Arg  
145 150 155 160

Arg Arg Leu Ala Met Tyr Ile His Pro Glu Val Ser Pro Ser Cys Leu  
165 170 175

Leu Leu Met Gly Ile Thr Asp Leu Ala Glu Gly Ser Ala Trp Asn Thr  
180 185 190

Met Pro Pro His Leu His Glu Arg Arg Met Glu Ala Tyr Cys Tyr Phe  
195 200 205

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

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

Ala Trp Ser Ile His Met Gly Ala Gly Thr Gly Pro Tyr Ala Phe Val  
245 250 255

Trp Gly Met Thr Gly Glu Asn Gln Glu Tyr Asn Asp Val Ala Pro Val  
260 265 270

Ala Val Ala Asp Leu Lys  
275

<210> 10  
<211> 274  
<212> PRT  
<213> Pannonibacter phragmitetus

<400> 10

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

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

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

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

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

Val Val Asn Val Gly Ala Ser Gly Lys Val Ser Ala Ala Gly Glu Thr  
85 90 95

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

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

Ala His Ala Ala Tyr Pro Ala Arg Leu Ile Arg Ile Gly Glu Ala Glu  
 130 135 140

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

Gln Phe Val His Pro Ala Val Met Thr Ser Cys Gln Leu Val Val Gly  
 165 170 175

Tyr Thr Gln Leu His Asn Gly Ser Val Trp Asn Thr Met Pro Ala His  
 180 185 190

Val His Asp Arg Arg Met Glu Ala Tyr Leu Tyr Phe Asp Met Lys Pro  
 195 200 205

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

Leu Val Met Lys Asn Glu Asp Ala Val Val Ser Pro Pro Trp Ser Ile  
 225 230 235 240

His Cys Gly Ala Gly Thr Gly Ser Tyr Thr Phe Ile Trp Ala Met Ala  
 245 250 255

Gly Asp Asn Val Asp Tyr Lys Asp Val Glu Met Val Ala Met Glu Asp  
 260 265 270

Leu Arg

<210> 11

<211> 271

<212> PRT

<213> Bacillus subtilis

<400> 11

Met Ser Tyr Leu Leu Arg Lys Pro Gln Ser Asn Glu Val Ser Asn Gly

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Val Lys Leu Val His Glu Val Thr Lys Ser Asn Ser Asp Leu Thr Tyr
    20              25              30

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

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

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

Ser Val Phe Glu Arg Lys Pro Thr Asp Ser Val Tyr Ile Ser Asn Asp
    85              90              95

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

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

Asp Asn Gly Ile Glu His Arg Gly Lys Phe Ser Asn Lys Arg Thr Val
    130             135             140

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

Val Glu Val Tyr Thr Asp Ser Gly Asn Trp Ser Ser Tyr Pro Pro His
    165             170             175

Lys His Asp Gln Asp Asn Leu Pro Glu Glu Ser Phe Leu Glu Glu Thr
    180             185             190

Tyr Tyr His Glu Leu Asp Pro Gly Gln Gly Phe Val Phe Gln Arg Val
    195             200             205

Tyr Thr Asp Asp Arg Ser Ile Asp Glu Thr Met Thr Val Glu Asn Glu

```

210

215

220

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

Gly Tyr Thr Ser Tyr Tyr Leu Asn Val Met Ala Gly Pro Thr Arg Lys  
 245 250 255

Trp Lys Phe His Asn Asp Pro Ala His Glu Trp Ile Leu Glu Arg  
 260 265 270

&lt;210&gt; 12

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Ochrobactrum anthropi

&lt;400&gt; 12

Met Ala Asn Leu Leu Arg Lys Pro Asn Gly Thr His Gly Lys Val His  
 1 5 10 15

Asp Ile Thr Pro Glu Asn Ala Lys Trp Gly Tyr Val Gly Phe Gly Leu  
 20 25 30

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

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

Gly Glu Asp Phe Gly Glu Met Gly Glu Arg Leu Asn Val Phe Glu Lys  
 65 70 75 80

Leu Pro Pro His Cys Leu Tyr Val Pro Ala Glu Ser Asp Trp His Ala  
 85 90 95

Thr Ala Thr Thr Asp Cys Val Leu Ala Val Cys Thr Ala Pro Gly Lys  
 100 105 110

Pro Gly Arg Lys Ala Gln Lys Leu Gly Pro Glu Ser Leu Thr Leu Glu  
 115 120 125

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Gln Arg Gly Lys Gly Ala Asn Thr Arg Phe Ile His Asn Ile Ala Met  
130 135 140

Glu Ser Arg Asp Val Ala Asp Ser Leu Leu Val Thr Glu Val Phe Thr  
145 150 155 160

Pro Gln Gly Asn Trp Ser Ser Tyr Pro Pro His Arg His Asp Glu Asp  
165 170 175

Asn Phe Pro Asp Met Thr Tyr Leu Glu Glu Thr Tyr Tyr His Arg Leu  
180 185 190

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

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

Pro Lys Gly His His Pro Cys Gly Ala Pro Tyr Gly Tyr Glu Met Tyr  
225 230 235 240

Tyr Leu Asn Val Met Ala Gly Pro Leu Arg Lys Trp Arg Phe Lys Asn  
245 250 255

His Pro Asp His Asp Trp Ile Phe Lys Arg Asp Asn Pro  
260 265

<210> 13  
<211> 268  
<212> PRT  
<213> Halomonas titanicae

<400> 13

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

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

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

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

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

Glu Gln Ile Pro Pro Tyr Ala Val Tyr Leu Pro Asp His Val Ser Tyr  
85 90 95

Ala Val Glu Ala Thr Thr Asp Leu Glu Leu Ala Val Cys Thr Ala Pro  
100 105 110

Gly His Gly Asn His Ala Pro Arg Leu Ile Ala Pro Asp Asn Ile Lys  
115 120 125

Gln Ser Thr Arg Gly Gln Gly Thr Asn Thr Arg His Val His Asp Ile  
130 135 140

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

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

Asp Asn Leu Pro His Glu Ser His Leu Glu Glu Thr Tyr Tyr His Arg  
180 185 190

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

Arg Ser Leu Asp Glu Thr Met Ala Val Glu Asn Gly Cys Cys Val Leu  
210 215 220

Val Pro Lys Gly Tyr His Pro Val Gly Ala Ser His Gly Tyr Ser Leu  
225 230 235 240

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Tyr Tyr Leu Asn Val Met Ala Gly Pro Lys Arg Ala Trp Lys Phe His  
                     245                    250                    255

Asn Asp Pro Asp His Glu Trp Leu Met Asn Ala Gly  
                     260                    265

<210> 14

<211> 264

<212> PRT

<213> Acidiphilium multivorum

<400> 14

Met Pro Asp Leu Leu Arg Lys Pro Phe Gly Thr His Gly Lys Val His  
   1                    5                    10                    15

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

Tyr Arg Leu Arg Ala Gly Glu Phe Ala Ala Glu Ala Thr Gly Gly Asn  
                     35                    40                    45

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

Gly Arg Asp Trp Gly Val Leu Gly Glu Arg Met Ser Val Phe Glu Lys  
   65                    70                    75                    80

Ser Pro Pro His Ser Leu Tyr Val Pro Asn Gly Ala Glu Trp Ala Leu  
                     85                    90                    95

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

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

Ala Arg Gly Glu Gly Thr Asn Thr Arg His Ile Asn Asn Ile Ala Met  
   130                    135                    140

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Glu Ala Glu Asp Tyr Cys Asp Ala Leu Leu Val Thr Glu Val Phe Thr  
145 150 155 160

Pro Ala Gly His Trp Ser Ser Tyr Pro Ser His Arg His Asp Glu Asp  
165 170 175

Asp Asp Pro Arg Ile Thr Tyr Leu Glu Glu Thr Tyr Tyr His Arg Leu  
180 185 190

Asn Pro Ala Ser Gly Phe Gly Val Gln Arg Val Tyr Thr Asp Asp Arg  
195 200 205

Ala Leu Asp Gln Thr Met Ala Val Ser Asp Gly Asp Val Val Leu Val  
210 215 220

Pro Arg Gly His His Pro Cys Ala Ala Pro Tyr Gly Ile Glu Met Tyr  
225 230 235 240

Tyr Leu Asn Val Met Ala Gly Pro Leu Arg Lys Trp Arg Phe Leu Pro  
245 250 255

Asp Pro Glu Leu Gly Ile Ala Lys  
260

<210> 15  
<211> 271  
<212> PRT  
<213> Lactobacillus casei

<400> 15

Met Ser Leu Leu Tyr His Lys Gln Asn Gln Glu Leu Ser Ser Gly Val  
1 5 10 15

Arg Leu Ile Gln Asp Val Asn Ala Ser Asn Ser Pro Met Lys Tyr Thr  
20 25 30

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

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

50

55

60

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

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

Ala Phe Gly Ile Arg Ala Lys Gln Ala Ala Lys Ile Leu Ile Ala Tyr  
 100 105 110

Ala Pro Thr Asn Gln Thr Phe Pro Val Arg Leu Ile Arg Gly Asn Ile  
 115 120 125

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

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

Glu Val Tyr Thr Asp Ser Ala Asn Trp Ser Ser Tyr Pro Pro His Arg  
 165 170 175

His Asp His Asp Asp Leu Pro Ala Glu Ser Leu Leu Glu Glu Ile Tyr  
 180 185 190

Tyr His Glu Met Arg Pro Lys Gln Gly Phe Val Phe Gln Arg Val Tyr  
 195 200 205

Thr Asp Asp Leu Ser Leu Asp Glu Thr Met Ala Val Gln Asn Gln Asp  
 210 215 220

Val Val Val Val Pro Lys Gly Tyr His Pro Val Gly Val Pro Asp Gly  
 225 230 235 240

Tyr Asp Ser Tyr Tyr Leu Asn Val Met Ala Gly Pro Thr Arg Val Trp  
 245 250 255

His Phe His Asn Ala Pro Glu His Ala Trp Ile Ile Asp Arg Gln

260

265

270

&lt;210&gt; 16

&lt;211&gt; 466

&lt;212&gt; PRT

&lt;213&gt; Bacteroides sp.

&lt;400&gt; 16

Met Lys Lys Phe Met Asp Glu Asn Phe Leu Leu Gln Thr Glu Thr Ala  
 1 5 10 15

Gln Lys Leu Tyr His Asn His Ala Ala Asn Met Pro Ile Phe Asp Tyr  
 20 25 30

His Cys His Ile Asn Pro Lys Asp Ile Ala Glu Asp Arg Met Phe Lys  
 35 40 45

Thr Ile Thr Glu Ile Trp Leu Tyr Gly Asp His Tyr Lys Trp Arg Ala  
 50 55 60

Met Arg Thr Asn Gly Val Asp Glu Arg Phe Cys Thr Gly Asp Ala Ser  
 65 70 75 80

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

Arg Asn Pro Leu Tyr His Trp Thr His Leu Glu Leu Lys Lys Phe Phe  
 100 105 110

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

Ala Cys Asn Glu Lys Leu Gln Thr Pro Ala Tyr Ser Cys Arg Asn Ile  
 130 135 140

Ile Arg Met Ala Asn Val His Thr Ile Cys Thr Thr Asp Asp Pro Val  
 145 150 155 160

Asp Thr Leu Glu Tyr His Gln Gln Ile Lys Glu Asp Gly Phe Glu Val  
 165 170 175

SGI1660-1WO\_ST25.txt

Ala Val Leu Pro Ala Trp Arg Pro Asp Lys Ala Met Met Val Glu Asp  
180 185 190

Pro Lys Phe Phe Asn Asp Tyr Met Asp Gln Leu Ala Glu Ala Ala Gly  
195 200 205

Ile His Ile Glu Ser Phe Glu Asp Leu Met Glu Ala Leu Asp Thr Arg  
210 215 220

His Gln Tyr Phe His Asp Asn Gly Cys Arg Leu Ser Asp His Gly Leu  
225 230 235 240

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

Phe Lys Lys Ile Arg Gly Gly Ser Arg Leu Ser Glu Thr Glu Ile Leu  
260 265 270

Lys Phe Lys Ser Cys Met Leu Tyr Glu Tyr Gly Val Met Asp His Ser  
275 280 285

Arg Gly Trp Thr Gln Gln Leu His Ile Gly Ala Gln Arg Asn Asn Asn  
290 295 300

Thr Arg Leu Phe Lys Lys Leu Gly Pro Asp Thr Gly Phe Asp Ser Ile  
305 310 315 320

Gly Asp Lys Pro Ile Ala Glu Pro Leu Ala Lys Leu Leu Asp Arg Leu  
325 330 335

Asp Gln Glu Asn Lys Leu Cys Lys Thr Val Leu Tyr Asn Leu Asn Pro  
340 345 350

Arg Asp Asn Glu Leu Tyr Ala Thr Met Leu Gly Asn Phe Gln Asp Gly  
355 360 365

Ser Val Pro Gly Lys Ile Gln Tyr Gly Ser Gly Trp Trp Phe Leu Asp  
370 375 380

SGI1660-1WO\_ST25.txt

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

Leu Leu Ser Arg Phe Val Gly Met Leu Thr Asp Ser Arg Ser Phe Leu  
405 410 415

Ser Tyr Thr Arg His Glu Tyr Phe Arg Arg Thr Leu Cys Asn Leu Leu  
420 425 430

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

Gly Ser Met Val Glu Asn Ile Cys Phe Asn Asn Ala Lys Asn Tyr Phe  
450 455 460

Asn Phe  
465

<210> 17  
<211> 451  
<212> PRT  
<213> Thermotoga maritima MSB8

<400> 17

Met Phe Leu Gly Glu Asp Tyr Leu Leu Thr Asn Arg Ala Ala Val Arg  
1 5 10 15

Leu Phe Asn Glu Val Lys Asp Leu Pro Ile Val Asp Pro His Asn His  
20 25 30

Leu Asp Ala Lys Asp Ile Val Glu Asn Lys Pro Trp Asn Asp Ile Trp  
35 40 45

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

Cys Gly Val Ser Glu Glu Tyr Ile Thr Gly Ser Arg Ser Asn Lys Glu  
65 70 75 80

SGI1660-1WO\_ST25.txt

Lys Trp Leu Ala Leu Ala Lys Val Phe Pro Arg Phe Val Gly Asn Pro  
85 90 95

Thr Tyr Glu Trp Ile His Leu Asp Leu Trp Arg Arg Phe Asn Ile Lys  
100 105 110

Lys Val Ile Ser Glu Glu Thr Ala Glu Glu Ile Trp Glu Glu Thr Lys  
115 120 125

Lys Lys Leu Pro Glu Met Thr Pro Gln Lys Leu Leu Arg Asp Met Lys  
130 135 140

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

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

Trp Arg Pro Asp Arg Ala Met Asn Val Asp Lys Glu Gly Trp Arg Glu  
180 185 190

Tyr Val Glu Lys Met Gly Glu Arg Tyr Gly Glu Asp Thr Ser Thr Leu  
195 200 205

Asp Gly Phe Leu Asn Ala Leu Trp Lys Ser His Glu His Phe Lys Glu  
210 215 220

His Gly Cys Val Ala Ser Asp His Ala Leu Leu Glu Pro Ser Val Tyr  
225 230 235 240

Tyr Val Asp Glu Asn Arg Ala Arg Ala Val His Glu Lys Ala Phe Ser  
245 250 255

Gly Glu Lys Leu Thr Gln Asp Glu Ile Asn Asp Tyr Lys Ala Phe Met  
260 265 270

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

SGI1660-1W0\_ST25.txt

Leu His Ile Gly Ala Leu Arg Asp Tyr Arg Asp Ser Leu Phe Lys Thr  
 290 295 300

Leu Gly Pro Asp Ser Gly Gly Asp Ile Ser Thr Asn Phe Leu Arg Ile  
 305 310 315 320

Ala Glu Gly Leu Arg Tyr Phe Leu Asn Glu Phe Asp Gly Lys Leu Lys  
 325 330 335

Ile Val Leu Tyr Val Leu Asp Pro Thr His Leu Pro Thr Ile Ser Thr  
 340 345 350

Ile Ala Arg Ala Phe Pro Asn Val Tyr Val Gly Ala Pro Trp Trp Phe  
 355 360 365

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

Val Asp Leu Leu Tyr Asn Leu Ala Gly Met Val Thr Asp Ser Arg Lys  
 385 390 395 400

Leu Leu Ser Phe Gly Ser Arg Thr Glu Met Phe Arg Arg Val Leu Ser  
 405 410 415

Asn Val Val Gly Glu Met Val Glu Lys Gly Gln Ile Pro Ile Lys Glu  
 420 425 430

Ala Arg Glu Leu Val Lys His Val Ser Tyr Asp Gly Pro Lys Ala Leu  
 435 440 445

Phe Phe Gly  
 450

<210> 18

<211> 427

<212> PRT

<213> Bacillus halodurans

<400> 18

## SGI1660-1WO\_ST25.txt

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

Val Asn Asn Gln Pro Val Thr Asp Met His Thr His Leu Phe Ser Pro  
 20 25 30

Asn Phe Gly Glu Ile Leu Leu Trp Asp Ile Asp Glu Leu Leu Thr Tyr  
 35 40 45

His Tyr Leu Val Ala Glu Val Met Arg Trp Thr Asp Val Ser Ile Glu  
 50 55 60

Ala Phe Trp Ala Met Ser Lys Arg Glu Gln Ala Asp Leu Ile Trp Glu  
 65 70 75 80

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

Leu Thr Cys Leu Gln Gly Leu Gly Leu Asp Pro Ala Thr Arg Asp Leu  
 100 105 110

Gln Val Tyr Arg Glu Tyr Phe Ala Lys Lys Thr Ser Glu Glu Gln Val  
 115 120 125

Asp Thr Val Leu Gln Leu Ala Asn Val Ser Asp Val Val Met Thr Asn  
 130 135 140

Asp Pro Phe Asp Asp Asn Glu Arg Ile Ser Trp Leu Glu Gly Lys Gln  
 145 150 155 160

Pro Asp Ser Arg Phe His Ala Ala Leu Arg Leu Asp Pro Leu Leu Asn  
 165 170 175

Glu Tyr Glu Gln Thr Lys His Arg Leu Arg Asp Trp Gly Tyr Lys Val  
 180 185 190

Asn Asp Glu Trp Asn Glu Gly Ser Ile Gln Glu Val Lys Arg Phe Leu  
 195 200 205

## SGI1660-1WO\_ST25.txt

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

Pro Pro Thr Phe Ser Phe Pro Glu Glu Ser Asn Arg Gly Arg Ile Ile  
 225 230 235 240

Arg Asp Cys Leu Leu Pro Val Ala Glu Lys His Asn Ile Pro Phe Ala  
 245 250 255

Met Met Ile Gly Val Lys Lys Arg Val His Pro Ala Leu Gly Asp Ala  
 260 265 270

Gly Asp Phe Val Gly Lys Ala Ser Met Asp Gly Val Glu His Leu Leu  
 275 280 285

Arg Glu Tyr Pro Asn Asn Lys Phe Leu Val Thr Met Leu Ser Arg Glu  
 290 295 300

Asn Gln His Glu Leu Val Val Leu Ala Arg Lys Phe Ser Asn Leu Met  
 305 310 315 320

Ile Phe Gly Cys Trp Trp Phe Met Asn Asn Pro Glu Ile Ile Asn Glu  
 325 330 335

Met Thr Arg Met Arg Met Glu Met Leu Gly Thr Ser Phe Ile Pro Gln  
 340 345 350

His Ser Asp Ala Arg Val Leu Glu Gln Leu Ile Tyr Lys Trp His His  
 355 360 365

Ser Lys Ser Ile Ile Ala Glu Val Leu Ile Asp Lys Tyr Asp Asp Ile  
 370 375 380

Leu Gln Ala Gly Trp Glu Val Thr Glu Glu Glu Ile Lys Arg Asp Val  
 385 390 395 400

Ala Asp Leu Phe Ser Arg Asn Phe Trp Arg Phe Val Gly Arg Asn Asp  
 405 410 415

SGI1660-1WO\_ST25.txt

His Val Thr Ser Val Lys Val Glu Gln Gln Thr  
420 425

<210> 19  
<211> 473  
<212> PRT  
<213> Bacillus subtilis  
  
<400> 19

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

Val Ser Leu Tyr His Asn Tyr Ala Lys Asp Met Pro Ile Ile Asp Tyr  
20 25 30

His Cys His Leu Ser Pro Lys Glu Ile Tyr Glu Asn Lys Thr Phe Gln  
35 40 45

Asn Ile Thr Glu Ala Trp Leu Tyr Gly Asp His Tyr Lys Trp Arg Ile  
50 55 60

Met Arg Ala Asn Gly Ile Glu Glu Thr Tyr Ile Thr Gly Asp Ala Pro  
65 70 75 80

Asp Glu Glu Lys Phe Met Ala Trp Ala Lys Thr Val Pro Met Ala Ile  
85 90 95

Gly Asn Pro Leu Tyr Asn Trp Thr His Leu Glu Leu Gln Arg Phe Phe  
100 105 110

Gly Ile Tyr Glu Ile Leu Asn Glu Lys Ser Gly Ser Ala Ile Trp Lys  
115 120 125

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

Ile Val Lys Ser Asn Val Lys Val Val Cys Thr Thr Asp Asp Pro Val  
145 150 155 160

Asp Ser Leu Glu Tyr His Leu Leu Leu Lys Glu Asp Lys Asp Phe Pro

165

170

175

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

Arg Glu Gly Phe Pro Glu Trp Val Gln Ala Leu Glu Asp Ala Ala Ala  
 195 200 205

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

Val Arg Phe Phe His Ser Ala Gly Gly Arg Val Ser Asp His Ala Ile  
 225 230 235 240

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

Phe Ser Asp Arg Leu Gln Gly Thr Glu Val Ser Cys Glu Asp Glu Lys  
 260 265 270

Lys Phe Lys Thr Tyr Thr Leu Gln Phe Leu Cys Gly Leu Tyr Ala Glu  
 275 280 285

Leu Asp Trp Ala Met Gln Phe His Ile Asn Ala Leu Arg Asn Thr Asn  
 290 295 300

Thr Lys Met Met Lys Arg Leu Gly Pro Asp Thr Gly Tyr Asp Ser Met  
 305 310 315 320

Asn Asp Glu Glu Ile Ala Lys Pro Leu Tyr Lys Leu Leu Asn Ser Val  
 325 330 335

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

Asn Asp Asn Tyr Val Ile Ala Ser Met Ile Asn Ser Phe Gln Asp Gly  
 355 360 365

Ile Thr Pro Gly Lys Ile Gln Phe Gly Thr Ala Trp Trp Phe Asn Asp

370

375

380

Thr Lys Asp Gly Met Leu Asp Gln Met Lys Ala Leu Ser Asn Val Gly  
 385 390 395 400

Leu Phe Ser Arg Phe Ile Gly Met Leu Thr Asp Ser Arg Ser Phe Leu  
 405 410 415

Ser Tyr Thr Arg His Glu Tyr Phe Arg Arg Ile Val Cys Asn Leu Ile  
 420 425 430

Gly Glu Trp Val Glu Asn Gly Glu Val Pro Arg Asp Met Glu Leu Leu  
 435 440 445

Gly Ser Ile Val Gln Gly Ile Cys Tyr Asp Asn Ala Lys His Tyr Phe  
 450 455 460

Gln Phe Gln Glu Glu Lys Ala Asn Val  
 465 470

&lt;210&gt; 20

&lt;211&gt; 825

&lt;212&gt; DNA

&lt;213&gt; Rhizobium sp.

&lt;400&gt; 20

atgctcaacg tggaaacgag gcacgccgtt cacgcggatc acgcgagatc actcgacaca 60

gagggcctgc gccggcactt cctggcccag ggcctgtttg cggagggcga gatacggctg 120

atctatacgc attatgatcg attcgtcatg ggaggcgccg tgccggacgg cgcgccactt 180

gtgctcgatc atgtcgagga gacgaaaacg ccgggctttc tcgaccgacg ggagatggga 240

atcgtcaata tcggtgctga gggcagcgtg catgccggca acgaaagctg gtcgctgaac 300

cgtggtgacg tactttatct cggcatgggg gcgggaccgg tcaccttcga aggggctggg 360

cgcttctacc tcgtctcggc accggcgcac cgagcctgc ccaaccggct cgtcacgccg 420

gccgacagca aggaggtcaa gcttggcgct ctcgagactt ccaacaaacg caccatcaat 480

cagttcattc atcccctggg catggaaaagc tgccagctcg tgctgggata taccacgctg 540

gaggacggct cggctctggaa taccatgccc gcgcatgtgc acgaccgacg catggaggcc 600

SGI1660-1WO\_ST25.txt

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| tatctctatt tcggcatgga tgagacatcg cgggttctgc atctgatggg cgagccgcag   | 660 |
| caaacgaggc atctcttcgt cgccaatgag gaaggggcga tctctccgcc gtggtccatc   | 720 |
| catgcggggag caggcattgg cagctatacc ttcattctggg ccatggcggg cgacaatgtc | 780 |
| gattataccg acatggagtt catccagccg ggagatcttc gatga                   | 825 |

<210> 21  
 <211> 837  
 <212> DNA  
 <213> Escherichia coli

|                                                                              |     |
|------------------------------------------------------------------------------|-----|
| <400> 21<br>atggacgtaa gacagagcat ccacagtgcg caccgaaaaa cgctggatac ccaagggtg | 60  |
| cgcaatgaat ttttggttga aaaggtatct gtcgccgatg agtacaccat ggtttacagc            | 120 |
| cacattgacc gaattattgt tggcggcatt atgccgataa ctaaaacggg ttccgttggc            | 180 |
| ggggaagttg gtaaacaact cggcgtaagc tatttccttg aacgtcgcga gttaggtgtt            | 240 |
| atcaatatgt gcggtgccgg tacgattact gtcgatggcc aatgctatga aatcggtcac            | 300 |
| cgcgacgccc tgtatgttgg taaaggtgca aaagaagttg tctttgccag tattgatacc            | 360 |
| ggcactccgg cgaagtctta ttacaattgc gcacccgcgc atacgacgta tcccacaaa             | 420 |
| aaagtcacac cggacgaagt atctccagtc acgttaggcg ataacctcac cagtaaccgt            | 480 |
| cgcacgatta acaaatatct tgtcccggat gtactggaaa cctgccaatt gaggatgggg            | 540 |
| ctgacggagc tggctccggg taacttgtgg aacaccatgc cgtgtcacac ccacgagcgc            | 600 |
| cggatggaag tttatttcta tttcaatatg gatgatgacg cctgcgtttt ccacatgatg            | 660 |
| gggcagccgc aagaaacgcg tcatattgtg atgcataacg agcaggcggg gatctccccg            | 720 |
| agctgggtcga tccattccgg tgtcggaacc aaagcttata cctttatctg gggcatggtc           | 780 |
| ggtgaaaacc aggtctttga tgatatggac catgtggccg tttaaagattt gcgctag              | 837 |

<210> 22  
 <211> 837  
 <212> DNA  
 <213> Rhizobium sp.

|                                                                               |    |
|-------------------------------------------------------------------------------|----|
| <400> 22<br>atgacgatga agatactcta cggcgccgga ccggaggatg tgaaagggtg tgacacgcag | 60 |
|-------------------------------------------------------------------------------|----|

SGI1660-1WO\_ST25.txt

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| cgctgcgcg acgccttcct gctggacgac ctcttcgccg acgaccgggt cagtttcaca  | 120 |
| tatacccatg tcgatcgctt catcctcggc ggggccgtcc cggtgacgac gagcctcacc | 180 |
| ttcggctccg gcacggagat cggaacgccc tacctgcttt ccgcccgcga gatggggatc | 240 |
| gccaatctcg gcggcacggg cacgatcgag gtggatggcc agcgcttcac gctcgaaaac | 300 |
| cgcgacgtgc tctatgtcgg tcgcggcgcc cggcagatga ccgcctccag cctgtcggcg | 360 |
| gagaggccag cccgcttcta catgaattcc gtgcccgcgc gcgccgattt cccgcaccgt | 420 |
| ctgatcaccg gcgggagagg caagcccctc gatctcggcg atgcgcgcgc ctcgaacagg | 480 |
| cgccggctcg caatgtacat ccatccggag gtctcgccgt cctgcctgct gctcatgggc | 540 |
| atcaccgatc ttgccgaggg cagcgcctgg aacaccatgc cgccgcatct gcacgagcgg | 600 |
| cggatggagg cctattgcta cttcgatctc tcgcccgagg accgggtcat ccacatgatg | 660 |
| ggtcggccgg acgaaacccg ccaccttgtc gtggccgacg gcgaggcggg cctctctccc | 720 |
| gcctggtcga tccatatggg tgccgggacg gggccctacg ccttcgtctg gggcatgacc | 780 |
| ggcgaaaacc aggaatacaa cgacgtcgct cccgtagccg tggctgatct caaatga    | 837 |

<210> 23

<211> 825

<212> DNA

<213> Pannonibacter phragmitetus

<400> 23

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atgctgaccg tcgaaacccg ccacgccatt gatccgcaga ccgcaaagcg gatggacacg | 60  |
| gaagagctgc gcaagcattt ccacatgggc agcctgtttg ctgccggtga aatccgcctc | 120 |
| gtctacaccg actatgaccg catgatcgtc ggcgctgccg tgccctcggg cgcgccgctg | 180 |
| gtgctggatc aggtcaagga atgcggcacc gccagcatcc tcgaccgccg cgagatggct | 240 |
| gtcgtcaacg tcggcgccag cggcaaggct tctgcagcag gcgaaaccta cgccatggaa | 300 |
| cgcggcgacg tgctctatct gccgctgggc tccggcaagg tgaccttcga aggcaaggc  | 360 |
| cgcttctaca ttctctccgc tccggccac gctgcttacc cggcccgcct gatccgcac   | 420 |
| ggcgaggccg agaaggtaa gctcggctcg gccgagacct ccaacgaccg caccatctac  | 480 |
| cagttcgtgc atccggcggg gatgacttcc tgccaactcg tcgtcggcta caccagctg  | 540 |

## SGI1660-1WO\_ST25.txt

cacaacggct ctgtctggaa caccatgccc gccacgtgc atgaccggcg catggaggcc 600  
 tatctctatt tcgacatgaa gccggagcag cgcgtgttcc acttcatggg cgagccgcag 660  
 gaaacccgcc atctgggtcat gaagaacgag gatgcggtgg tctccccgcc ctggtccatc 720  
 cactgcggcg caggcaccgg cagctacacc ttcatctggg ccatggccgg cgacaacgtc 780  
 gactacaagg acgtggaaat ggtcgccatg gaggatctgc ggtga 825

<210> 24  
 <211> 816  
 <212> DNA  
 <213> *Bacillus subtilis*

<400> 24  
 atgagttatt tgttgcgtaa gccgcagtcg aatgaagtgt ctaatggggt caaactggtg 60  
 cacgaagtaa cgaaatccaa ctctgatctc acctatgtag agtttaaagt gttagatctc 120  
 gcttccgggt ccagctatgc agaagaattg aaaaaacagg aaatctgtat tgtcgcggta 180  
 acgggaaaca ttacagtgc cgatcacgag tcgacttttg agaatatcgg cacgcgtgaa 240  
 agcgtattcg aacgaaaacc gacagacagc gtctatatctt caaatgaccg ttcctttgag 300  
 atcacagcgg tcagcgacgc aagagtggcg ctttgctatt ctccatcgga aaaacagctt 360  
 ccgacaaagc tgatcaaagc ggaagacaat ggcatgagc atcgcgggaa gttttcaaac 420  
 aaacgtactg ttcacaacat tcttccggat tcagaccctt cagctaacag cctattagta 480  
 gttgaagtct atacagacag cggcaactgg tccagctatc cgcctcataa acatgatcaa 540  
 gacaatttgc cggaggaatc ttttttagaa gaaacgtact accatgagtt agacccggga 600  
 cagggttttg tgtttcagcg tgtatacaca gatgaccgct cgattgacga gacaatgact 660  
 gtagaaaatg aaaacgttgt catcgttcct gcaggatacc acccggtagg cgtgccggac 720  
 ggatacacat cctactatctt aaatgtcatg gcagggccga cgcggaaatg gaagtttcat 780  
 aatgaccggc cgcatgagtg gatttttagaa cgtaa 816

<210> 25  
 <211> 810  
 <212> DNA  
 <213> *Ochrobactrum anthropi*

<400> 25

## SGI1660-1WO\_ST25.txt

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atggccaatt tgttgcgcaa gccaacggc acgcatggca aggtccacga catcactccg   | 60  |
| gaaaacgcca aatgggggtta tgtcgggttc gggctctttc gtctcaaata cggcgagagt | 120 |
| gtctccgaaa agaccggatc gacggaggtg atccttggtc ttgtggaagg caaggcaaag  | 180 |
| atttccgctt ctggcgagga tttcggcgag atgggtgaac gcttaaactg gttcgagaaa  | 240 |
| ctgccgccac actgcctcta tgtgcctgct gaaagcgact ggcatgcaac cgccacgaca  | 300 |
| gatttgtgtc tggctgtttg caccgcaccg ggcaagccag gccgcaaggc acagaagctt  | 360 |
| gggccggaaa gcttgacact tgaacaacgc ggaaaagggtg ccaatacccg ctttatccat | 420 |
| aatatcgcaa tggaaagccg cgatgttgcc gatagccttc ttgttaccga ggtattcaca  | 480 |
| ccgcagggaa actggtcgtc ctatccaccc cacagacacg acgaagacaa ttttccggat  | 540 |
| atgacctatc tggaagagac ctattatcac cgtctcaacc cggcgcaggg cttcggcttc  | 600 |
| cagcgtgttt tcaccgaaga cggaagcctt gatgaaacca tggcgggtctc tgacggagac | 660 |
| gtcgtgcttg taccaaaagg ccaccatcca tgtggcgcg cctatggcta cgagatgtat   | 720 |
| tatctcaatg tgatggccgg tcccttgcg aaatggcgct tcaagaacca tcccgaccat   | 780 |
| gactggattt tcaaacgcga caatccgtaa                                   | 810 |

&lt;210&gt; 26

&lt;211&gt; 807

&lt;212&gt; DNA

&lt;213&gt; Halomonas titanicae

&lt;400&gt; 26

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atggcttccc tactggtacg cccacccgcc ccagatgccc agggcaccgt gattgacgtt | 60  |
| accctgaat ctgctggctg gacgcacgtt ggctttcggg tgcataaact cgccaagggc  | 120 |
| cagcgcttg aggccagcag cgatgatcag gaagtctgcc tggctgtgct caccggtcgc  | 180 |
| gccacggtaa cttgcggcga gcaccgctt gaagatattg gccagcgtat ggatattttt  | 240 |
| gagcagatcc ctccctatgc ggtttaccta cctgaccatg ttagctacgc ggtggaagcg | 300 |
| accacagact tagagctagc ggtgtgcacc gccctgggc atggcaacca tgccccacgg  | 360 |
| ctcatcgcg ctgacaacat caagcaaagc acccggtggc agggcaccaa caccgccat   | 420 |
| gttcacgata ttctgccgga aaccgagccc gccgatagcc tattagtagt cgaagtattc | 480 |
| acacctgcgg gtaactggtc gagctacccg cccacaaac acgatgtgga taacttacc   | 540 |

SGI1660-1W0\_ST25.txt

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| cacgaatcac atctggaaga gacctactac caccgcatta accctgaaca agggttcgcc | 600 |
| ttccagcgcg ttacaccga tgaccgcagc cttgatgaaa ccatggcggt ggaaaacggc  | 660 |
| tgctgtgtgt tggttcccaa gggttaccat ccggtgggcg cctcccatgg ctactcgctc | 720 |
| tactacttaa atgtgatggc ggggcccaag cgggcatgga aatttcacaa cgaccccgac | 780 |
| cacgaatggc tgatgaacgc tggatag                                     | 807 |

<210> 27  
 <211> 795  
 <212> DNA  
 <213> Acidiphilium multivorum

|                                                                               |     |
|-------------------------------------------------------------------------------|-----|
| <400> 27<br>atgccggact tactgagaaa accgtttggc acccatggca aagtgcacga tattacccca | 60  |
| gcagcagcag gttggagaca tgttggtttt ggcttatatc gcttaagagc gggcgaattt             | 120 |
| gcagcagaag cgacaggcgg caatgaagtt attctggtga tggttgaggg caaagcgtct             | 180 |
| attagagcag caggcagaga ttggggcggt ttaggcgaac gtatgagcgt cttcgaaaaa             | 240 |
| agtccaccac attccctgta tgtcccgaat ggtgcagaat gggccttagt agccgaaaca             | 300 |
| gattgcattg tagcagtgtg tagcgctccg ggtagaggag gtcattgctgc aagaagaatt            | 360 |
| ggtcctgaag gtattgtgtt aaccgccaga ggtgaaggca ccaatacacg ccacatcaac             | 420 |
| aacatcgcca tggaagccga agattattgt gatgccctgt tagtcaccga agtgttcacc             | 480 |
| ccagccggcc attggagctc ttatccatct catcgtcatg atgaagacga cgatccgcgc             | 540 |
| atcacctatt tagaagagac ctactatcat cgcttaaadc ctgcctcggg ctttggcggt             | 600 |
| caacgcgtct ataccgatga tcgcgcctta gatcaaacca tggcggtttc tgatggcgat             | 660 |
| gttggttttag ttcctcgccg ccatcatccg tgtgcagccc cgtatggtat tgaaatgtat            | 720 |
| tacctgaacg tcatggccgg cccgttacgt aaatggcgct ttttacctga tcctgaactt             | 780 |
| ggcattgcga aataa                                                              | 795 |

<210> 28  
 <211> 816  
 <212> DNA  
 <213> Lactobacillus casei

## SGI1660-1W0\_ST25.txt

&lt;400&gt; 28

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgtctctgc tgtaccacaa gcagaaccag gaactgagta gtggtgtgcg cctgatccaa  | 60  |
| gatgttaatg ccagcaatag cccgatgaaa tataccgccg tgaaagtgct ggagtttagc  | 120 |
| gccgatagca gctatgagga aaccttagag gcctttgaag ccggcattgt tgtgttagag  | 180 |
| ggcaaagtga ccatcaccgc cgacgatcaa accttcgaag atgtgggtca aagaacctcg  | 240 |
| atcttcgaca aaatcccgac cgatagcggt tatgtgtcta ccggttttagc cttcggtatt | 300 |
| cgcgccaaac aagccgcaa aatcttaatc gcgtatgctc cgaccaatca gaccttccca   | 360 |
| gttcgcttaa ttcgcggcaa tatccaccag gtggaacatc gcggcaagta caacaacaaa  | 420 |
| cgcttagtgc agaacattct cccggataat ctcccgttcg ccgataaatt actgctgggt  | 480 |
| gaggtgtaca ccgatagcgc caattggagc tcctatccgc cgcatagaca tgatcacgat  | 540 |
| gatttaccgg ccgaaagtct gttagaggag atctactatc acgaaatgcg cccgaagcag  | 600 |
| ggcttcgtct ttcaacgcgt gtataccgat gatctgagtc tggatgagac catggccggt  | 660 |
| caaaatcaag atgttgtcgt tgtcccgaag ggctatcatc cggttggtgt ccccgacggc  | 720 |
| tatgattcgt attacctgaa cgtgatggcc ggcccgaag gagtgtggca ttttcataat   | 780 |
| gctccggaac atgcctggat tattgatcgc cagtaa                            | 816 |

&lt;210&gt; 29

&lt;211&gt; 1401

&lt;212&gt; DNA

&lt;213&gt; Bacteroides sp.

&lt;400&gt; 29

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atgaaaaaat ttatggatga aaatcttctg ttgcaaaccg aaacagcgca gaaattgtat | 60  |
| cataatcacg cggcaaacat gccgattttc gattaccact gccacattaa ccccaaagac | 120 |
| atcgcggaag accggatgtt taaaaccatc accgaaatct gggtgtacgg cgatcattat | 180 |
| aaatggcgcg ccatgcgtac aaacggcggt gacgagcgct tttgcaccgg cgatgcaagc | 240 |
| gattgggaaa agtttgaaaa gtgggcccga acggttcctc ataccctgcg taatccgctt | 300 |
| tatcactgga cacacctgga gctaaagaaa tttttcggga ttaacgagat cctgagtccg | 360 |
| aaaaatgccc gggaaattta tgatgcctgt aacgaaaaac tgcaaacgcc cgcgtatagt | 420 |
| tgccgcaaca tcatccggat ggccaatgtg catacaatct gtaccaccga cgaccgggtt | 480 |

## SGI1660-1W0\_ST25.txt

gacacactgg aatatcatca gcaaattaaa gaagacggct ttgaagtggc ggttttacct 540  
 gcctggcgtc cggataaagc gatgatgggtg gaagacccga agttctttaa cgactatatg 600  
 gaccagttgg ccgaagctgc cggatatccat atcgaatcgt ttgaggattt gatggaagcc 660  
 ttggatacgc gtcaccagta ttttcatgat aatggttgcc gtttgtccga ccacgggctg 720  
 gataccgttt ttgctgaaga ttatacggag gaagaaatta aagcgatctt caaaaaaatc 780  
 cgtggcggca gcaggcttag cgaaacggaa atcctgaaat tcaagtcctg catgttgtac 840  
 gaatatgggg tgatggacca ttcgcgcggc tggacacaac aattgcacat tggcgcacaa 900  
 cgcaacaaca acacccgttt gttcaaaaaa ttaggtcccg aacttggttt cgattcgatt 960  
 ggcgataagc cgatcgctga accattggcc aaattgctcg accgcctgga tcaggaaaac 1020  
 aaattgtgca aaacggtttt gtataatctg aatccgcgtg ataacgagtt gtacgctacc 1080  
 atgttgggca actttcagga cggatcggtt cccgggaaaa ttcaatacgg ctcgggttgg 1140  
 tggtttctcg atcagaaaaga cggcatgatt aaacagatga atgccctttc caatctgggt 1200  
 ttgctgagcc gtttcgtagg catgctgacc gactcaagga gcttcctttc gtacaccctg 1260  
 cacgaatatt tccgtcgtac cttttgcaac ctgcttgga atgatgttga aaacggggag 1320  
 attccggcag atatggagct tttgggcagt atggttgaga atatttggtt taataacgcg 1380  
 aagaactatt ttaattttta g 1401

&lt;210&gt; 30

&lt;211&gt; 1356

&lt;212&gt; DNA

&lt;213&gt; Thermotoga maritima MSB8

&lt;400&gt; 30

atgtttctgg gcgaagacta tctgctgacc aatcgtgcgg cagttcgtct gttcaacgaa 60  
 gtgaaagatc tgccgatcgt tgatccgcat aaccacctgg atgcgaaaga tatcgtggaa 120  
 aacaaaccgt ggaacgacat ctgggaagtg gaagggtcga ccgatcacta tgtgtgggaa 180  
 ctgatgcgtc gttgtggtgt tagcgaagaa tatattaccg gctctcgtag caacaaagaa 240  
 aaatggctgg cgctggcgaa agtgtttccg cgttttgtgg gtaatccgac gtacgaatgg 300  
 atccacctgg atctgtggcg tcgtttcaac atcaaaaaag tcatcagcga agaaaccgcg 360  
 gaagaaatct gggaagaaac caaaaaaaaaa ctgccggaga tgaccccgca gaaactgctg 420

## SGI1660-1WO\_ST25.txt

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cgcgacatga aagtggaaat cctgtgcacc accgatgatac cgggtgtctac cctggaacat | 480  |
| caccgtaaag cgaaagaagc cgtggaaggc gtgaccattt taccgacctg gcgtccggat   | 540  |
| cgtgcaatga atgttgataa agaaggttgg cgtgaatatg ttgaaaaaat gggatgaacgc  | 600  |
| tatggcgaag ataccagcac cctggatggg tttctgaatg ccctgtggaa aagccacgaa   | 660  |
| cacttcaaag aacacggctg tgtggcgagc gatcatgcgc tgctggaacc gagcgtgtac   | 720  |
| tacgtggatg aaaaccgcgc gcgtgcagtt catgaaaaag ctttttctgg tgaaaaactg   | 780  |
| actcaagatg aaatcaacga ctataaagcg ttcgatgatg tgcagttcgg caaatgaac    | 840  |
| caggaaacca actgggtgac ccagctgcac attgggtgcc tgcgcgatta ccgcgatagc   | 900  |
| ctgttcaaaa ccctggggccc ggattctggg ggcgatatca gcaccaactt tctgcgtatt  | 960  |
| gctgaaggctc tgcgttattt tctgaacgaa ttgatggta aactgaaaat tgtgctgtac   | 1020 |
| gtgctggatc cgaccattt accgaccatt tcgaccattg cacgtgcgtt cccgaacgtg    | 1080 |
| tatgtgggtg caccgtgggt gttcaacgat agcccgttcg gcatggaaat gcacctgaaa   | 1140 |
| tacctggcga gcgttgatct gctgtacaat ctggctggta tggttaccga ttcacgtaaa   | 1200 |
| ttactgagtt ttggttctcg taccgaaatg tttcgtcgcg ttctgtctaa tgtggttggc   | 1260 |
| gaaatgggtg aaaaaggcca gatcccgatc aaagaagcgc gcgaactggg gaaacacgtg   | 1320 |
| agctacgacg gcccgaagc cctgttcttt ggctga                              | 1356 |

<210> 31  
 <211> 1284  
 <212> DNA  
 <213> Bacillus halodurans

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| <400> 31                                                          |     |
| atgagcatca acagccgtga agttctggcg gaaaaagtga aaaacgcggt gaacaaccag | 60  |
| ccggttaccg atatgcatac ccacctgttt agcccgaact ttggcgaaat tctgctgtgg | 120 |
| gacatcgatg aactgctgac ctatcactac ctggttgcgg aagttatgcg ttggaccgat | 180 |
| gtgagcattg aagcgttttg ggcaatgagc aaacgtgaac aggccgatct gatttgggaa | 240 |
| gaactgttca tcaaacgcag cccggtgagc gaagcatgtc gtggcgttct gacctgttta | 300 |
| caaggtttag gtctggatcc ggcaactcgt gatttacagg tgtatcgtga atacttcgcc | 360 |

## SGI1660-1W0\_ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aaaaaaacca gcgaggaaca ggtggatacc gttctgcagc tggcaaagt gagcgatgtg   | 420  |
| gtgatgacca atgatccgtt cgatgataat gaacgcatca gctggctgga aggcaaacag  | 480  |
| ccggatagcc gctttcatgc agcgttacgt ctggatccgc tgctgaatga atatgaacag  | 540  |
| accaaacatc gtctgcgtga ttgggggttat aaagtgaacg acgaatggaa cgaaggcagc | 600  |
| atccaggaag tgaaacgctt tctgaccgac tggattgaac gtatggatcc ggtgtatatg  | 660  |
| gcggtgagct taccgccgac cttcagcttt ccggaagaat cgaaccgtgg ccgcattatc  | 720  |
| cgtgattgtc tgttaccggt tgcagaaaaa cataacatcc cgtttgcaat gatgattggc  | 780  |
| gtgaaaaaac gcgtgcatcc ggcgttaggt gatgcaggcg attttgtggg taaagcaagt  | 840  |
| atggatggcg ttgaacacct gctgcgcgaa taccgaaca acaaattcct ggtgaccatg   | 900  |
| ctgagccgcg aaaaccagca cgaactgggt gttctggcgc gtaaatttag taacctgatg  | 960  |
| atttttgggt gttggtggtt tatgaacaac ccggagatca tcaacgaaat gacccgcatg  | 1020 |
| cgcatggaaa tgctgggtac cagctttatc ccgcagcaca gcgatgcccg tgttctggaa  | 1080 |
| cagctgatct ataaatggca ccacagcaaa agcatcatcg cggaagtcct gatcgacaaa  | 1140 |
| tacgacgaca tcctgcaagc aggttgggaa gttaccgaag aagaaatcaa acgtgatgtg  | 1200 |
| gcagatctgt ttagccgcaa cttttggcgc tttgtgggcc gtaacgatca cgtgaccagc  | 1260 |
| gtgaaagtgg aacagcagac ctga                                         | 1284 |

&lt;210&gt; 32

&lt;211&gt; 1422

&lt;212&gt; DNA

&lt;213&gt; Bacillus halodurans

&lt;400&gt; 32

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atggaaccgt ttatgggcaa aaacttcctg ctgaaaaacg agaccgcggt gagcctgtac | 60  |
| cacaactacg cgaaagatat gccgatcatc gactaccatt gccatctgag cccgaaagaa | 120 |
| atctacgaga acaaaacctt ccagaacatc accgaagcgt ggctgtacgg cgatcactac | 180 |
| aatggcgca tcatgcgtgc gaatggcatc gaagaaacct atattaccgg tgatgcaccg  | 240 |
| gacgaagaaa aattcatggc gtgggcgaaa accgtgccga tggccattgg taatccgctg | 300 |
| tataactgga cccatctgga actgcaacgt ttttttggca tctacgaaat cctgaacgaa | 360 |
| aaaagcggca gcgcgatctg gaaacagacc acaaaactgc tgaaaggcga aggctttggt | 420 |

SGI1660-1W0\_ST25.txt

```

gcgcgtgatac tgatcgtgaa aagcaacgtt aaagtgggtgt gcaccaccga cgatccgggtg      480
gattctcttgg aataccatct gctgctgaaa gaagacaaag acttcccgggt tagcgtttta      540
ccgggttttc gtccggataa aggtctggaa atcaaccgtg aaggctttcc ggaatgggtt      600
caagcccctgg aagatgcggc cgcaattagc attacgacct atgatgaatt tctgaaagcg      660
ctggaaaaaac gcgtgcgctt cttccatagt gcgggtgggtc gtgttagcga tcatgcaatc      720
gataccatgg ttttcgccga aaccaccaa gaagaagcgg gtcgcatttt tagtgatcgt      780
ctgcaaggca ccgaagttag ctgcgaagac gagaaaaaat tcaaaaccta caccctgcag      840
tttctgtgtg gcctgtatgc cgaactggac tgggcaatgc agtttcacat caacgcgctg      900
cgcaacacca acaccaaagt gatgaaacgc ctgggtccgg ataccggtta tgatagcatg      960
aacgatgaag aaatcgcgaa accgctgtac aaactgctga acagcgtgga aatgaaaaac     1020
caactgccga aaaccatcct gtacagcctg aaccgaacg acaactacgt gatcgcgagc     1080
atgatcaaca gcttccagga tggcatcacc ccgggcaaaa ttcagtttgg caccgcatgg     1140
tggttcaacg ataccaaaga tggtagctg gatcagatga aagcactgag caatgtgggc     1200
ctgttttagcc gttttattgg catgctgacc gatagccgta gctttctgag ctatacccg     1260
cacgaatact ttcgccgcat tgtgtgtaac ctgatcggcg aatgggtgga aaacggcgaa     1320
gttccgcgcg atatggaact gctgggtagt attgtgcaag gtatttgcta cgataacgcg     1380
aaacattact tccagttcca ggaggaaaaa gcgaacgtgt ga                        1422

```

<210> 33  
 <211> 593  
 <212> PRT  
 <213> *Achromobacter piechaudii*

<400> 33

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Thr | Pro | Arg | Lys | Leu | Arg | Ser | Gln | Lys | Trp | Phe | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | His | Ala | Asp | Met | Thr | Ala | Ile | Tyr | Val | Glu | Arg | Tyr | Leu | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Gly | Leu | Thr | Arg | Gln | Glu | Leu | Gln | Ser | Gly | Arg | Pro | Ile | Ile | Gly |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

35

40

45

Ile Ala Gln Thr Gly Ser Asp Leu Ala Pro Cys Asn Arg His His Leu  
 50 55 60

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

Pro Met Glu Phe Pro Val His Pro Leu Ala Glu Gln Gly Arg Arg Pro  
 85 90 95

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

Leu His Gly Tyr Pro Leu Asp Gly Val Val Leu Thr Thr Gly Cys Asp  
 115 120 125

Lys Thr Thr Pro Ala Cys Leu Met Ala Ala Ala Thr Val Asp Leu Pro  
 130 135 140

Ala Ile Val Leu Ser Gly Gly Pro Met Leu Asp Gly Trp His Asp Gly  
 145 150 155 160

Gln Arg Val Gly Ser Gly Thr Val Ile Trp His Ala Arg Asn Leu Met  
 165 170 175

Ala Ala Gly Lys Leu Asp Tyr Glu Gly Phe Met Thr Leu Ala Thr Ala  
 180 185 190

Ser Ser Pro Ser Val Gly His Cys Asn Thr Met Gly Thr Ala Leu Ser  
 195 200 205

Met Asn Ser Leu Ala Glu Ala Leu Gly Met Ser Leu Pro Thr Cys Ala  
 210 215 220

Ser Ile Pro Ala Pro Tyr Arg Glu Arg Ala Gln Met Ala Tyr Ala Thr  
 225 230 235 240

Gly Met Arg Ile Cys Asp Met Val Arg Glu Asp Leu Arg Pro Ser His

245

250

255

Ile Leu Thr Arg Gln Ala Phe Glu Asn Ala Ile Val Val Ala Ser Ala  
 260 265 270

Leu Gly Ala Ser Thr Asn Cys Pro Pro His Leu Ile Ala Met Ala Arg  
 275 280 285

His Ala Gly Ile Asp Leu Ser Leu Asp Asp Trp Gln Arg Leu Gly Glu  
 290 295 300

Asp Val Pro Leu Leu Val Asn Cys Val Pro Ala Gly Glu His Leu Gly  
 305 310 315 320

Glu Gly Phe His Arg Ala Gly Gly Val Pro Ala Val Met His Glu Leu  
 325 330 335

Phe Ala Ala Gly Arg Leu His Pro Asp Cys Pro Thr Val Ser Gly Lys  
 340 345 350

Thr Ile Gly Asp Ile Ala Ala Gly Ala Lys Thr Arg Asp Ala Asp Val  
 355 360 365

Ile Arg Ser Cys Ala Ala Pro Leu Lys His Arg Ala Gly Phe Ile Val  
 370 375 380

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

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

Ala Phe Glu Ala Arg Ala Ile Val Phe Glu Gly Pro Glu Asp Tyr His  
 420 425 430

Ala Arg Ile Glu Asp Pro Ala Leu Asn Ile Asp Glu His Cys Ile Leu  
 435 440 445

Val Ile Arg Gly Ala Gly Thr Val Gly Tyr Pro Gly Ser Ala Glu Val

450

455

460

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

Leu Pro Cys Leu Gly Asp Gly Arg Gln Ser Gly Thr Ser Gly Ser Pro  
 485 490 495

Ser Ile Leu Asn Met Ser Pro Glu Ala Ala Val Gly Gly Gly Leu Ala  
 500 505 510

Leu Leu Arg Thr Gly Asp Lys Ile Arg Val Asp Leu Asn Gln Arg Ser  
 515 520 525

Val Thr Ala Leu Val Asp Asp Ala Glu Met Ala Arg Arg Lys Gln Glu  
 530 535 540

Pro Pro Tyr Gln Ala Pro Ala Ser Gln Thr Pro Trp Gln Glu Leu Tyr  
 545 550 555 560

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

Thr Leu Tyr Leu Lys Val Ile Glu Thr Arg Gly Asp Pro Arg His Ser  
 580 585 590

His

&lt;210&gt; 34

&lt;211&gt; 602

&lt;212&gt; PRT

&lt;213&gt; Acinetobacter sp.

&lt;400&gt; 34

Met Ser Glu Arg Ile Lys Lys Met Asn Asp Gln Asn Lys Arg Ile Phe  
 1 5 10 15

Leu Arg Ser Gln Glu Trp Phe Asp Asp Pro Glu His Ala Asp Met Thr  
 20 25 30

SGI1660-1W0\_ST25.txt

Ala Leu Tyr Val Glu Arg Tyr Met Asn Tyr Gly Leu Thr Arg Ala Glu  
35 40 45

Leu Gln Ser Gly Arg Pro Ile Ile Gly Ile Ala Gln Thr Gly Ser Asp  
50 55 60

Leu Thr Pro Cys Asn Arg His His Lys Glu Leu Ala Glu Arg Val Lys  
65 70 75 80

Ala Gly Ile Arg Asp Ala Gly Gly Ile Pro Met Glu Phe Pro Val His  
85 90 95

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

Leu Ala Tyr Leu Gly Leu Val Glu Ile Leu His Gly Tyr Pro Leu Asp  
115 120 125

Gly Val Val Leu Thr Thr Gly Cys Asp Lys Thr Thr Pro Ala Cys Leu  
130 135 140

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

Pro Met Leu Asp Gly His Phe Lys Gly Glu Leu Ile Gly Ser Gly Thr  
165 170 175

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

Glu Gly Phe Met Glu Met Thr Thr Ser Ala Ser Pro Ser Val Gly His  
195 200 205

Cys Asn Thr Met Gly Thr Ala Leu Ser Met Asn Ala Leu Ala Glu Ala  
210 215 220

Leu Gly Met Ser Leu Pro Thr Cys Ala Ser Ile Pro Ala Pro Tyr Arg  
225 230 235 240

SGI1660-1W0\_ST25.txt

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

Val Leu Glu Asp Leu Arg Pro Ser Lys Ile Met Asn Lys Gln Ser Phe  
260 265 270

Glu Asn Ala Ile Ala Val Ala Ser Ala Leu Gly Ala Ser Ser Asn Cys  
275 280 285

Pro Pro His Leu Ile Ala Ile Ala Arg His Met Gly Ile Glu Leu Ser  
290 295 300

Leu Glu Asp Trp Gln Arg Val Gly Glu Asn Ile Pro Leu Ile Val Asn  
305 310 315 320

Cys Met Pro Ala Gly Lys Tyr Leu Gly Glu Gly Phe His Arg Ala Gly  
325 330 335

Gly Val Pro Ala Val Leu His Glu Leu Gln Lys Ala Ser Val Leu His  
340 345 350

Glu Gly Cys Ala Ser Val Ser Gly Lys Thr Met Gly Glu Ile Ala Lys  
355 360 365

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

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

Ser Ala Ile Met Lys Met Ser Val Val Gly Glu Ala Phe Lys Lys Thr  
405 410 415

Tyr Leu Ser Asp Pro Asn Gly Glu Asn Ser Phe Glu Ala Arg Ala Ile  
420 425 430

Val Phe Glu Gly Pro Glu Asp Tyr His Ala Arg Ile Asn Asp Pro Ala  
435 440 445

SGI1660-1W0\_ST25.txt

Leu Asp Ile Asp Glu His Cys Ile Leu Val Ile Arg Gly Ala Gly Thr  
450 455 460

Val Gly Tyr Pro Gly Ser Ala Glu Val Val Asn Met Ala Pro Pro Ala  
465 470 475 480

Glu Leu Ile Lys Lys Gly Ile Asp Ser Leu Pro Cys Leu Gly Asp Gly  
485 490 495

Arg Gln Ser Gly Thr Ser Ala Ser Pro Ser Ile Leu Asn Met Ser Pro  
500 505 510

Glu Ala Ala Val Gly Gly Gly Ile Ala Leu Leu Lys Thr Asn Asp Arg  
515 520 525

Leu Arg Ile Asp Leu Asn Lys Arg Ser Val Asn Val Leu Ile Ser Asp  
530 535 540

Glu Glu Leu Glu Gln Arg Arg Arg Glu Trp Lys Pro Thr Val Ser Ser  
545 550 555 560

Ser Gln Thr Pro Trp Gln Glu Met Tyr Arg Asn Met Val Gly Gln Leu  
565 570 575

Ser Thr Gly Gly Cys Leu Glu Pro Ala Thr Leu Tyr Met Arg Val Ile  
580 585 590

Asn Gln Asp Asn Leu Pro Arg His Ser His  
595 600

<210> 35

<211> 593

<212> PRT

<213> Achromobacter xylosoxidans

<400> 35

Met Ser Gln Thr Pro Arg Lys Leu Arg Ser Gln Lys Trp Phe Asp Asp  
1 5 10 15

SGI1660-1W0\_ST25.txt

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

Tyr Gly Leu Thr Arg Gln Glu Leu Gln Ser Gly Arg Pro Ile Ile Gly  
35 40 45

Ile Ala Gln Thr Gly Ser Asp Leu Ala Pro Cys Asn Arg His His Leu  
50 55 60

Ala Leu Ala Glu Arg Ile Lys Ala Gly Ile Arg Asp Ala Gly Gly Ile  
65 70 75 80

Pro Met Glu Phe Pro Val His Pro Leu Ala Glu Gln Gly Arg Arg Pro  
85 90 95

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

Leu His Gly Tyr Pro Leu Asp Gly Val Val Leu Thr Thr Gly Cys Asp  
115 120 125

Lys Thr Thr Pro Ala Cys Leu Met Ala Ala Ala Thr Val Asp Ile Pro  
130 135 140

Ala Ile Val Leu Ser Gly Gly Pro Met Leu Asp Gly Trp His Asp Gly  
145 150 155 160

Gln Arg Val Gly Ser Gly Thr Val Ile Trp His Ala Arg Asn Leu Met  
165 170 175

Ala Ala Gly Lys Leu Asp Tyr Glu Gly Phe Met Thr Leu Ala Thr Ala  
180 185 190

Ser Ser Pro Ser Ile Gly His Cys Asn Thr Met Gly Thr Ala Leu Ser  
195 200 205

Met Asn Ser Leu Ala Glu Ala Leu Gly Met Ser Leu Pro Thr Cys Ala  
210 215 220

## SGI1660-1W0\_ST25.txt

Ser Ile Pro Ala Pro Tyr Arg Glu Arg Gly Gln Met Ala Tyr Ala Thr  
 225 230 235 240

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

Val Leu Thr Arg Gln Ala Phe Glu Asn Ala Ile Val Val Ala Ser Ala  
 260 265 270

Leu Gly Ala Ser Ser Asn Cys Pro Pro His Leu Ile Ala Met Ala Arg  
 275 280 285

His Ala Gly Ile Asp Leu Ser Leu Asp Asp Trp Gln Arg Leu Gly Glu  
 290 295 300

Asp Val Pro Leu Leu Val Asn Cys Val Pro Ala Gly Glu His Leu Gly  
 305 310 315 320

Glu Gly Phe His Arg Ala Gly Gly Val Pro Ala Val Leu His Glu Leu  
 325 330 335

Ala Ala Ala Gly Arg Leu His Met Asp Cys Ala Thr Val Ser Gly Lys  
 340 345 350

Thr Ile Gly Glu Ile Ala Ala Ala Ala Lys Thr Asn Asn Ala Asp Val  
 355 360 365

Ile Arg Ser Cys Asp Ala Pro Leu Lys His Arg Ala Gly Phe Ile Val  
 370 375 380

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

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

Ala Phe Glu Ala Arg Ala Ile Val Phe Glu Gly Pro Glu Asp Tyr His  
 420 425 430

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Ala Arg Ile Glu Asp Pro Thr Leu Asn Ile Asp Glu His Cys Ile Leu  
435 440 445

Val Ile Arg Gly Ala Gly Thr Val Gly Tyr Pro Gly Ser Ala Glu Val  
450 455 460

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

Leu Pro Cys Leu Gly Asp Gly Arg Gln Ser Gly Thr Ser Ala Ser Pro  
485 490 495

Ser Ile Leu Asn Met Ser Pro Glu Ala Ala Val Gly Gly Gly Leu Ala  
500 505 510

Leu Leu Arg Thr Gly Asp Arg Ile Arg Val Asp Leu Asn Gln Arg Ser  
515 520 525

Val Ile Ala Leu Val Asp Gln Thr Glu Met Glu Arg Arg Lys Leu Glu  
530 535 540

Pro Pro Tyr Gln Ala Pro Glu Ser Gln Thr Pro Trp Gln Glu Leu Tyr  
545 550 555 560

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

Thr Leu Tyr Leu Lys Val Val Glu Thr Arg Gly Asp Pro Arg His Ser  
580 585 590

His

<210> 36

<211> 1782

<212> DNA

<213> Achromobacter piechaudii

<400> 36

atgtctcaga caccgccgaa gttgcgcagc cagaaatggt tcgacgaccc tgcgcatgcc

60

## SGI1660-1W0\_ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gatatgacgg cgatttacgt cgagcgttat ctgaattacg gcctgacgcg gcaagagttg  | 120  |
| cagtccgggc ggccgatcat cggcatcgcc cagaccggca gcgatctggc gccctgcaac  | 180  |
| cgccatcacc tggcgctggc cgagcgcgtc aaagcgggca tccgggacgc gggcggcatc  | 240  |
| ccgatggagt tccccgtgca cccgctggcc gaacaaggcc ggcgggcccac ggccgcgctg | 300  |
| gaccgcaacc tggcctatct gggcctggtc gaaatcctgc acggctaccc cttggacggg  | 360  |
| gtgggtgctga cgactggctg cgacaagacc acgcctgcct gcctgatggc cgccgccacg | 420  |
| gtcgacctgc ccgcatcgt gctgtccggc ggccccatgc tggacggctg gcacgacggc   | 480  |
| cagcgcgtcg gttccggcac cgtcatctgg cacgcgcgca acctgatggc ggccggcaag  | 540  |
| cttgattacg aaggcttcat gacgtggcc accgcgtctt cgccgtcggc cggccactgc   | 600  |
| aacaccatgg gcacggcgtt gtcgatgaat tcgctggccg aagcgtggg catgtcgctg   | 660  |
| cccacctgcg ccagcattcc cgccccctac cgcgaaacgcg ccagatggc ctacgccacc  | 720  |
| ggcatgcgca tctgcgacat ggtgcgcgaa gacctgcgac cctcccatat cctgacacgg  | 780  |
| caggcattcg agaacgccat cgtcgtggca tcggcgctgg gcgcgtccac caattgcccg  | 840  |
| ccgcacctga tcgcgatggc ccgccacgcc ggcatcgacc ttagcctgga cgactggcag  | 900  |
| cgcttggggtg aagacgtgcc gctgctggtc aactgcgtgc cggcgggga gcatctgggc  | 960  |
| gagggcttcc accgcgcggg cggcgtcccc gcggtcatgc atgaactgtt cgccgccggg  | 1020 |
| cgcttcacc ccgactgccc caccgtatcc ggcaagacca tcggggacat cgccgcgggc   | 1080 |
| gccaagaccc gcgacgccga cgtcatccgc agctgcgccg ccccgctgaa acaccgggca  | 1140 |
| ggcttcatcg tgctgtcggg caatttcttc gacagcgcca tcatcaagat gtcggtcgta  | 1200 |
| ggcgaagcgt tccgccgcgc ctacctgtcc gaaccgggt cagagaacgc cttcgaggcc   | 1260 |
| cgcgccatcg tgttcgaagg ccccgaggac taccacgcgc gcatcgaaga cccggcgctg  | 1320 |
| aacatcgacg aacctgcat ccttgtcatc cgcggcgccg gcaccgtggg ctaccgggc    | 1380 |
| agcgccgaag tggatcaacat ggcgccgccg tcccacctga tcaagcgcg cgtggattcc  | 1440 |
| ctgccgtgcc tgggggatgg caggcaaagc ggcaattccg gcagcccgtc cttttgaac   | 1500 |
| atgtcccctg aagcagcagt cgggggagga ttggcgctgc tgcgcaccgg cgacaagatc  | 1560 |
| cgtgtcgatc tgaaccagcg cagcgtcacc gccttggtcg acgacgcgga aatggcaaga  | 1620 |

## SGI1660-1W0\_ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| cggaagcaag aaccgcccta ccaggcacccg gcctcgcaaa cgccctggca agagctgtac | 1680 |
| cggcaactgg tcggccagtt gtcgacgggc ggctgcctgg agcccgcgac gctatatctg  | 1740 |
| aaagtcacg aaacgcgcgg cgatccccgg cactctcact ga                      | 1782 |

&lt;210&gt; 37

&lt;211&gt; 1809

&lt;212&gt; DNA

&lt;213&gt; Acinetobacter sp.

&lt;400&gt; 37

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atgagtgaag ggatcaaaaa aatgaatgat caaaataaac ggattttttt acgtagccaa   | 60   |
| gaatggtttg atgacctga acatgctgac atgacagcac tctatgttga gcgttatatg    | 120  |
| aattatggcc tgacccgtgc cgagctacaa tcaggccgcc cgattattgg tattgcacaa   | 180  |
| actggcagtg atttaactcc atgtaaccgt caccacaaag aacttgctga acgggttaaa   | 240  |
| gcaggatattc gagatgcggg aggtattccc atggaattcc ccgttcaccc gattgcagaa  | 300  |
| caaaccgctc gccctactgc tgcacttgat agaaatttag cttacttagg cttagttaga   | 360  |
| atattgcatg gttatccgct tgatgggtg gtgctaacca caggttgtga caaaactaca    | 420  |
| cctgcttggt taatggctgc cgcaacgaca gatataccag ccattgtgtt gtctgggtga   | 480  |
| ccaatgctag atggatcattt taaagggtgag ttaattgggt ctgggactgt gctttggcat | 540  |
| gcaagaaatt tacttgccac gggtgaaatt gattatgaag gggtcatgga aatgaccact   | 600  |
| tcagcatcgc cttcggctcg acattgcaac accatgggca ctgcactttc tatgaatgcc   | 660  |
| ttggcagaag ctttgggcat gtctttaccg acatgtgcaa gtattccagc gccgtatcgc   | 720  |
| gaacgagggc aaatggccta tatgacaggc aaaagaattt gtgaaatggt tttagaagat   | 780  |
| ttacgccctt ctaaaatcat gaacaacaa tcatttgaaa atgccatcgc ggtagcttca    | 840  |
| gcattagggg catcaagtaa ttgccctcct cacctcattg caattgcccg tcatatgggc   | 900  |
| attgagctca gtttagaaga ctggcaacgc gttggggaga acattcctct cattgtgaac   | 960  |
| tgtatgcctg cgggtaaata tttagggtgaa ggttttcacc gtgctggcgg tgttcctgct  | 1020 |
| gttttgcatg aattacaaaa ggccagcgtt ttacatgaag gctgtgcatc agtcagcggg   | 1080 |
| aaaacgatgg gagaaattgc taaaaatgct aaaacctcca atgtagatgt tatttttcca   | 1140 |

## SGI1660-1W0\_ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tatgaacaac cattaataca tgggtgcaggt tttattgtgc ttagtggcaa tttcttcgac | 1200 |
| agcgccatta tgaaaatgtc tgttgtgggt gaagcattta agaaaaccta tttatctgac  | 1260 |
| ccaaatgggg aaaatagctt tgaagcacgg gcaatcgttt ttgaagggcc agaggactac  | 1320 |
| catgcacgaa ttaatgatcc agccttagac attgatgaac attgtatttt ggtcattcgt  | 1380 |
| ggcgctggaa cagtgggcta tccaggtagt gcagaagttg taaatatggc tccacccgca  | 1440 |
| gagttaatta aaaaaggcat cgattcactg ccttgcttag gagatggccg ccaaagtgg   | 1500 |
| acgtctgcca gcccttctat tttaaatatg tcacccgaag cggcggtagg cggtggaatt  | 1560 |
| gcattattaa agaccaatga ccgtttacgc attgatctca ataaacgctc cgtcaacgta  | 1620 |
| ctcatttctg acgaagagtt agaacaacgc cgccgtgagt ggaaaccgac ggtctcttca  | 1680 |
| tctcaaacac ctggcaaga aatgtatcgc aacatgggtg gtcaattatc cactggcggt   | 1740 |
| tgtttggaac ctgcaacttt atatatgcga gtcataaatc aagacaacct tccaagacac  | 1800 |
| tctcattaa                                                          | 1809 |

&lt;210&gt; 38

&lt;211&gt; 1782

&lt;212&gt; DNA

&lt;213&gt; Achromobacter xylosoxidans

&lt;400&gt; 38

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| atgagccaaa caccgcgtaa attacgcagc cagaagtgggt ttgacgatcc tgcacatgcc   | 60  |
| gatatgaccg ccatctatgt tgaacgctac ctgaactatg gcttaaccg ccaagaactg     | 120 |
| caaagtggtc gcccgattat tggatttgcc caaaccggca gcgatttagc cccgtgtaat    | 180 |
| cgccatcatt tagccttagc cgaacgcatt aaagcaggca ttagagatgc aggcggcatt    | 240 |
| cctatggaat ttcccgttca tccgctggcc gaacaaggta gacgtcctac agcagcatta    | 300 |
| gatcgcaatt tagcctatit aggcctgggtg gaaattttac acggctatcc cctggacggt   | 360 |
| gtgggtgctga caaccggttg cgataaaaaca acaccggcgt gtttaattggc agctgcaaca | 420 |
| gttgatattc cggcgatcgt gttatcagggt ggtccgatgt tagatggctg gcatgatggc   | 480 |
| caaagagttg gcagtggtag cgtgatttgg catgcacgca atttaattggc agcaggcaaa   | 540 |
| ctggattatg aaggcttcat gaccctggcg acagcctctt ctccgagtat tggacactgt    | 600 |
| aataccatgg gcacagcctt aagcatgaat agtctggcag aagccctggg tatgtcttta    | 660 |

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```

ccgacctgtg cgtctattcc agccccgtat agagaacgcg gtcaaattggc gtatgctact      720
ggtttacgca tttgcgatat ggtgcgcgaa gatttacgcc cgtcacatgt ttttaaccgc      780
caagccttcg aaaatgccat tgttggtgcc tcagccttag gtgcaagctc taattgtccc      840
cctcatttaa ttgccatggc ccgtcatgcc ggtatcgact taagcctgga tgactggcaa      900
cgcttaggcg aagatgttcc gttactggtc aattgtgtgc ctgccggtga acatttaggt      960
gaaggatttc atcgcgcggg tgggtgttcc gctgttttac atgaattagc tgccgcaggt     1020
cgtttacata tggattgtgc taccgtttct ggcaagacca tcggcgaaat tgcagctgcc     1080
gcaaaaacca acaacgcaga cgtgattcgc tcgtgtgatg ccccgttaaa acatagagcc     1140
ggctttattg tgtaagcgg caatttcttc gactccgcca tcatcaagat gtccgttgtg     1200
ggatgaagcct ttcgcagagc ctatttaagt gaacctggca gcgaaaatgc ctttgaagcc     1260
cgtgccatcg tgtttgaagg cccggaagac tatcatgccc gcattgaaga tccgaccctg     1320
aatattgatg aacactgcat tctggtgatt cgcggcgcag gtaccgttgg ttatcctggt     1380
agtgtgaag ttgtgaatat ggccccgccg agccatttat taaaacgcgg tattgattca     1440
ttaccttgcc tgggagatgg ccgcaaaagt ggtacctcag ctagtccgtc tatcctgaat     1500
atgagccctg aagccgccgt tggaggaggt ttagcattat taagaaccgg tgatcgcatt     1560
cgcgtcgatc tgaatcaacg ctcagtcatt gcattagtcg accagaccga aatggaacgc     1620
cgcaaattag aaccaccgta tcaagcacct gaaagccaaa ccccgtaggca agaactgtat     1680
cgccaattag tcggtcaact gtcaacaggc ggctgcctgg aaccagccac cttatatatta     1740
aaagtcgtgg aaacccgtgg agatcctcgt catagccatt aa                        1782

```

<210> 39  
 <211> 451  
 <212> PRT  
 <213> Terriglobuds roseus

<400> 39

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

Ala Pro Leu Ala Arg Ala Ala Asn Val Pro Glu Asp His Ala Asn Val

20

25

30

Pro Arg Thr Asn Trp Ser Lys Asn Phe His Tyr Ser Thr Ser Arg Val  
 35 40 45

Tyr Ala Pro Thr Thr Pro Glu Glu Val Pro Ala Ile Val Leu Glu Asn  
 50 55 60

Gly His Leu Lys Gly Leu Gly Ser Arg His Cys Phe Asn Asn Ile Ala  
 65 70 75 80

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

Ile Asp Glu Ala Ala Gln Thr Val Thr Val Gly Ala Gly Ile Ala Tyr  
 100 105 110

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

Leu Ala Ser Leu Pro His Ile Ser Val Gly Gly Thr Ile Ala Thr Ala  
 130 135 140

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

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

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

Leu Gly Val Leu Thr Lys Val Thr Leu Asp Ile Val Pro Arg Phe Asp  
 195 200 205

Met Ser Gln Val Val Tyr Arg Asn Leu Ser Phe Asp Gln Leu Glu His  
 210 215 220

Asn Leu Asp Thr Ile Leu Ser Ser Gly Tyr Ser Val Ser Leu Phe Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 |     | 230 |     | 235 |     | 240 |     |     |     |     |     |     |     |     |     |
| Asp | Trp | Gln | Arg | Asn | Arg | Val | Asn | Gln | Val | Trp | Ile | Lys | Asp | Lys | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Ala | Asp | Ala | Pro | Gln | Lys | Pro | Leu | Pro | Pro | Met | Phe | Tyr | Gly | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Leu | Gln | Thr | Ala | Lys | Leu | His | Pro | Ile | Asp | Asp | His | Pro | Ala | Asp |
|     |     | 275 |     |     |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Ala | Cys | Thr | Glu | Gln | Met | Gly | Ser | Val | Gly | Pro | Trp | Tyr | Leu | Arg | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | His | Phe | Lys | Met | Glu | Phe | Thr | Pro | Ser | Ser | Gly | Glu | Glu | Leu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Glu | Tyr | Phe | Val | Ala | Arg | Lys | Asp | Gly | Tyr | Arg | Ala | Ile | Arg | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Glu | Lys | Leu | Arg | Asp | Lys | Ile | Thr | Pro | His | Leu | Phe | Ile | Thr | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Arg | Thr | Ile | Ala | Ala | Asp | Asp | Leu | Pro | Met | Ser | Met | Ala | Tyr | Gln |
|     |     | 355 |     |     |     |     |     | 360 |     |     |     | 365 |     |     |     |
| Arg | Asp | Ser | Met | Ala | Ile | His | Phe | Thr | Trp | Lys | Pro | Glu | Glu | Pro | Thr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Arg | Lys | Leu | Leu | Pro | Glu | Ile | Glu | Ala | Ala | Leu | Ala | Pro | Phe | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Val | Arg | Pro | His | Trp | Gly | Lys | Ile | Phe | Glu | Ile | Pro | Pro | Ser | Tyr | Leu |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |     |
| His | Lys | Gln | Tyr | Pro | Ala | Leu | Pro | Arg | Phe | Arg | Ala | Met | Ala | Gln | Ala |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     | 430 |     |     |     |
| Leu | Asp | Pro | Gly | Gly | Lys | Phe | Arg | Asn | Ala | Tyr | Leu | Asp | Arg | Asn | Ile |

435

440

445

Phe Gly Ala  
450

&lt;210&gt; 40

&lt;211&gt; 450

&lt;212&gt; PRT

&lt;213&gt; Granulicella mallensis

&lt;400&gt; 40

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

Leu Met Met Gly Leu Asn Glu Ser Lys Ala Phe Ala Asp Asp Ser Val  
20 25 30

Pro Arg Thr Asn Trp Ser Gly Asn Tyr His Tyr Ser Thr Asn Lys Val  
35 40 45

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

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

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

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

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

Leu Ala Ser Leu Pro His Ile Ser Val Gly Gly Ala Cys Ala Thr Ala  
130 135 140

Thr His Gly Ser Gly Met Gly Asn Gly Asn Leu Ala Thr Ala Val Lys  
145 150 155 160

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

Asp Arg Asp Gly Asp Arg Phe Ala Gly Ser Val Val Gly Leu Gly Ala  
180 185 190

Leu Gly Val Val Thr His Leu Thr Leu Gln Val Gln Pro Arg Phe Glu  
195 200 205

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

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

Asp Trp Gln Asn Gly Arg Ala Gly Glu Val Trp Ile Lys Arg Arg Val  
245 250 255

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

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

Cys Thr Asp Gln Leu Asn Thr Val Gly Pro Trp Tyr Glu Arg Leu Pro  
290 295 300

His Phe Lys Leu Asn Phe Thr Pro Ser Ser Gly Gln Glu Leu Gln Thr  
305 310 315 320

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

Glu Thr Leu Arg Asp Val Ile Thr Pro His Leu Tyr Ile Thr Glu Leu  
340 345 350

Arg Ala Val Ala Ala Asp Asp Leu Trp Met Ser Met Ala Tyr Gln Arg  
355 360 365

SGI1660-1W0\_ST25.txt

Pro Ser Leu Ala Ile His Phe Thr Trp Lys Pro Glu Thr Asp Ala Val  
370 375 380

Leu Lys Leu Leu Pro Gln Ile Glu Ala Lys Leu Ala Pro Phe Gly Ala  
385 390 395 400

Arg Pro His Trp Ala Lys Val Phe Thr Met Lys Ser Ser His Val Ala  
405 410 415

Pro Leu Tyr Pro Arg Leu Lys Asp Phe Leu Val Leu Ala Lys Ser Phe  
420 425 430

Asp Pro Lys Gly Lys Phe Gln Asn Ala Phe Leu Gln Asp His Val Asp  
435 440 445

Ile Ala  
450

<210> 41  
<211> 414  
<212> PRT  
<213> Streptomyces acidiscabies

<400> 41

Met Thr Ala Ser Val Thr Asn Trp Ala Gly Asn Ile Ser Phe Val Ala  
1 5 10 15

Lys Asp Val Val Arg Pro Gly Gly Val Glu Ala Leu Arg Lys Val Val  
20 25 30

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

Arg Ile Ala Glu Pro Gly Ala Asp Gly Val Leu Val Ser Leu Asp Ala  
50 55 60

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

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

Gly Leu Ala Leu Pro Asn Met Ala Ser Leu Pro His Ile Ser Val Ala  
100 105 110

Gly Ser Val Ala Thr Gly Thr His Gly Ser Gly Val Asn Asn Gly Pro  
115 120 125

Leu Ala Thr Pro Val Arg Glu Val Glu Leu Leu Thr Ala Asp Gly Ser  
130 135 140

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

Ser Leu Gly Ala Leu Gly Val Val Val Ala Leu Thr Leu Asp Leu Glu  
165 170 175

Pro Ala Tyr Gly Val Glu Gln Tyr Thr Phe Thr Glu Leu Pro Leu Glu  
180 185 190

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

Phe Thr Asp Trp Arg Glu Ala Gly Phe Arg Gln Val Trp Val Lys Arg  
210 215 220

Arg Ile Asp Glu Pro Tyr Ala Gly Phe Pro Trp Ala Ala Pro Ala Thr  
225 230 235 240

Glu Lys Leu His Pro Val Pro Gly Met Pro Ala Glu Asn Cys Thr Asp  
245 250 255

Gln Phe Gly Ala Ala Gly Pro Trp His Glu Arg Leu Pro His Phe Lys  
260 265 270

Ala Glu Phe Thr Pro Ser Ser Gly Asp Glu Leu Gln Ser Glu Tyr Leu  
275 280 285

SGI1660-1W0\_ST25.txt

Leu Pro Arg Glu His Ala Leu Ala Ala Leu Asp Ala Val Gly Asn Val  
290 295 300

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

Ala Ala Asp Thr Gln Trp Leu Ser Pro Ala Tyr Gly Arg Asp Ser Val  
325 330 335

Ala Leu His Phe Thr Trp Thr Asp Asp Met Asp Ala Val Leu Pro Ala  
340 345 350

Val Arg Ala Val Glu Ser Ala Leu Asp Gly Phe Gly Ala Arg Pro His  
355 360 365

Trp Gly Lys Val Phe Thr Thr Ala Pro Ala Ala Leu Arg Glu Arg Tyr  
370 375 380

Pro Arg Leu Asp Asp Phe Arg Thr Leu Arg Asp Glu Leu Asp Pro Ala  
385 390 395 400

Gly Lys Phe Thr Asn Ala Phe Val Arg Asp Val Leu Glu Gly  
405 410

<210> 42

<211> 427

<212> PRT

<213> Actinomycetales

<400> 42

Met Thr Leu Glu Arg Asn Trp Ala Gly Thr His Thr Phe Ala Ala Pro  
1 5 10 15

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

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

## SGI1660-1W0\_ST25.txt

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

Asp Ile Pro Ala Asp Pro Val Phe Asp Glu Ala Ala Gly Ser Val Thr  
 65 70 75 80

Ile Gly Ala Gly Thr Arg Tyr Gly Ile Ala Ala Ala Trp Leu Ala Glu  
 85 90 95

His Gly Leu Ala Phe His Asn Met Gly Ser Leu Pro His Ile Ser Val  
 100 105 110

Gly Gly Ala Ile Ala Thr Gly Thr His Gly Ser Gly Asn Asp Asn Gly  
 115 120 125

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

Glu Leu Val His Val Arg Arg Gly Asp Pro Gly Phe Asp Gly Leu Val  
 145 150 155 160

Val Gly Leu Gly Ala Tyr Gly Ile Val Val Arg Val Thr Val Asp Val  
 165 170 175

Gln Pro Ala Tyr Arg Val Arg Gln Asp Val Tyr Arg Asp Val Pro Trp  
 180 185 190

Asp Ala Val Leu Ala Asp Phe Glu Gly Val Thr Gly Gly Ala Tyr Ser  
 195 200 205

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

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

Glu Ser Trp Leu Gly Val Gln Arg Asp Ser Leu Thr Ala Gly Asn Leu  
 245 250 255

SGI1660-1W0\_ST25.txt

Val Glu Thr Asp Pro Asp Asn Leu Thr Leu Gln Gly Gly Val Pro Gly  
260 265 270

Asp Trp Trp Glu Arg Leu Pro His Phe Arg Leu Glu Ser Thr Pro Ser  
275 280 285

Asn Gly Asp Glu Ile Gln Thr Glu Tyr Phe Ile Asp Arg Ala Asp Gly  
290 295 300

Pro Ala Ala Ile Thr Ala Leu Arg Ala Leu Gly Asp Arg Ile Ala Pro  
305 310 315 320

Leu Leu Leu Val Thr Glu Leu Arg Thr Ala Ala Pro Asp Lys Leu Trp  
325 330 335

Leu Ser Gly Ala Tyr His Arg Glu Met Leu Ala Val His Phe Thr Trp  
340 345 350

Arg Asn Leu Pro Glu Glu Val Arg Ala Val Leu Pro Ala Ile Glu Glu  
355 360 365

Ala Leu Ala Pro Phe Asp Ala Arg Pro His Trp Gly Lys Leu Asn Leu  
370 375 380

Leu Thr Ala Glu Arg Ile Ala Glu Val Val Pro Arg Leu Ala Asp Ala  
385 390 395 400

Arg Asp Leu Phe Glu Glu Leu Asp Pro Ala Gly Thr Phe Ser Asn Ala  
405 410 415

His Leu Glu Arg Ile Gly Val Arg Leu Pro Arg  
420 425

<210> 43

<211> 419

<212> PRT

<213> Frankia sp.

<400> 43

Met Arg Asp Ala Ala Ala Asn Trp Ala Gly Asn Val Arg Phe Gly

## SGI1660-1W0\_ST25.txt

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

210

215

220

Asp Gly Pro Gly Asp Asp Gly Glu Pro Pro Ala Glu Arg Phe Gly Ala  
 225 230 235 240

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

His Thr Thr Gln Gln Leu Gly Val Pro Gly Pro Trp His Glu Arg Leu  
 260 265 270

Pro His Phe Arg Leu Asp Phe Thr Pro Ser Ala Gly Asp Glu Leu Gln  
 275 280 285

Thr Glu Tyr Phe Val Ala Arg Glu His Ala Ala Ala Ile Glu Ala  
 290 295 300

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

Ile Arg Thr Val Ala Ala Asp Ala Leu Trp Leu Ser Pro Ala Tyr Arg  
 325 330 335

Arg Asp Val Met Ala Leu His Phe Thr Trp Ile Ser Ala Glu Gly Thr  
 340 345 350

Val Met Pro Ala Val Ala Ala Val Glu Arg Ala Leu Ala Pro Phe Asp  
 355 360 365

Pro Val Pro His Trp Gly Lys Val Phe Ala Leu Pro Pro Ala Ala Val  
 370 375 380

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

Arg Asp Pro Glu Ala Val Phe Arg Asn Gln Tyr Leu Asp Ala Tyr Leu  
 405 410 415

Pro Ala Ala

<210> 44  
 <211> 413  
 <212> PRT  
 <213> Propionibacteriaceae

<400> 44

Met Thr Gln Arg Asn Trp Ala Gly Asn Val Ser Tyr Ser Ser Ser Arg  
 1 5 10 15

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

Glu Pro Arg Val Arg Pro Leu Gly Ser Arg His Cys Phe Asn Asp Ile  
 35 40 45

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

Glu Pro Arg Leu Thr Ala Pro Gly Thr Leu Arg Thr Pro Ala Trp Leu  
 65 70 75 80

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

Ala Asn Leu Ala Ser Leu Pro His Ile Ser Val Ala Gly Ala Val Gln  
 100 105 110

Thr Gly Thr His Gly Ser Gly Asp Arg Ile Gly Thr Leu Ala Thr Gln  
 115 120 125

Val Ser Ala Leu Glu Leu Val Thr Gly Thr Gly Glu Val Leu Arg Leu  
 130 135 140

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

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

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Val Ala Gln His Val Tyr Glu Gly Val Arg Leu Asp Asp Val Leu Ala  
180 185 190

Asp Leu Gly Ala Val Thr Gly Ala Gly Asp Ser Val Ser Met Phe Thr  
195 200 205

His Trp Gln Asp Pro Ala Val Val Ser Gln Val Trp Val Lys Ser Gly  
210 215 220

Gly Asp Val Asp Asp Ala Ala Ile Arg Asp Ala Gly Gly Arg Pro Ala  
225 230 235 240

Asp Gly Pro Arg His Pro Ile Ala Gly Ile Asp Pro Thr Pro Cys Thr  
245 250 255

Pro Gln Leu Gly Glu Pro Gly Pro Trp Tyr Asp Arg Leu Pro His Phe  
260 265 270

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

Leu Val Asp Arg Asp Asp Ala Val Asp Ala Ile Arg Ala Val Gln Asp  
290 295 300

Leu Ala Pro Arg Ile Ala Pro Leu Leu Phe Val Cys Glu Ile Arg Thr  
305 310 315 320

Met Ala Ser Asp Gly Leu Trp Leu Ser Pro Ala Gln Gly Arg Asp Thr  
325 330 335

Val Gly Leu His Phe Thr Trp Arg Pro Asp Glu Ser Ala Val Arg Gln  
340 345 350

Leu Leu Pro Glu Ile Glu Arg Ala Leu Pro Ala Ser Ala Arg Pro His  
355 360 365

Trp Gly Lys Val Phe Thr Leu Pro Gly His Asp Val Ala Ala Arg Tyr  
370 375 380

Pro Arg Trp Ala Asp Phe Val Ala Leu Arg Arg Arg Leu Asp Pro Glu  
385 390 395 400

Arg Arg Phe Ala Asn Ala Tyr Leu Glu Arg Leu Gly Leu  
405 410

<210> 45

<211> 420

<212> PRT

<213> Streptomyces sp.

<400> 45

Met Thr Pro Ala Glu Lys Asn Trp Ala Gly Asn Ile Thr Phe Gly Ala  
1 5 10 15

Lys Arg Leu Cys Val Pro Arg Ser Val Arg Glu Leu Arg Glu Thr Val  
20 25 30

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

Thr Val Ala Asp Thr Ser Gly Asp His Val Ser Leu Ala Gly Leu Pro  
50 55 60

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

Gly Leu Arg Phe Gly Glu Phe Ala Ala Glu Leu His Ala Arg Gly Leu  
85 90 95

Ala Leu Ala Asn Leu Gly Ser Leu Pro His Ile Ser Val Ala Gly Ala  
100 105 110

Val Ala Thr Gly Thr His Gly Ser Gly Val Gly Asn Arg Ser Leu Ala  
115 120 125

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

## SGI1660-1W0\_ST25.txt

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

Gly Ala Leu Gly Val Val Thr Ser Leu Glu Leu Asp Leu Val Pro Ala  
 165 170 175

Phe Glu Val Arg Gln Trp Val Tyr Glu Asp Leu Pro Glu Ala Thr Leu  
 180 185 190

Ala Ala Arg Phe Asp Glu Val Met Ser Ala Ala Tyr Ser Val Ser Val  
 195 200 205

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

Arg Val Gly Asp Glu Gly Ala Arg Ser Val Met Pro Ala Glu Trp Leu  
 225 230 235 240

Gly Ala Arg Leu Ala Asp Gly Pro Arg His Pro Val Pro Gly Met Pro  
 245 250 255

Ala Gly Asn Cys Thr Ala Gln Gln Gly Val Pro Gly Pro Trp His Glu  
 260 265 270

Arg Leu Pro His Phe Arg Met Glu Phe Thr Pro Ser Asn Gly Asp Glu  
 275 280 285

Leu Gln Ser Glu Tyr Phe Val Ala Arg Ala Asp Ala Val Ala Ala Tyr  
 290 295 300

Glu Ala Leu Ala Arg Leu Arg Asp Arg Ile Ala Pro Val Leu Gln Val  
 305 310 315 320

Ser Glu Leu Arg Thr Val Ala Ala Asp Asp Leu Trp Leu Ser Pro Ala  
 325 330 335

His Gly Arg Asp Ser Val Ala Phe His Phe Thr Trp Val Pro Asp Ala  
 340 345 350

SGI1660-1W0\_ST25.txt

Ala Ala Val Ala Pro Val Ala Gly Ala Ile Glu Glu Ala Leu Ala Pro  
355 360 365

Phe Gly Ala Arg Pro His Trp Gly Lys Val Phe Ser Thr Ala Pro Glu  
370 375 380

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

Gly Arg His Asp Pro Glu Gly Thr Phe Arg Asn Ala Phe Leu Asp Arg  
405 410 415

Tyr Phe Arg Arg  
420

<210> 46

<211> 419

<212> PRT

<213> Paenibacillus sp.

<400> 46

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

Glu Leu Leu Glu Pro Lys Ser Leu Glu Glu Val Lys Asp Leu Val Val  
20 25 30

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

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

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

Ile Arg Tyr Gly Asp Leu Cys Arg Tyr Leu Asn Asp His Gly Tyr Ala  
85 90 95

## SGI1660-1W0\_ST25.txt

Leu His Asn Leu Ala Ser Leu Pro His Ile Ser Val Ala Gly Ala Val  
 100 105 110

Ala Thr Ala Thr His Gly Ser Gly Asp Leu Asn Ala Ser Leu Ala Ser  
 115 120 125

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

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

Gly Gly Leu Gly Val Val Thr Lys Leu Lys Leu Asp Leu Val Pro Ser  
 165 170 175

Phe Gln Val Ser Gln Thr Val Tyr Asp Arg Leu Pro Phe Ser Ala Leu  
 180 185 190

Asp His Gly Ile Asp Glu Ile Leu Ser Ser Ala Tyr Ser Val Ser Leu  
 195 200 205

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

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

Ala Leu Pro Ala Pro Glu Lys Arg His Met Val Leu Gly Gln Ser Val  
 245 250 255

Val Asn Cys Ser Glu Gln Met Gly Asp Pro Gly Pro Trp Tyr Glu Arg  
 260 265 270

Leu Pro His Phe Arg Met Glu Phe Thr Pro Ser Ala Gly Asn Glu Leu  
 275 280 285

Gln Ser Glu Tyr Phe Val Pro Arg Arg His Ala Val Glu Ala Met Arg  
 290 295 300

## SGI1660-1W0\_ST25.txt

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

Glu Ile Arg Thr Ile Ala Ser Asp Thr Phe Trp Met Ser Pro Cys Tyr  
 325 330 335

Arg Gln Asp Ser Val Gly Leu His Phe Thr Trp Lys Pro Asp Trp Glu  
 340 345 350

Arg Val Arg Gln Leu Leu Pro Leu Ile Glu Arg Glu Leu Glu Pro Phe  
 355 360 365

Ala Ala Arg Pro His Trp Ala Lys Leu Phe Thr Met Glu Ser Glu Met  
 370 375 380

Ile Gln Ala Arg Tyr Glu Arg Leu Ala Asp Phe Arg Gln Leu Leu Leu  
 385 390 395 400

Arg Tyr Asp Pro Ile Gly Lys Phe Arg Asn Thr Phe Leu Asp His Tyr  
 405 410 415

Ile Met His

<210> 47

<211> 1356

<212> DNA

<213> Terriglobuds roseus

<400> 47

atggatcgtc gtgaactgct gaaaacctct gcactgctga tggcagcagc accgttagca 60

cgtgcagcaa atgttccgga agatcatgca aatgttccgc gtaccaattg gagcaaaaac 120

ttccactata gcaccagccg cgtttatgca ccgactaccc cggaagaagt tccggcaatt 180

gttctggaaa atggatcatct gaaaggctctg ggttctcgtc actgcttcaa caacatcgcc 240

gatagccagt atgcgcagat cagcatgcgc gaagttaaag gcattcagat cgatgaagcc 300

gcacaaaccg ttaccgtggg tgcaggtatt gcgtatgggtg aattagcacc ggtgctggat 360

aaagcggggtt ttgactggc aaatttagca agtttaccgc atatcagcgt gggtggcacc 420

## SGI1660-1WO\_ST25.txt

|                                                                     |      |
|---------------------------------------------------------------------|------|
| attgcaaccg caacacatgg ctctggcggt ggtaacaaaa acctgtcttc tgcaaccctg   | 480  |
| gcaattgaaa tcgtgaaagc ggatggcagc attctgcgtc tgtcgcgtga tactgatggt   | 540  |
| gaacgttttc gtatggcggt ggttcacatg ggtgcattag gtgttttaac caaagttacc   | 600  |
| ctggatatcg tgccgcgctt cgatatgtct cagggtggtgt atcgcaacct gtcctttgat  | 660  |
| cagctggaac acaacctgga taccattctg agctctggct atagcgttag cctgttcacc   | 720  |
| gactggcagc gtaatcgtgt taatcagggtg tggatcaaag ataaagcgac cgcggatgca  | 780  |
| ccgcaaaaaac cgttacctcc gatgttttat ggtgcgaccc tgcaaaccgc aaaactgcat  | 840  |
| ccgatcgatg atcatccggc agatgcatgt accgaacaaa tgggtagtgt tgggccgtgg   | 900  |
| tattttacgtc tgccgcattt caaaatggag tttaccccga gcagcgggtga agaattacag | 960  |
| accgaatact tcgtggcgcg caaagatggc tatcgcgcaa ttcgtgccgt ggaaaaactg   | 1020 |
| cgcgataaaa ttaccccga cctgtttatc accgaaatcc gcaccattgc agcagatgat    | 1080 |
| ctgccgatga gcatggcata tcaacgtgac agtatggcga ttcattttac ctggaaaccg   | 1140 |
| gaagaaccga ccgtgcgtaa attactgccg gaaatcgaag cagcactggc gccgtttggt   | 1200 |
| gttcgtccgc attggggcaa aatttttgaa attccgccga gctatctgca taaacagtat   | 1260 |
| ccggcactgc cgcgttttcg cgcaatggca caggcattag atcctggtgg caaatttcgt   | 1320 |
| aatgcatatc tggatcgtaa catctttggc gcgtag                             | 1356 |

&lt;210&gt; 48

&lt;211&gt; 1353

&lt;212&gt; DNA

&lt;213&gt; Granulicella mallensis

&lt;400&gt; 48

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atggacaaac gcgatttcct gaaaggtagc gcaaccaccg cagttgcact gatgatgggt  | 60  |
| ctgaatgaaa gcaaagcggt tgcggatgat agcgttccgc gtaccaattg gagcggcaac  | 120 |
| taccattata gcaccaacaa agtgctgcag ccggcaagtg ttgcagaaac ccaagatgca  | 180 |
| gttcgtagtg ttgcagggtg tcgtgcatta ggtactcgtc atagctttta cggcatcgcg  | 240 |
| gatagccaga ttgcccagat tagtaccctg aaactgaaag atgtgagcct ggatgcgaaa  | 300 |
| agctcgaccg tgaccgttgg tgcagggtatt cgttatgggt atctggcggt tcagctggat | 360 |
| gcgaaagggt ttgctctgca taatctggca agtctgccgc atatttctgt tgggtggtgca | 420 |

## SGI1660-1W0\_ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgtgcaactg cgacccatgg ttcaggtatg ggtaatggta atttagcaac cgcagttaaa  | 480  |
| gcggtggaat ttgttgcggc ggatggtagc gtgcataccc tgtctcgtga tcgtgatgg   | 540  |
| gatcgttttg cgggctctgt tgttggtctg ggtgcattag gtgttggttac ccatttaacc | 600  |
| ctgcaagttc agccacgttt cgaaatgacc caggtgggtg accgtgatct gccatttagt  | 660  |
| gaactggaac atcatctgcc ggaaattatg ggtgccgggt atagcgtgtc cctgtttacc  | 720  |
| gattggcaga atggtcgtgc aggtgaagtg tggatcaaac gtcgcgtgga tcaaggtgg   | 780  |
| gcaagtgtc ctccagctcg tttttttaat gcaaccttag caaccaccaa actgcacccg   | 840  |
| atcctggatc atcctgctga agcatgtacc gatcagttaa ataccgtagg tccgtggtat  | 900  |
| gaacgtttac cgcacttcaa actgaacttc accccgagca gtggccaaga attacagacc  | 960  |
| gagtttttcg tgccgttcga tcgcggctat gacgccattc gtgccgttga aactttacgt  | 1020 |
| gatgtgatta ccccgacact gtatatcacc gaactgcgtg cagttgcagc tgatgattta  | 1080 |
| tggatgagca tggcatatca acgtccgagt ctggcaatcc attttacctg gaaaccggaa  | 1140 |
| accgatgcag tgctgaaatt actgccgcag attgaagcga aactggcccc gtttggtgct  | 1200 |
| cgtccgcatt gggcaaaaagt ttttaccatg aaaagcagcc atgtggcacc gctgtatccg | 1260 |
| cgcctgaaag attttctggt tctggcaaaa tcctttgatc cgaaaggcaa attccaaaac  | 1320 |
| gcgtttctgc aggaccatgt ggacatcgca tag                               | 1353 |

&lt;210&gt; 49

&lt;211&gt; 1245

&lt;212&gt; DNA

&lt;213&gt; Streptomyces acidiscabies

&lt;400&gt; 49

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgaccgcat ctgtgaccaa ttgggcgggt aacatcagct ttgtggcgaa agatgttggt  | 60  |
| cgtccgggtg gtgttgaaagc actgcgtaaa gttgttgctg gtaatgatcg tgttcgtgtt | 120 |
| ctgggttctg gtcataagctt taaccgtatc gctgaaccgg gtgctgatgg tgttctggtt | 180 |
| agcctggatg cattaccgca agtgattgat gttgataccg aacgtcgtac cgtgcgtgtt  | 240 |
| ggtggtggtg ttaaatacgc ggaactggct cgtcatgtga atgaatctgg tctggcactg  | 300 |
| ccgaatatgg catctctgcc gcatatttct gttgcagggt ctgttgcaac tggtagccat  | 360 |

## SGI1660-1W0\_ST25.txt

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ggttctggtg tgaataatgg cccgttagca accccggttc gtgaagttga attattaacc  | 420  |
| gcggatggct ctctggtgac catcggtaaa gatgatgcgc gttttccggg tgcagttact  | 480  |
| tctctgggtg cgctgggtgt tgttggtgca ctgaccttag atttagaacc ggcgtatggt  | 540  |
| gttgaacagt atacctttac cgaattaccg ctggaaggtc tggacttcga agcagttgcg  | 600  |
| agtgcagcat attctgtag cctgttcacc gattggcgtg aagctggttt tcgccaagtt   | 660  |
| tgggtgaaac gccgcattga tgaaccgtac gcgggctttc cgtgggcagc accggcaact  | 720  |
| gaaaaattac atccggttcc gggtagcca gcagaaaatt gtactgatca atttggtgca   | 780  |
| gcaggtccat ggcatgaacg tttaccgcat tttaaagcgg aatttaccct gtctagcgtt  | 840  |
| gatgaattac agagcgaata tctgctgccg cgtgaacatg cactggcggc actggatgca  | 900  |
| gtgggcaacg tgcgtgaaac cgtttctacc gtgctgcaga tttgcgaagt tcgtaccatt  | 960  |
| gcagcagata cccagtgggt aagtccggct tatggctcgtg atagtgttgc attacatttt | 1020 |
| acttggaccg atgatatgga tgcagtttta cctgcagttc gtgccgttga aagcgcgctg  | 1080 |
| gatggctttg gtgctcgccc gcattgggggt aaagtgttta ccaccgcacc ggcagcatta | 1140 |
| cgtgaacgtt atccgcgtct ggatgatattt cgtaccctgc gtgatgaatt agatccggca | 1200 |
| ggcaaattta ctaatgcatt tgttcgtgat gttctggaag gttag                  | 1245 |

&lt;210&gt; 50

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Actinomycetales

&lt;400&gt; 50

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgaccctgg aacgtaattg ggcaggtacc catacctttg cagcaccgcg tattgttaat  | 60  |
| gcaaccagca tcgatgaagt tcgtgcgtta gtggcagaag cagcacgtac cggtacccgt  | 120 |
| gttcgtgcat taggtactcg tcattctttt accgatctgg cagatagcga tggtagcctg  | 180 |
| attaccgtgc tggatattcc ggcagatcca gttttcgatg aagcagcagg tagcgttacc  | 240 |
| attggtgcag gtacccgtta tggtagttgca gcagcatggt tagcagaaca tggtagcgcg | 300 |
| tttcacaaca tgggttagcct gccgcatatt agcgttggtg gtgcaattgc aaccggtacc | 360 |
| catggttagtg gtaatgataa cggcattctg agtagcgag ttagtggtct ggaatatgtt  | 420 |
| gatgcgaccg gtgaactgggt tcatgtgcgt cgtggtgatc ctggttttga tggtagcgtt | 480 |

SGI1660-1W0\_ST25.txt

|                                                                      |      |
|----------------------------------------------------------------------|------|
| gttggttttag ggcgctatgg tattgtgggt cgtgtgacgg tggatgttca accggcatat   | 540  |
| cgtgttcgcc aggatgtgta tcgtgatgtt ccgtgggatg cagttctggc agattttgaa    | 600  |
| gggtgttacag gtgggtgcgta tagcgttagc atctttacca actggctggg tgatacgggtg | 660  |
| gaacagattt ggtggaaaac ccgtctgggt gcaggatgat atgaactgcc ggtgggttccg   | 720  |
| gaaagctggc tgggtgttca acgtgattct ttaaccgcag gtaatctggt tgaaaccgat    | 780  |
| ccggataatt taaccctgca aggtgggtgtt ccgggtgatt ggtgggaacg tttaccgcat   | 840  |
| tttcgtctgg aaagtacccc gtctaattgg gatgaaatcc agaccgaata cttcatcgat    | 900  |
| cgcgcgggatg gtccggcggc aattaccgca ctgcgtgcat taggtgatcg tattgctccg   | 960  |
| ttactgttag ttaccgaatt acgtaccgca gctccagata aactgtggct gagtggcgca    | 1020 |
| tatcatcgcg aaatgttagc ggtccatttt acctggcgta atttaccgga agaagtgcgt    | 1080 |
| gcagttttac cagcgatcga agaagccctg gcgccgtttg atgctcgtcc gcattgggggt   | 1140 |
| aaactgaatc tgtaaccgc agaacgtatt gcagaagttg ttccgcgtct ggctgatgca     | 1200 |
| cgtgatctgt ttgaagaact ggacccggct ggtacctttt ctaatgctca tctggaacgt    | 1260 |
| attggtgttc gtttaccgcg ttag                                           | 1284 |

<210> 51  
 <211> 1260  
 <212> DNA  
 <213> Frankia sp.

|                                                                                |     |
|--------------------------------------------------------------------------------|-----|
| <400> 51<br>atgcgtgatg cagcagcagc aaattgggca ggtaatgtgc gttttgggtgc agcacgtgtt | 60  |
| gttgcaccgg aaagtgttgg tgaactgcag gaaattgttg caggtagccg taaagcacgt              | 120 |
| gcattaggta ccggtcatag ctttagccgt attgcagata ccgatggtag cctgattgct              | 180 |
| accgcacgtt taccacgtcg tattcagatc gatgatggca gcgttaccgt ttctgggtgt              | 240 |
| atccgttatg gcgatctggc ccgtgaatta gcaccgaatg gttgggcatt acgtaatctg              | 300 |
| ggttcttttac cgcacatttc agttgcaggc gcatgtgcaa ccggtacca tggttcaggc              | 360 |
| gatcgtaatg gtagtctggc aacctctgtt gcagcgtag aattagttac cgcgtctggt               | 420 |
| gaattagtga gcgttcgtcg tggcgatgaa gatttcgatg gccatgtgat tgcgctgggt              | 480 |

## SGI1660-1W0\_ST25.txt

gcactgggtg ttactgttgc agttaccctg gatttagttc cgggttttca ggttcgtcag 540  
ctgggtgatg aaggtctgac ccgtgatacc ttactggaaa gtgtgcagga aatctttgct 600  
gcgagctata gtgttagcgt gtttaccggt tgggacccgg aaagttctca actgtggctg 660  
aaacagcgcg ttgatgggcc gggcgatgat ggtgaaccac cggcagaacg ttttggtgca 720  
cgtttagcaa ctcgtccgtt acatccagtt ccgggtattg atccgactca tactactcaa 780  
caattagggtg ttccagggtc gtggcatgaa cgtttaccgc attttcgtct ggattttacc 840  
ccttctgcag gtgatgaact gcaaaccgaa tacttcgtgg cccgcgaaca tgcagcggcg 900  
gcgattgaag cactgtttgc gattgggtgc gttgttcgtc cggcattaca aattagcgaa 960  
attcgtaccg ttgcagctga tgcattatgg ctgtctccgg catatcgtcg tgatgttatg 1020  
gcgttacatt ttacctggat tagcgcagaa ggtaccgtta tgccagcagt tgcagcagtg 1080  
gaacgtgcac tggcgccgtt tgatccggtt cctcattggg gtaaagtttt tgcgctgccg 1140  
ccagcagcag ttcgtgctgg ttatcctcgt gcagcagaat ttttagcatt agcagctcgt 1200  
cgtgatccgg aagcagtttt tcgtaatcag tatttagatg catatttacc ggcagcatag 1260

&lt;210&gt; 52

&lt;211&gt; 1242

&lt;212&gt; DNA

&lt;213&gt; Propionibacteriaceae

&lt;400&gt; 52

atgacccagc gtaattgggc gggtaatgtg agctatagta gcagccgtgt tgcagaacca 60  
gcaagtgtgg atgatttaac cgcaactggt gaaagtgaac cgcgtgttcg tccgttaggt 120  
agtcgtcatt gcttcaacga tatcgccgat accccagggt ttcattgtttc tctggcacgt 180  
ctgcgtgggtg aagaaccgcg tttaacagca ccgggtacct tacgtactcc agcttggtta 240  
cgttatgggtg atttagttcc ggttctgcgt gaagcagggt cagcattagc aaatttagca 300  
tctctgccgc atattagcgt tgcagggtgca gttcaaaccg gtacccatgg ttcagggtgat 360  
cgtattggca ctctggcaac ccaagttagc gccctggaat tagtgaccgg caccggtgaa 420  
gttttacgct tagaacgtgg tgaacctgat tttgatgggt cggttggtgg tttagggtgcg 480  
ttaggtgttc tgactcatgt ggaattagat gtagtccgg cgcgtgatgt tgcacagcac 540  
gtgtatgaag gtgttcgtct ggatgatgtt ctggcggatt taggcgcgggt tactggcgca 600

## SGI1660-1W0\_ST25.txt

ggtgattcgg tgagcatggt tacccattgg caagatccgg cagttgttag tcaggtttgg 660  
 gttaaaagtg gcggtgatgt ggatgatgca gcaattcgtg atgcaggtgg tcgtccggca 720  
 gatggtccgc gtcatccaat tgcaggtatt gatccgactc catgtactcc acaattaggt 780  
 gaaccaggtc cgtggtatga tcgtctgccg ctttttcgtc tggaatttac cccgagtgtt 840  
 ggtgaagaac tgcaaagtga atatctgggt gatcgcgatg atgccgttga tgcaattcgt 900  
 gcggtgcagg atttagcccc gcgtattgca ccgctgctgt ttgtttgcga aattcgtacc 960  
 atggcaagtg atggtttatg gctgagcccc gcacaaggtc gtgataccgt tggctctgcat 1020  
 ttacctggc gtcctgatga atctgcagtt cgtcaattat taccggaaat tgaacgtgct 1080  
 ttaccggcaa gtgctcgtcc gcattggggg aaagtgttta ccctgccggg ccatgatgtt 1140  
 gcagcacgtt atccgcgttg ggcagatttt gttgcattac gtcgtcgttt agatccggaa 1200  
 cgtcgtttcg cgaatgcata cctggaacgt ttaggtctgt ag 1242

&lt;210&gt; 53

&lt;211&gt; 1263

&lt;212&gt; DNA

&lt;213&gt; Streptomyces sp.

&lt;400&gt; 53

atgactccgg cggaaaaaaa ttgggcgggc aacatcacct ttggtgcaaa acgtctgtgt 60  
 gttccgcgtt ctgttcgtga actgcgtgaa accgttgcaag catctgggtg agttcgtccg 120  
 ttaggtactc gtcataagct taataaccgt gcagatacca gtggtgatca tgttagtctg 180  
 gcaggtttac cgcgtgttgt ggacatcgat gttccgggtc gtgcagtttc tctgtctgct 240  
 ggtctgcgtt ttggtgaatt tgcggctgaa ttacatgcac gtggtctggc gctggcaaat 300  
 ttaggttctc tgccgcatat tagcgttgca ggtgcagttg caaccggtag tcatggttct 360  
 ggtgttggtg atcgttcttt agcaggtgca gttcgtgctt tatctctggt aaccgccgat 420  
 ggtgaaaccc gtaccttacg tcgtaccgat gaagattttg caggtgcagt ggtttctctg 480  
 ggtgcactgg gtgttggttac ttctctggaa ctggatttag ttccggcggt cgaagtgcgt 540  
 cagtgggtgt acgaagatct gccggaagca actttagcag ctcgttttga tgaagttatg 600  
 tcagcagcgt atagcgtgtc cgtgttcacc gattggcgtc cgggtcctgt tgggtcaagtt 660

## SGI1660-1WO\_ST25.txt

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| tggtgtaa    | aacgtgttgg | tgatgaaggt | gctcgtagtg | ttatgccagc | agaatggtta  | 720  |
| gggtgcacgtt | tagcagatgg | tccgcgtcat | ccagttccag | gtatgcctgc | aggtaattgt  | 780  |
| acagcacaac  | aaggtgttcc | aggtccgtgg | catgaacgtt | taccgcattt | tcgcatggaa  | 840  |
| tttaccctcgt | ctaacggcga | tgaactgcaa | agcgaatatt | ttgtggcgcg | tgcatgatgca | 900  |
| gttgacgagct | atgaagcatt | agcacgtctg | cgtgatcgta | ttgcgccggg | tctgcaagtt  | 960  |
| agcgaattac  | gtaccgttgc | agcagatgat | ctgtggctga | gtccggcaca | tggtcgtgat  | 1020 |
| agtgttgctg  | ttcattttac | ctgggttccg | gatgcagcag | cagttgcacc | ggttgcaggt  | 1080 |
| gctattgaag  | aagcattagc | accgtttggg | gcacgtccac | attggggtaa | agtttttagc  | 1140 |
| accgcaccgg  | aagttttacg | taccttatat | ccgcgttatg | ccgatttcga | agaactgggtg | 1200 |
| ggccgccatg  | atccggaagg | cacctttcgt | aatgcatttt | tagatcgcta | ctttcgtcgc  | 1260 |
| tag         |            |            |            |            |             | 1263 |

&lt;210&gt; 54

&lt;211&gt; 1260

&lt;212&gt; DNA

&lt;213&gt; Paenibacillus sp.

&lt;400&gt; 54

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| atgggcgata  | aactgaattg | ggcgggcaac  | tatcgttatc  | gcagcatgga | actgctggaa  | 60  |
| ccgaaaagcc  | tggaagaagt | gaaagatctg  | gtgggttagcc | gtaccagcat | tcgtgttctg  | 120 |
| ggtagctgtc  | atagctttaa | cggcattgctg | gataccgggtg | gtagtcatct | gagtctgcgc  | 180 |
| aaaatgaacc  | gcgtgattga | tctggatcgt  | gttcagcgta  | ccgttaccgt | tgaagggtgg  | 240 |
| attcgttacg  | gtgatctgtg | ccgctatctg  | aacgatcatg  | gttatgccct | gcataatctg  | 300 |
| gcaagcttac  | cgcacatcag | cgttgacaggt | gcagttgcaa  | ccgcaacca  | tggttctggg  | 360 |
| gatctgaatg  | caagtctggc | aagctctgtt  | cgtgcaattg  | aactgatgaa | aagcgatggc  | 420 |
| gaagttacgg  | ttctgacccg | tggtaccgat  | ccggaatttg  | atggtgcagt | tggttggtctg | 480 |
| gggtggtttag | gtgttgtagc | caaaactgaaa | ctggatctgg  | ttccgagctt | tcaggtgtcg  | 540 |
| cagaccgtgt  | atgatcgtct | gccgttttagc | gcactggatc  | atggcatcga | tgaaattctg  | 600 |
| agtagtgcac  | atagcgttag | cctgttcacc  | gattgggcgg  | aaccgatctt | taatcaggtg  | 660 |
| tggtgtaa    | gcaaagtggg | cattaacggc  | gaagatgaaa  | ccagtccgga | tttttttggc  | 720 |

SGI1660-1W0\_ST25.txt

gcattaccgg caccggaaaa acgccacatg gttctgggtc agagcgtggt gaattgcagc 780  
gaacaaatgg gtgatcctgg tccgtggtat gaacgtttac cgcattttcg catggaattt 840  
accccgagtg caggcaatga attacagagc gaatattttg tgccgcgtcg tcatgcggtt 900  
gaagcaatgc gtgcgttagg taaactgcgt gatcgtattg caccactgct gttcatcagc 960  
gaaatccgca ccattgcgag cgataccttc tggatgagcc cgtgttatcg tcaggattct 1020  
gttggctctgc attttacctg gaaaccggat tgggaacgtg ttcgtcagtt attaccgctg 1080  
attgaacgtg aactggaacc gtttgcgga cgtccgcatt gggcgaaact gtttaccatg 1140  
gaaagcgaaa tgattcaggc gcgctatgaa cgtctggcgg attttcgtca gctgctgctg 1200  
cgttatgatc cgattggcaa attccgtaac acctttctgg atcactacat catgcactaa 1260

<210> 55  
<211> 205  
<212> PRT  
<213> Thermus thermophilus

<400> 55

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

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

Leu Arg Glu Ile Leu Glu Ala Ala Leu Arg Ala Pro Ser Ala Trp Asn  
35 40 45

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

Ala Leu Arg Glu Ala Ala Phe Gly Gln Ala His Val Glu Glu Ala Pro  
65 70 75 80

Val Val Leu Val Leu Tyr Ala Asp Leu Glu Asp Ala Leu Ala His Leu  
85 90 95

Asp Glu Val Ile His Pro Gly Val Gln Gly Glu Arg Arg Glu Ala Gln

100

105

110

Lys Gln Ala Ile Gln Arg Ala Phe Ala Ala Met Gly Gln Glu Ala Arg  
 115 120 125

Lys Ala Trp Ala Ser Gly Gln Ser Tyr Ile Leu Leu Gly Tyr Leu Leu  
 130 135 140

Leu Leu Leu Glu Ala Tyr Gly Leu Gly Ser Val Pro Met Leu Gly Phe  
 145 150 155 160

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

Ile Pro Ala Leu Val Ala Leu Gly Tyr Pro Ala Glu Glu Gly Tyr Pro  
 180 185 190

Ser His Arg Leu Pro Leu Glu Arg Val Val Leu Trp Arg  
 195 200 205

<210> 56  
 <211> 618  
 <212> DNA  
 <213> Thermus thermophilus

<400> 56  
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 cgccgttatc gcaaagatcc agttccggaa ggtttactgc gcgaaattct ggaagcagca 120  
 ttacgtgcac cgtctgcatg gaatttaca ccgtggcgta ttgtggtggt tcgtgatccg 180  
 gcaactaaac gtgcattacg tgaagcagca tttgggtcaag cccatgtgga agaagcaccg 240  
 gttgttctgg ttctgtacgc agatctggaa gatgcactgg cacatctgga tgaagtgatt 300  
 catccgggcg ttcaagggtga acgtcgtgaa gcgcagaaac aagcaattca gcgtgcattt 360  
 gcagcaatgg gtcaggaagc tcgtaaagct tgggcaagcg gtcaaagtta tattctgctg 420  
 ggttatctgc tgctgctgct ggaagcatat ggtctgggtt ctgttccgat gctggggttt 480  
 gatcctgaac gtgttaaagc gattctgggc ctgccgtcac atgcagcgat tccggcatta 540  
 gttgcactgg gttatccggc tgaagaaggt tatccgagtc atcgtttacc gctggaacgt 600

gttgttttat ggcgttga

618

&lt;210&gt; 57

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Agrobacterium sp.

&lt;400&gt; 57

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Pro | Phe | Ser | Leu | Gln | Gly | Arg | Lys | Ala | Leu | Val | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Thr | Gly | Leu | Gly | Gln | Ala | Ile | Ala | Val | Gly | Leu | Ala | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Glu | Val | Val | Cys | Ala | Ala | Arg | Arg | Ala | Pro | Asp | Glu | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Met | Ile | Ala | Ser | Asp | Gly | Gly | Lys | Ala | Ser | Ala | Leu | Ser | Ile | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ala | Asp | Pro | Leu | Ala | Ala | Lys | Asp | Ser | Phe | Ala | Gly | Ala | Gly | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Leu | Val | Asn | Asn | Ala | Gly | Ile | Ile | Arg | Arg | Ala | Asp | Ser | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Phe | Ser | Glu | Leu | Asp | Trp | Asp | Glu | Val | Met | Asp | Val | Asn | Leu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Phe | Phe | Thr | Thr | Gln | Ala | Phe | Ala | Lys | Glu | Leu | Leu | Ala | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Ser | Gly | Lys | Val | Val | Asn | Ile | Ala | Ser | Leu | Leu | Ser | Phe | Gln |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Ile | Arg | Val | Pro | Ser | Tyr | Thr | Ala | Ala | Lys | His | Gly | Val | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Thr | Lys | Leu | Leu | Ala | Asn | Glu | Trp | Ala | Ala | Lys | Gly | Ile | Asn |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

165

170

175

Val Asn Ala Ile Ala Pro Gly Tyr Ile Glu Thr Asn Asn Thr Glu Ala  
 180 185 190

Leu Arg Ala Asp Ala Ala Arg Asn Lys Ala Ile Leu Glu Arg Ile Pro  
 195 200 205

Ala Gly Arg Trp Gly Arg Ser Glu Asp Ile Ala Gly Ala Ala Val Phe  
 210 215 220

Leu Ser Ser Ala Ala Ala Asp Tyr Val His Gly Ala Ile Leu Asn Val  
 225 230 235 240

Asp Gly Gly Trp Leu Ala Arg  
 245

<210> 58

<211> 198

<212> PRT

<213> Agrobacterium tumefaciens

<400> 58

Met Ile Ala Gly Val Gly Gly Glu Ala Arg Glu Leu Ala Leu Asp Leu  
 1 5 10 15

Ser Asp Pro Met Ala Ala Lys Asp Val Phe Ala Glu Gly Ala Tyr Asp  
 20 25 30

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

Phe Ser Glu Asp Asp Trp Asp Ala Val Met Asp Val Asn Leu Lys Ala  
 50 55 60

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

Ala Ser Gly Lys Ile Val Asn Ile Ala Ser Leu Leu Ser Phe Gln Gly  
 85 90 95

Gly Ile Arg Val Ala Ser Tyr Thr Ala Ala Lys His Gly Val Ala Gly  
 100 105 110

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

Asn Ala Ile Ala Pro Gly Tyr Ile Ala Thr Asn Asn Thr Glu Ala Leu  
 130 135 140

Arg Ala Asp Glu Glu Arg Asn Ala Ala Ile Leu Ala Arg Ile Pro Ala  
 145 150 155 160

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

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

Gly Gly Trp Leu Ala Arg  
 195

<210> 59  
 <211> 253  
 <212> PRT  
 <213> Escherichia coli

<400> 59

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

Gly Cys Asp Thr Gly Leu Gly Gln Gly Met Ala Leu Gly Leu Ala Gln  
 20 25 30

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

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

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

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

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

Met Asn Leu Asn Ile Lys Ser Val Phe Phe Met Ser Gln Ala Ala Ala  
115 120 125

Lys His Phe Ile Ala Gln Gly Asn Gly Gly Lys Ile Ile Asn Ile Ala  
130 135 140

Ser Met Leu Ser Phe Gln Gly Gly Ile Arg Val Pro Ser Tyr Thr Ala  
145 150 155 160

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

Ala Lys His Asn Ile Asn Val Asn Ala Ile Ala Pro Gly Tyr Met Ala  
180 185 190

Thr Asn Asn Thr Gln Gln Leu Arg Ala Asp Glu Gln Arg Ser Ala Glu  
195 200 205

Ile Leu Asp Arg Ile Pro Ala Gly Arg Trp Gly Leu Pro Ser Asp Leu  
210 215 220

Met Gly Pro Ile Val Phe Leu Ala Ser Ser Ala Ser Asp Tyr Val Asn  
225 230 235 240

Gly Tyr Thr Ile Ala Val Asp Gly Gly Trp Leu Ala Arg  
245 250

<210> 60  
<211> 254  
<212> PRT

&lt;213&gt; Sphingomonas sp.

&lt;400&gt; 60

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

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

Ala Gln Ala Gly Ala Asp Ile Ala Ala Val Gly Arg Thr Pro Ala Gln  
 35 40 45

Asp Thr Val Asp Gln Val Arg Ala Leu Gly Arg Arg Ala Asp Ile Ile  
 50 55 60

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

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

Ile Ile Arg Arg Ala Asp Ser Val Asp Phe Thr Glu Glu Asp Trp Asp  
 100 105 110

Ala Val Ile Asp Thr Asn Leu Lys Thr Thr Phe Phe Leu Cys Gln Ala  
 115 120 125

Ala Gly Arg His Met Leu Ala Gln Gly Ala Gly Lys Ile Ile Asn Ile  
 130 135 140

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

Ala Ser Lys Ser Gly Val Ala Gly Leu Thr Lys Leu Leu Ala Asn Glu  
 165 170 175

Trp Ala Ala Lys Gly Val Asn Val Asn Ala Ile Ala Pro Gly Tyr Ile  
 180 185 190

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Ala Thr Asn Asn Thr Ala Ala Leu Gln Ala Asp Glu Thr Arg Asn Arg  
195 200 205

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

Ile Gly Gly Ala Ala Val Phe Leu Ala Ser Ser Ala Ala Asp Tyr Ile  
225 230 235 240

His Gly His Thr Leu Ala Val Asp Gly Gly Trp Leu Ala Arg  
245 250

<210> 61  
<211> 246  
<212> PRT  
<213> Hoeflea phototrophica

<400> 61

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

Asn Thr Gly Ile Gly Gln Ala Ile Ala Met Ala Leu Gly Arg Ala Gly  
20 25 30

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

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

Ala Asp Pro Met Ala Ala Arg Asp Val Phe Ala Ala Glu Pro Val Asp  
65 70 75 80

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

Phe Thr Glu Ala Asp Trp Asp Glu Val Met Asp Val Asn Leu Lys Ala  
100 105 110

Val Phe Phe Thr Cys Gln Ala Phe Gly Lys Ala Val Leu Gly Arg Gly

115

120

125

Gly Asn Gly Lys Ile Val Asn Ile Ala Ser Leu Leu Ser Phe Gln Gly  
 130 135 140

Gly Ile Arg Val Pro Ser Tyr Thr Ala Ser Lys His Gly Val Ala Gly  
 145 150 155 160

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

Asn Ala Ile Ala Pro Gly Tyr Ile Glu Thr Asn Asn Thr Glu Ala Leu  
 180 185 190

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

Gly Arg Trp Gly Gln Ala Ser Asp Ile Gly Glu Ala Ala Val Phe Leu  
 210 215 220

Ala Ser Pro Ala Ala Asn Tyr Ile His Gly Ala Val Leu Asn Val Asp  
 225 230 235 240

Gly Gly Trp Leu Ala Arg  
 245

&lt;210&gt; 62

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Agrobacterium sp.

&lt;400&gt; 62

atgaagaatc ccttttcgct tcaggggctg aaggcgctcg tcaccggcgc gaatacgggg 60

cttggccagg cgattgcggt tgggctcgcc gcggccggtg cggaggtggt ctgcgccgcc 120

cgccgcgcgc cggatgaaac gctggagatg atcgccagcg acggcggcaa ggccagcgca 180

ttgtccatcg attttgccga tccgctggcg gcgaaggaca gttttgccgg cgccggtttc 240

gatattctcg tcaacaatgc cggtatcatc cgccgtgccg attccgtcga gttctccgaa 300

ctcgactggg acgaggtgat ggacgtcaat ctcaaggcgc tgtttttcac caccaggct 360

SGI1660-1W0\_ST25.txt

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| tttgcgaaag agctgctggc gaaaggccgg tccggcaagg tggatcaatat cgcttcgctc  | 420 |
| ctttcctttc agggcggtat tcgctgcccgc tcctatacgg cggcgaaaca tgggtgcccgc | 480 |
| ggcctaacca aactcctggc gaatgaatgg gccgccaagg gcatcaatgt gaatgccatt   | 540 |
| gcgcccgggtt atatcgaaac caacaatacc gaggcgctac gcgccgatgc ggctcgtaac  | 600 |
| aaggccattc tcgagcgcat cccggccggc cgctgggggc gctcgaaga catcgccggg    | 660 |
| gcggcggttt tcctgtcatc tgcggcggcg gactatgtgc atggcgccat tctcaacgtc   | 720 |
| gatggcggct ggctggcgcg ctga                                          | 744 |

<210> 63  
 <211> 597  
 <212> DNA  
 <213> Agrobacterium tumefaciens

|                                                                               |     |
|-------------------------------------------------------------------------------|-----|
| <400> 63<br>atgatcgccg gcgtgggggg agaagcaagg gagctggcgc tcgatctgtc cgatcccatg | 60  |
| gcggcaaaaag atgtttttgc tgaaggcgct tacgacctcc tcatcaacaa tgccggcatc            | 120 |
| atccgccgtg ccgatgcagt cgatttctcc gaggatgact gggacgcggt gatggacgtg             | 180 |
| aacctgaaaag ccgtcttctt cacctcgcaa gcctttgcgc gggctctcat gtccagaaac            | 240 |
| gcaagcggaa agatcgttaa cattgcatcc cttctgtcgt ttcaaggcgg cattcgcgtt             | 300 |
| gcctcctaca cggccgcaa gcacggtgtg gcaggcatca ccagactgtt ggcaaacgaa              | 360 |
| tgggcgtccc gcggcatcaa cgtcaatgcg atagcgccc gttacattgc cacgaacaac              | 420 |
| acggaagcgc ttcgagccga cgaggagcgc aacgcggcga tcctcgcacg cattccggct             | 480 |
| ggccgctggg ggccggcgga ggatattgcg ggtactgctg tctatctttg ttcgccggca             | 540 |
| gccgattatg ttcattggcg cattctaaac gtcgatggcg gttggctcgc gcgctga                | 597 |

<210> 64  
 <211> 762  
 <212> DNA  
 <213> Escherichia coli

|                                                                              |     |
|------------------------------------------------------------------------------|-----|
| <400> 64<br>atgattttta gtgcattttc tctcgaagg aaagttgcgg tcgtcactgg ttgtgatact | 60  |
| ggactgggtc aggggatggc gttggggctg gcgcaagcgg gctgtgacat tgttggcatt            | 120 |

## SGI1660-1W0\_ST25.txt

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aacatcgttg aaccgactga aaccatcgag caggtcacag cgctggggcg tcgtttttta   | 180 |
| agcctgaccg ccgatctgcg aaagattgat ggtattccag cactgctgga tcgcgcggtta  | 240 |
| gcggagtttg gtcataattga taccctgggtg aataacgccg gattgattcg ccgcgaagat | 300 |
| gctctcgagt tcagcgaaaa ggactgggac gatgtcatga acctgaatat caagagcgta   | 360 |
| ttcttcatgt ctcaggcagc ggcgaaacac tttatcgcg caggcaatgg cggcaagatt    | 420 |
| atcaatatcg cgtcaatgct ctccctccag ggccgggatcc gtgtgccttc ttataccgca  | 480 |
| tcaaaaagcg gcgtgatggg tgtgacgcga ttgatggcga acgaatgggc taaacacaac   | 540 |
| attaatgtta atgcgatagc cccgggttac atggcgacca acaatactca acaactacgg   | 600 |
| gcagatgaac aacgtagcgc ggaaattctc gaccgcattc cagctggtcg ttggggactg   | 660 |
| ccgagtgacc tgatggggcc gatagtgttc cttgcctcca gcgcttcaga ttatgtgaat   | 720 |
| ggttatacca ttgccgtgga tggcggttgg ctggcgcggt aa                      | 762 |

&lt;210&gt; 65

&lt;211&gt; 765

&lt;212&gt; DNA

<213> *Sphingomonas* sp.

&lt;400&gt; 65

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgcccggca tgaccactcc tttcgatctt catggcaaga ccgcgatcgt caccggcgcc  | 60  |
| aataccggca tcggccaggc cattgccctg tcgctcgcg aggccggcg ggatatcgcc    | 120 |
| gccgtcggcc gcacggcg acaggacac gtcgatcagg tccgcgcgct cggccgccgg     | 180 |
| gcggacatta tctcggccga cttttcgacc atcgaaccgg tccagcgcg cctcgacgaa   | 240 |
| acgctggaaa agcttggtgc cttggacata ctggtcaaca atgccggcat catccgccgc  | 300 |
| gccgacagcg tcgatttcac cgaggaggat tgggacgcgg tgatcgacac caatctcaag  | 360 |
| accaccttct tcctctgtca ggccgccggt cgccacatgc ttgcccaagg cgctggcaag  | 420 |
| atcatcaaca tcgcctcgct tctttccttc caggcgggca ttcgctgcc gagctacacc   | 480 |
| gcgtccaaaa gcggcgtcgc gggcctgacc aagctgctcg ccaacgaatg ggccggccaag | 540 |
| ggcgtcaatg tgaacgcat cgccggggc tatatcgcca ccaacaacac cgccgcgctc    | 600 |
| caggccgacg aaacccgcaa ccgccagatc caggagcgca tcccggctgg ccgctggggc  | 660 |

SGI1660-1W0\_ST25.txt

gaccccgccg acattggcgg cgcgcccggtg ttcctggcgt ccagcgccgc cgattatata 720  
catggccaca cgctcgccgt cgacggcggc tggctcgcg gctga 765

<210> 66  
<211> 741  
<212> DNA  
<213> Hoeflea phototrophica

<400> 66  
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ggtcaggcca tcgccatggc gcttggccgc gccggggcgg acgtcatctg cgcgggacgc 120  
tcgtcctgtg cggagaccgt tgccctcatc gctggcagca agggcaaggc gcgcgaactg 180  
gtgctcgact tcgccgaccc gatggccgcc cgtgacgtgt tcgccgccga accggtggac 240  
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gactgggatg aggtgatgga cgtgaacctg aaggccgtgt tcttcacctg ccaggccttc 360  
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tcattccagg gtggtatccg ggtgccgtcc tacacggcct cgaagcatgg tgttgcaggc 480  
atcaccaagc ttctggccaa cgaatgggcg gcgaaggga tcaatgtgaa tgccatcgcc 540  
cccggttaca tcgaaacgaa caataccgaa gcaactgcggg cggacccggt gcgcaacaag 600  
gccatccttg agcgtatccc tgccggccgc tggggccagg cctcggacat cggcgaagcc 660  
gccgtgttcc ttgcctctcc ggctgccaat tacatccatg gtgcagtgt gaatgttgac 720  
ggaggctggc ttgcccgtg a 741

<210> 67  
<211> 446  
<212> PRT  
<213> Escherichia coli

<400> 67

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

## SGI1660-1W0\_ST25.txt

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

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

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

Lys Asn Val Leu Thr Leu Val Arg Asn Thr Phe Ala Asp Arg Asp Ala  
 85 90 95

Gly Gly Arg Gly Leu Gln Thr Phe Asp Leu Arg Thr Thr Ile His Val  
 100 105 110

Val Thr Gly Ile Glu Ala Ala Met Leu Asp Leu Leu Gly Gln His Leu  
 115 120 125

Gly Val Asn Val Ala Ser Leu Leu Gly Asp Gly Gln Gln Arg Ser Glu  
 130 135 140

Val Glu Met Leu Gly Tyr Leu Phe Phe Val Gly Asn Arg Lys Ala Thr  
 145 150 155 160

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

Leu Arg His Glu Glu Ala Met Thr Pro Asp Ala Val Val Arg Leu Ala  
 180 185 190

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

Gly Val Leu Ala Gly Glu Glu Glu Ala Glu Ser Ile Val Ala Leu Ala  
 210 215 220

Gln Arg Phe Pro Gln Ala Arg Ile Thr Leu Asp Pro Asn Gly Ala Trp  
 225 230 235 240

SGI1660-1W0\_ST25.txt

Ser Leu Asn Glu Ala Ile Lys Ile Gly Lys Tyr Leu Lys Gly Ser Leu  
245 250 255

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

Glu Val Met Ala Glu Phe Arg Arg Ala Thr Gly Leu Pro Thr Ala Thr  
275 280 285

Asn Met Ile Ala Thr Asp Trp Arg Gln Met Gly His Thr Leu Ser Leu  
290 295 300

Gln Ser Val Asp Ile Pro Leu Ala Asp Pro His Phe Trp Thr Met Gln  
305 310 315 320

Gly Ser Val Arg Val Ala Gln Met Cys His Glu Phe Gly Leu Thr Trp  
325 330 335

Gly Ser His Ser Asn Asn His Phe Asp Ile Ser Leu Ala Met Phe Thr  
340 345 350

His Val Ala Ala Ala Ala Pro Gly Lys Ile Thr Ala Ile Asp Thr His  
355 360 365

Trp Ile Trp Gln Glu Gly Asn Gln Arg Leu Thr Lys Glu Pro Phe Glu  
370 375 380

Ile Lys Gly Gly Leu Val Gln Val Pro Glu Lys Pro Gly Leu Gly Val  
385 390 395 400

Glu Ile Asp Met Asp Gln Val Met Lys Ala His Glu Leu Tyr Gln Lys  
405 410 415

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

Pro Gly Trp Thr Phe Asp Asn Lys Arg Pro Cys Met Val Arg  
435 440 445

&lt;210&gt; 68

&lt;211&gt; 446

&lt;212&gt; PRT

&lt;213&gt; Pseudomonas stutzeri

&lt;400&gt; 68

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

Val Pro Val Ala Gly Gln Asp Ser Met Leu Met Asn Leu Ser Gly Ala  
 20 25 30

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

Gly His Val Gly Val Gly Glu Val Pro Gly Gly Glu Ala Ile Arg Gln  
 50 55 60

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

Tyr Asn Ala Leu Leu Gly Lys Val Arg Arg Ala Phe Ala Asp Arg Asp  
 85 90 95

Ala Gly Gly Arg Gly Leu Gln Thr Phe Asp Leu Arg Ile Ala Ile His  
 100 105 110

Ala Val Thr Ala Leu Glu Ser Ala Leu Leu Asp Leu Leu Gly Gln His  
 115 120 125

Leu Glu Val Pro Val Ala Ala Leu Leu Gly Glu Gly Gln Gln Arg Asp  
 130 135 140

Glu Val Glu Met Leu Gly Tyr Leu Phe Phe Ile Gly Asp Arg Asn Arg  
 145 150 155 160

Thr Asp Leu Gly Tyr Arg Asp Glu Ser Asn Ser Asp Asp Ala Trp Phe  
 165 170 175

## SGI1660-1W0\_ST25.txt

Arg Val Arg Asn Glu Glu Ala Met Thr Pro Glu Arg Ile Val Arg Gln  
 180 185 190

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

Gly Gly Val Leu Arg Gly Glu Glu Glu Val Glu Ala Ile Arg Ala Leu  
 210 215 220

Ala Gln Arg Phe Pro Asp Ala Arg Val Thr Leu Asp Pro Asn Gly Ala  
 225 230 235 240

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

Leu Ala Tyr Ala Glu Asp Pro Cys Gly Ala Glu Asn Gly Tyr Ser Gly  
 260 265 270

Arg Glu Val Met Ala Glu Phe Arg Arg Ala Thr Gly Leu Pro Thr Ala  
 275 280 285

Thr Asn Met Ile Ala Thr Asp Trp Arg Gln Met Ser His Ala Val Cys  
 290 295 300

Leu His Ser Val Asp Ile Pro Leu Ala Asp Pro His Phe Trp Thr Met  
 305 310 315 320

Ala Gly Ser Val Arg Val Ala Gln Met Cys Ala Asp Phe Gly Leu Thr  
 325 330 335

Trp Gly Ser His Ser Asn Asn His Phe Asp Ile Ser Leu Ala Met Phe  
 340 345 350

Thr His Val Ala Ala Ala Ala Pro Gly Arg Val Thr Ala Ile Asp Thr  
 355 360 365

His Trp Ile Trp Gln Asp Gly Gln His Leu Thr Arg Glu Pro Leu Lys  
 370 375 380

SGI1660-1W0\_ST25.txt

Ile Val Ser Gly Lys Val Ala Val Pro Gln Lys Pro Gly Leu Gly Val  
385 390 395 400

Glu Leu Asp Trp Asp Ala Leu Glu Gln Ala His Ala His Tyr Gln Glu  
405 410 415

Lys Gly Leu Gly Ala Arg Asp Asp Ala Ile Ala Met Gln Tyr Leu Ile  
420 425 430

Pro Asn Trp Thr Phe Asn Asn Lys Lys Pro Cys Met Val Arg  
435 440 445

<210> 69  
<211> 1341  
<212> DNA  
<213> Escherichia coli

<400> 69  
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catgacagta tgctgatgaa tctgagtggg gcacacgcac cgttctttac gcgtaatatt 120  
gtgattatca aagataattc tggtcacact ggcgtagggg aaattcccgg cggcgagaaa 180  
atccgtaaaa cgctggaaga tgcgattccg ctgggtgtag gtaaaacgct ggggtgaatac 240  
aaaaacgttc tgacgctggg gcgtaatact tttgccgata gtgatgctgg tgggcgcggg 300  
ttgcagacat ttgacctacg taccactatt catgtagtta ccgggataga agcggcaatg 360  
ctggatctgc tggggcagca tctgggggta aacgtggcat cgctgctggg cgatgggtcaa 420  
cagcgtagcg aagtcgaaat gtcgggttat ctgttcttcg tcggtaatcg caaagccacg 480  
ccgctgccgt atcaaagcca gccggatgac tcatgacgact ggtatcgctt gcgtcatgaa 540  
gaagcgatga cgccggatgc ggtgggtgag ctggcggaag cggcatatga aaaatatggc 600  
ttcaacgatt tcaaactgaa gggcgggtgta ctggccgggg aagaagaggc cgagtctatt 660  
gtggcactgg cgcaacgctt cccgcaggcg cgtattacgc tcgatacctaa cggcgcctgg 720  
tcgctgaacg aagcgattaa aatcggtaaa tacctgaaag gttcgctggc ttatgcagaa 780  
gatccgtgtg gtgcggagca aggtttctcc gggcgtgaag tgatggcaga gttccgtcgc 840  
gcgacagggtc taccgactgc aaccaatatg atcgccaccg actggcggca aatgggcat 900

## SGI1660-1W0\_ST25.txt

acgctctccc tgcaatccgt tgatatcccc ctggcggatc cgcatttctg gacaatgcaa 960  
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 aacaaccact tcgatatttc cctggcgatg tttacccatg ttgccgccgc tgcaccgggt 1080  
 aaaattactg ctattgatac gcactggatt tggcaggaag gcaatcagcg cctgacaaaa 1140  
 gaaccgtttg agatcaaagg cgggctggta caggtgccag aaaaaccggg gctgggtgta 1200  
 gaaatcgata tggatcaagt gatgaaagcc catgagctgt atcagaaaca cgggcttggc 1260  
 gcgcgtgacg atgcgatggg aatgcagtat ctgattcctg gctggacgtt cgataacaag 1320  
 cgcccgtgca tgggtcggtta a 1341

&lt;210&gt; 70

&lt;211&gt; 1341

&lt;212&gt; DNA

&lt;213&gt; Pseudomonas stutzeri

&lt;400&gt; 70

atgaccaccg ccatgtcggg cacgccccgc atcaccgaac tcaccgtcgt gcccgtcgcc 60  
 gggcaggaca gcatgctgat gaacctcagc ggcgccccatg ggccctgggt caccgcgaac 120  
 atcctcatcc tcaaggacag cgccggccac gtcggcgctc gcgaagtgcc gggcggcgaa 180  
 gccatccgcc agaccctcga cgatgcccgt gccctgctgg tcggcgaacc gatcggccag 240  
 tacaacgcgc tgctcggcaa ggtgcgccgc gccttcgccg accgtgacgc cggcggccgc 300  
 ggcttcgaga ccttcgacct gcgcatcgcc attcacgccg tcaccgcgct ggagtcggcg 360  
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 cagcagcgtg acgaagtgga aatgctcggc tacctgttct tcacggcgga tcgcaacagg 480  
 accgacctcg gctaccgcga cgaatccaac tccgacgacg cctggtttcg cgtgcgcaac 540  
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 tggtcgctgg acgaagccag cggcctgtgt cgcgacctgc acggcgtgct ggcctatgcc 780  
 gaagaccctt gcggtgccga gaacggctat tccggccgcg aggtgatggc cgagttccgc 840  
 cgcgccaccg gtctgcccac cgcgaccaac atgatcgcca ccgactggcg acagatgagt 900

SGI1660-1W0\_ST25.txt

```

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gccggctctg tgcgcgtggc gcagatgtgc gccgacttcg gcctgacctg gggttcgcac      1020
tcgaacaacc acttcgacat ctccctggcg atgttcaccc acgtggcggc cgccgcgccg      1080
ggtcgcgtca ccgccatcga caccactgg atctggcagg acggccagca cctgaccgcg      1140
gagccgctga agatcgtcag cggcaagggt gcggtgccgc agaagccggg gctgggcgtc      1200
gagctggact gggatgccct ggagcaggcg catgcccact accaagagaa aggcctgggt      1260
gcccgcgatg acgccatcgc catgcagtac ctgatcccca actggacctt caacaacaag      1320
aagccgtgca tggcgcgtg a                                          1341

```

<210> 71  
 <211> 256  
 <212> PRT  
 <213> Gluconobacter oxydans

<400> 71

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

Thr Gly Ala Ser Arg Gly Ile Gly Leu Thr Leu Ala Lys Gly Leu Ala  
 20 25 30

Arg Tyr Gly Ala Glu Val Val Leu Asn Gly Arg Asn Ala Glu Ser Leu  
 35 40 45

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

Ala Val Phe Asp Val Thr Asp Gln Asp Ala Val Ile Asp Gly Val Ala  
 65 70 75 80

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

Gly Ile Gln Arg Arg Ala Pro Leu Glu Glu Phe Ser Arg Lys Asp Trp  
 100 105 110

## SGI1660-1W0\_ST25.txt

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

Ala Val Ala Arg His Met Ile Pro Arg Gly Arg Gly Lys Ile Val Asn  
 130 135 140

Ile Cys Ser Val Gln Ser Glu Leu Ala Arg Pro Gly Ile Ala Pro Tyr  
 145 150 155 160

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

Asp Trp Gly Arg His Gly Leu Gln Ile Asn Gly Leu Ala Pro Gly Tyr  
 180 185 190

Phe Ala Thr Glu Met Thr Glu Arg Leu Val Ala Asp Glu Glu Phe Thr  
 195 200 205

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

Glu Leu Val Gly Ala Ala Val Phe Leu Ser Ser Arg Ala Ser Ser Phe  
 225 230 235 240

Val Asn Gly Gln Val Leu Met Val Asp Gly Gly Ile Thr Val Ser Leu  
 245 250 255

<210> 72

<211> 771

<212> DNA

<213> Gluconobacter oxydans

<400> 72

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aatggccgta atgccgaaag cctggattct gcccaaagtg gctttgaagc cgaaggctta 180

aaagcatcta ccgctgtggt tgacgtgacc gatcaagatg cagtcattga cggcgtggca 240

gcaattgaac gcgatatggg tccgattgat atcctgatca acaatgcggg cattcaacgc 300

SGI1660-1W0\_ST25.txt

|                                                                    |     |
|--------------------------------------------------------------------|-----|
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| aacgccgtgt tctttgtggg acaagccgtt gccagacaca tgattcctag aggtcgcggt  | 420 |
| aaaatcgtca acatctgttc agtgcagagc gaactggcaa gaccgggtat tgcaccttat  | 480 |
| accgccacaa aaggagccgt caaaaatctg accaaaggta tggccaccga ttggggtcgt  | 540 |
| catggtttac agattaatgg cttagcacccg ggctattttg ccaccgagat gaccgaacgc | 600 |
| ttagttgccg acgaagaatt taccgactgg ttatgcaaac gcaccctgc aggcagatgg   | 660 |
| ggccaagttg aagaattagt aggcgcagcc gtgtttttaa gtagtagagc ctcaagcttc  | 720 |
| gtgaatggcc aagtcctgat ggttgatggt ggaattactg tgagcctgta a           | 771 |