

# SEQUENCE LISTING

<110> Rakuto Bio Technologies Ltd.  
Belinky, Paula  
Karmon, Yoram  
Cohen, Shaul  
Krinfeld, Bella  
Lasser, Haim

<120> ENZYMATIC SYSTEM-CONTAINING COSMETIC COMPOSITIONS

<130> 58615

<150> US 61/827,685

<151> 2013-05-27

<160> 27

<170> PatentIn version 3.5

<210> 1

<211> 371

<212> PRT

<213> Phanerochaete chrysosporium

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Leu Asp Asp Ile Gln Ala Asn Met Phe His Gly Gly Gln Cys Gly Ala  
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Glu Ala His Glu Ser Ile Arg Leu Val Phe His Asp Ser Ile Ala Ile  
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Ser Pro Ala Met Glu Ala Lys Gly Lys Phe Gly Gly Gly Gly Ala Asp  
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Gly Ser Ile Met Ile Phe Asp Thr Ile Glu Thr Ala Phe His Pro Asn  
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Ile Gly Leu Asp Glu Val Val Ala Met Gln Lys Pro Phe Val Gln Lys  
115 120 125

His Gly Val Thr Pro Gly Asp Phe Ile Ala Phe Ala Gly Ala Val Ala  
130 135 140

Leu Ser Asn Cys Pro Gly Ala Pro Gln Met Asn Phe Phe Thr Gly Arg  
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Lys Pro Ala Thr Gln Pro Ala Pro Asp Gly Leu Val Pro Glu Pro Phe  
Page 1

165 170 175  
 His Thr Val Asp Gln Ile Ile Ala Arg Val Asn Asp Ala Gly Glu Phe  
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 Asp Glu Leu Glu Leu Val Trp Met Leu Ser Ala His Ser Val Ala Ala  
 195 200 205  
 Val Asn Asp Val Asp Pro Thr Val Gln Gly Leu Pro Phe Asp Ser Thr  
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 Pro Gly Ile Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Phe Arg Gly  
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 Thr Leu Phe Pro Gly Ser Gly Gly Asn Gln Gly Glu Val Glu Ser Gly  
 245 250 255  
 Met Ala Gly Glu Ile Arg Ile Gln Thr Asp His Thr Leu Ala Arg Asp  
 260 265 270  
 Ser Arg Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Ser Lys  
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 Ser His Ser Asp Ile Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Ser  
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Leu Leu Asp Asn His Asp Thr Ile Val Cys His Glu Ile Gln Arg Phe  
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Gly Gly Arg Glu Val Asn Thr Ala Gly Asp Gly Phe Val Ala Thr Phe  
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370 375 380

Val Glu Val Arg Asp Ala Ser His Gly Thr Asp Val Ala Gly Val Ala  
385 390 395 400

Val His Ile Gly Ala Arg Val Cys Ala Leu Ala Gly Pro Ser Glu Val  
405 410 415

Leu Val Ser Ser Thr Val Arg Asp Ile Val Ala Gly Ser Arg His Arg  
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 <213> Mycobacterium bovis AF2122/97

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Pro Ser Leu Tyr Arg Phe His Arg Arg Leu Ala Ser Phe Ser Arg Val  
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Ile Arg Leu Asp His Arg Gly Val Gly Leu Ser Ser Arg Leu Ala Ala  
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Ile Thr Thr Leu Gly Pro Lys Phe Trp Ala Gln Asp Ala Ile Ala Val  
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Met Asp Ala Val Gly Cys Glu Gln Ala Thr Ile Phe Ala Pro Ser Phe  
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His Ala Met Asn Gly Leu Val Leu Ala Ala Asp Tyr Pro Glu Arg Val  
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Arg Ser Leu Ile Val Val Asn Gly Ser Ala Arg Pro Leu Trp Ala Pro  
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 Asp Tyr Pro Val Gly Ala Gln Val Arg Arg Ala Asp Pro Phe Leu Thr  
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 Asp Leu Ala Gly Asn Arg Ala Gly Pro Pro Ser Met Ala Arg Ala Val  
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 Ser Lys Val Ile Ala Glu Ala Asp Val Arg Asp Val Leu Gly His Ile  
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 Glu Ala Pro Thr Leu Ile Leu His Arg Val Gly Ser Thr Tyr Ile Pro  
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 Val Glu Val Arg Asp Ala Ser His Gly Thr Asp Val Ala Gly Val Ala  
 385 390 395 400

Val His Ile Gly Ala Arg Val Cys Ala Leu Ala Gly Pro Ser Glu Val  
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Leu Val Ser Ser Thr Val Arg Asp Ile Val Ala Gly Ser Arg His Arg  
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Phe Ala Glu Arg Gly Glu Gln Glu Leu Lys Gly Val Pro Gly Arg Trp  
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<213> Mycobacterium bovis BCG str. Pasteur 1173P2

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

Ile Thr Thr Leu Gly Pro Lys Phe Trp Ala Gln Asp Ala Ile Ala Val  
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Met Asp Ala Val Gly Cys Glu Gln Ala Thr Ile Phe Ala Pro Ser Phe  
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His Ala Met Asn Gly Leu Val Leu Ala Ala Asp Tyr Pro Glu Arg Val  
115 120 125

Arg Ser Leu Ile Val Val Asn Gly Ser Ala Arg Pro Leu Trp Ala Pro  
130 135 140

Asp Tyr Pro Val Gly Ala Gln Val Arg Arg Ala Asp Pro Phe Leu Thr  
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Val Ala Leu Glu Pro Asp Ala Val Glu Arg Gly Phe Asp Val Leu Ser  
165 170 175

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

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

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

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

Val Glu Leu Pro Gly Thr Asp Thr Leu Tyr Trp Val Gly Asp Thr Gly  
260 265 270

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

Ala Asp Ala Glu Arg Met Leu Ala Thr Ile Met Phe Thr Asp Ile Val  
290 295 300

Gly Ser Thr Gln His Ala Ala Ala Leu Gly Asp Asp Arg Trp Arg Asp  
305 310 315 320

Leu Leu Asp Asn His Asp Thr Ile Val Cys His Glu Ile Gln Arg Phe  
325 330 335

Gly Gly Arg Glu Val Asn Thr Ala Gly Asp Gly Phe Val Ala Thr Phe  
340 345 350

Thr Ser Pro Ser Ala Ala Ile Ala Cys Ala Asp Asp Ile Val Asp Ala  
355 360 365

Val Ala Ala Leu Gly Ile Glu Val Arg Ile Gly Ile His Ala Gly Glu  
370 375 380

Val Glu Val Arg Asp Ala Ser His Gly Thr Asp Val Ala Gly Val Ala  
385 390 395 400

Val His Ile Gly Ala Arg Val Cys Ala Leu Ala Gly Pro Ser Glu Val  
405 410 415

Leu Val Ser Ser Thr Val Arg Asp Ile Val Ala Gly Ser Arg His Arg  
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Phe Ala Glu Arg Gly Glu Gln Glu Leu Lys Gly Val Pro Gly Arg Trp  
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<213> Mycobacterium bovis BCG str. Tokyo 172

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

His Ala Met Asn Gly Leu Val Leu Ala Ala Asp Tyr Pro Glu Arg Val  
 115 120 125

Arg Ser Leu Ile Val Val Asn Gly Ser Ala Arg Pro Leu Trp Ala Pro  
 130 135 140

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

Asp Leu Ala Gly Asn Arg Ala Gly Pro Pro Ser Met Ala Arg Ala Val  
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Ser Lys Val Ile Ala Glu Ala Asp Val Arg Asp Val Leu Gly His Ile  
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Glu Ala Pro Thr Leu Ile Leu His Arg Val Gly Ser Thr Tyr Ile Pro  
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Val Gly His Gly Arg Tyr Leu Ala Glu His Ile Ala Gly Ser Arg Leu  
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Val Glu Leu Pro Gly Thr Asp Thr Leu Tyr Trp Val Gly Asp Thr Gly  
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Pro Met Leu Asp Glu Ile Glu Glu Phe Ile Thr Gly Val Arg Gly Gly  
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Ala Asp Ala Glu Arg Met Leu Ala Thr Ile Met Phe Thr Asp Ile Val  
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Leu Leu Asp Asn His Asp Thr Ile Val Cys His Glu Ile Gln Arg Phe  
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Gly Gly Arg Glu Val Asn Thr Ala Gly Asp Gly Phe Val Ala Thr Phe  
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Thr Ser Pro Ser Ala Ala Ile Ala Cys Ala Asp Asp Ile Val Asp Ala  
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Val Ala Ala Leu Gly Ile Glu Val Arg Ile Gly Ile His Ala Gly Glu  
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Val Glu Val Arg Asp Ala Ser His Gly Thr Asp Val Ala Gly Val Ala  
385 390 395 400

Val His Ile Gly Ala Arg Val Cys Ala Leu Ala Gly Pro Ser Glu Val  
405 410 415

Leu Val Ser Ser Thr Val Arg Asp Ile Val Ala Gly Ser Arg His Arg  
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 accgtgcgag acatcgtcgc cggatcacgg caccggttcg ccgagcgtgg tgagcaggaa 1320  
 ctcaagggcg taccgggcag atggcggcta tgcgtgctca tgcgcgacga cgccaccgcg 1380  
 acgcgctaa 1389

<210> 10  
 <211> 462  
 <212> PRT  
 <213> Mycobacterium tuberculosis H37Ra

<400> 10

Met Ala Gln Ala Pro His Ile His Arg Thr Arg Tyr Ala Lys Cys Gly  
 1 5 10 15

Asp Met Asp Ile Ala Tyr Gln Val Leu Gly Asp Gly Pro Thr Asp Leu  
 20 25 30

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

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

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

Ile Thr Thr Leu Gly Pro Lys Phe Trp Ala Gln Asp Ala Ile Ala Val  
 85 90 95

Met Asp Ala Val Gly Cys Glu Gln Ala Thr Ile Phe Ala Pro Ser Phe  
 100 105 110

His Ala Met Asn Gly Leu Val Leu Ala Ala Asp Tyr Pro Glu Arg Val  
 115 120 125

Arg Ser Leu Ile Val Val Asn Gly Ser Ala Arg Pro Leu Trp Ala Pro  
 130 135 140

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

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

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

Arg Leu Cys Val Leu Met Arg Asp Asp Ala Thr Arg Thr Arg  
 450 455 460

<210> 11  
 <211> 1389  
 <212> DNA  
 <213> Mycobacterium tuberculosis H37Ra

<400> 11  
 gtggcgagg ctccccacat tcacaggacc cgctacgcaa aatgcggcga catggatatc 60  
 gcctaccagg tgctgggtga cgggtccgacg gatctgctgg tgttgccggg gccgttcgtg 120  
 ccgatcgact cgatcgacga cgagccatcg ctgtaccgtt tccatcgccg tcttgcgta 180  
 ttcagcaggg tgatccgcct cgaccatcgt ggggtcggcc tgtcgtcacg gctcgccgag 240  
 ataaccacgc tggggccgaa gttctgggccc caggacgcga tcgcgggtgat ggacgcgggtc 300  
 ggatgcgagc aggcgacaat tttcgcgccc agtttccacg ccatgaacgg acttggttctc 360  
 gccgccgact accccgagcg ggtgcgcagc ctgatcgctg tcaacggctc ggcgcgccc 420  
 ctatggggcg ccgactaccc ggtaggcgcc cagggttcgtc gagctgacct gttcctgacg 480  
 gtggcgctgg aaccggatgc cgtcgagcgg ggcttcgacg tgctgagcat cgtggctcct 540  
 accgtggccg gagatgacgt gtttcgagcc tgggtgggac tcgccggcaa ccgtgccgga 600  
 ccgccgagca ttgcccgtgc cgtttcaaag gtcatacgcc aggccgacgt acgagatgtc 660  
 ttgggacaca tcgaggctcc aacactgatc ttgcaccgtg tcggatcgac gtacatccc 720  
 gtgggacatg gtcgctacct cgccgagcac atcgctggat cccgcttggg cgaactaccc 780  
 ggcaccgata ccctgtactg ggttggcgac accggggccga tgctcgatga aatcgaggaa 840  
 ttcatacccg gcgtgcgcgg cggcgctgac gccgagcgca tgcttgccac catcatgttt 900  
 accgacatcg tcggctcgac ccagcacgcc gccgcgctcg gcgacgaccg atggcgcgac 960  
 ctgttgga accacgacac catcgtgtgc cagaaatcc agcggttcgg cggtcgcgaa 1020  
 gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080  
 tgcgcggacg acatcgtcga cgcggtcgcc gcgctgggta ttgaggtccg gatcggtatt 1140  
 catgcggggc aggtcgaggt gcgcatgcc tcgcacggta ccgacgtcgc cggcgaggcc 1200  
 gtgcatatcg gtgcgcgcgt ctgcgcgctg gccggaccca gtgaggtgct ggtgtcctcg 1260  
 accgtgcgag acatcgtcgc cggatcacgg caccggttcg ccgagcgtgg tgagcaggaa 1320  
 ctcaagggcg taccgggcag atggcggcta tgcgtgctca tgcgcgacga cgccaccgcg 1380  
 acgcgctaa 1389

<210> 12  
 <211> 458  
 <212> PRT  
 <213> Mycobacterium ulcerans Agy99

<400> 12

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

Ala Leu Leu Asp Glu Val Glu Glu Phe Ile Thr Gly Val Arg Gly Gly  
 275 280 285

Phe Val Thr Glu Arg Val Leu Thr Ala Val Met Phe Thr Gly Ile Val  
 290 295 300

Gly Ser Thr Gln Arg Ala Ala Thr Val Gly Asp Leu Arg Trp Arg Asp  
 305 310 315 320

Leu Leu Asp Asn His Asp Asn Leu Val Arg His Glu Ile Gln Arg Phe  
 325 330 335

Gly Gly Arg Glu Val Asn Thr Ala Gly Asp Gly Phe Val Ala Thr Phe  
 340 345 350

Ser Ser Pro Ser Ala Ala Ile Asn Cys Ala Asp Ala Val Val Asp Ala  
 355 360 365

Val Ala Val Leu Gly Ile Glu Val Arg Val Gly Ile His Ala Gly Glu  
 370 375 380

Val Glu Val Arg Gly Ala Asp Val Ala Asp Leu Ala Val His Ile Gly  
 385 390 395 400

Ala Arg Val Cys Ala Leu Ala Gly Ser Ser Glu Val Leu Val Ser Ser  
 405 410 415

Thr Val Arg Asp Ile Val Thr Gly Ser Ser His Arg Phe Ala Glu Arg  
 420 425 430

Gly Glu His Glu Leu Lys Gly Val Pro Gly Arg Trp Arg Leu Cys Ala  
 435 440 445

Leu Val Arg Glu His Leu Thr Gly Gln Arg  
 450 455

<210> 13  
 <211> 1377  
 <212> DNA  
 <213> Mycobacterium ulcerans Agy99

<400> 13  
 gtgtcgcagg cgccccgaac tccccggact cgctacgcca ggtgcggcga cctggacatc 60  
 gcctaccagg tgatcgggga tcatccgatc gacctgctcg tcataccggg ggcctcgatt 120  
 ccggtcgaca ccatcgattc cgaaccgtcg atgtaccgct ttcaccgccg tctggcgctcg 180  
 ttttcccgcc tgatccggtt cgaccatcgc ggcgtcggcc tgtcatcgcg ggtttcgctcg 240  
 ccggtatgcg tcggcccag gttctgggcc gaggatgcga ttgcggtgat ggacgcggcc 300  
 ggatgccagc aagccacgat tcttgctctc gggttcaccg cgacgaccgc cctggtgctg 360  
 gccgccgact atcccagcgc ggtgcgcagc ctggtgctca tcaacgcctc cgcgcgga 420

ctgcatgcg cccgactacga actgggcatc aggtccaaca ccgccgaacc attcctcacc 480  
 ctcggaaccg atccccgacgc ggtcgagcag gggttcgacg tgctgcat catggcgccc 540  
 agtgtggccc atgacgacgc gttccgccac tgggtgggatc tggccgga aa ccgggaggcc 600  
 tcgcccagca cggcgcgcg cttcatcaac gcggttcaag cctcggatgc gcgcgactcg 660  
 ctgccccaca tcaccgcgcc gacgctgac ctgcatcggg tgggcaccaa gttcgttccg 720  
 gtcgagcagc gccgctatct ggccgagcac attgccgggt cgcgcttggt cgagcttccc 780  
 ggttccgatt cttgtattg ggtcggcgac accgccgagt tgctcgacga ggtcgaggag 840  
 ttcatacccg gcgtccgggg cggcttcgtc accgagcggg tactgaccgc ggtcatgttc 900  
 accggcatcg tcggctcgac ccagcgcgcg gccaccgtgg gtgacctgcg ctggcgcgac 960  
 ctgctcgata accacgacaa cctgggtccgc cagcagatcc agcggttcgg tgggcgagc 1020  
 gtcaataacc cgggagcagc gttcgtcgcg acgttcagca gcccgagtgc ggcaatcaac 1080  
 tgcgaggcag ccgtcgtcga cgcgctcgcg gtgctcgga tcgaggtccg ggtggggatt 1140  
 catgccggcg aggtcgaggt gcggggggcc gacgtcgccg acctggccgt acacatcggt 1200  
 gcccggttct gtgcgctggc cggctccagt gaggtgctgg tgcctcgac ggtgctgac 1260  
 atcgtcaccg gtcgagcca cagattcgcc gagcgaggcg aacacgaact caagggcggtg 1320  
 ccgggcccgat ggcgactttg tgcgctggtc cgggagcacc tcacgggcca gcggtag 1377

<210> 14  
 <211> 458  
 <212> PRT  
 <213> Mycobacterium marinum M  
 <400> 14

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

Asp Leu Asp Ile Ala Tyr Gln Val Ile Gly Asp His Pro Ile Asp Leu  
20 25 30

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

Pro Ser Met Tyr Arg Phe His Arg Arg Leu Ala Ser Phe Ser Arg Leu  
50 55 60

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

Pro Asp Ala Leu Gly Pro Arg Phe Trp Ala Glu Asp Ala Ile Ala Val  
85 90 95

Met Asp Ala Ala Gly Cys Gln Glu Ala Thr Ile Leu Ala Ser Gly Phe  
100 105 110

Thr Ala Thr Thr Ala Leu Val Leu Ala Ala Asp Tyr Pro Glu Arg Val  
 115 120 125  
 Arg Ser Leu Val Leu Ile Asn Ala Ser Ala Arg Thr Leu His Ala Pro  
 130 135 140  
 Asp Tyr Glu Leu Gly Ile Arg Ser Asn Thr Ala Glu Pro Phe Leu Thr  
 145 150 155 160  
 Leu Gly Thr Asp Pro Asp Ala Val Glu Gln Gly Phe Asp Val Leu Arg  
 165 170 175  
 Ile Met Ala Pro Ser Val Ala His Asp Asp Ala Phe Arg Asp Trp Trp  
 180 185 190  
 Asp Leu Ala Gly Asn Arg Ala Ala Ser Pro Ser Thr Ala Arg Ala Phe  
 195 200 205  
 Ile Asn Ala Val Gln Ala Ser Asp Ala Arg Asp Ser Leu Pro His Ile  
 210 215 220  
 Thr Ala Pro Thr Leu Ile Leu His Arg Val Gly Thr Lys Phe Val Pro  
 225 230 235 240  
 Val Glu His Gly Arg Tyr Leu Ala Glu His Ile Ala Gly Ser Arg Leu  
 245 250 255  
 Val Glu Leu Pro Gly Ser Asp Ser Leu Tyr Trp Val Gly Asp Thr Ala  
 260 265 270  
 Ala Leu Leu Asp Glu Val Glu Glu Phe Ile Thr Gly Val Arg Gly Gly  
 275 280 285  
 Phe Val Thr Glu Arg Val Leu Thr Thr Val Met Phe Thr Asp Ile Val  
 290 295 300  
 Gly Ser Thr Gln Arg Ala Ala Thr Val Gly Asp Leu Arg Trp Arg Asp  
 305 310 315 320  
 Leu Leu Asp Asn His Asp Asn Leu Val Arg His Glu Ile Gln Arg Phe  
 325 330 335  
 Gly Gly Arg Glu Val Asn Thr Ala Gly Asp Gly Phe Val Ala Thr Phe  
 340 345 350  
 Ser Ser Pro Ser Ala Ala Ile Asn Cys Ala Asp Ala Val Val Asp Ala  
 355 360 365  
 Val Ala Val Leu Gly Ile Glu Val Arg Val Gly Ile His Ala Gly Glu  
 370 375 380

Val Glu Val Arg Gly Ala Asp Val Ala Gly Leu Ala Val His Ile Gly  
385 390 395 400

Ala Arg Val Cys Ala Leu Ala Gly Ser Ser Glu Val Leu Val Ser Ser  
405 410 415

Thr Val Arg Asp Ile Val Thr Gly Ser Ser His Arg Phe Ala Glu Arg  
420 425 430

Gly Glu His Glu Leu Lys Gly Val Pro Gly Arg Trp Arg Leu Cys Ala  
435 440 445

Leu Val Arg Glu His Leu Thr Gly Gln Arg  
450 455

<210> 15

<211> 1377

<212> DNA

<213> Mycobacterium marinum M

<400> 15

|                                                                      |      |
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| gtgtcgcagg cgccccgaac tccccggact cgctacgcc a ggtgcggcga cctggacatc   | 60   |
| gcctaccagg tgatcgggga tcatccgatc gacctgctcg tcataccggg ggcctcgatt    | 120  |
| ccggtcgaca ccatcgattc cgaaccgtcg atgtaccgct ttcaccgccg tctggcgctcg   | 180  |
| ttttcccgcc tgatccgggt cgaccatcgc ggcgtcggcc tgtcatcgcg ggtttcgctcg   | 240  |
| ccggatgctc tcggccccgag gttctgggccc gaggatgcga ttgcgggtgat ggacgcggcc | 300  |
| ggatgccagg aagccacgat tcttgccctc gggttcaccg cgacgaccgc cctggtgctg    | 360  |
| gccgccgact atccccgagcg ggtgcgcgac ctggtgctca tcaacgcctc cgcgcggaaca  | 420  |
| ctgcatgctc ccgactacga actgggcatc aggtccaaca ccgccgaacc attcctcacc    | 480  |
| ctcggaaacc atccccgacg ggtcgagcag gggttcgacg tgctgcgcat catggcgccc    | 540  |
| agcgtggccc atgacgacg gttccgcgac tgggtgggatc tggccggaaa ccgggcggcc    | 600  |
| tcgcccagca cggcgcgctc cttcatcaac gcggttcaag cctcggtatc gcgcgactcg    | 660  |
| ctgccccaca tcaccgcgcc gacgtgatc ctgcatcggg tgggcaccaa gttcgttccg     | 720  |
| gtcgagcagc gccgctatct ggccgagcac attgccgggt cgcgcttggt cgagcttccc    | 780  |
| ggttccgatt cttgtattg ggtcggcgac accgccgctg tgctcgacga ggtcgaggag     | 840  |
| ttcatcaccg gcgtccgggg cggttcgtc accgagcggg tactgaccac ggtcatgttc     | 900  |
| accgacatcg tcggctcgac ccagcgcgca gccaccgtgg gtgacctgcg ctggcgcgac    | 960  |
| ctgctcgata accacgacaa cctggtccgc cacgagatcc agcggttcgg tgggcgcgag    | 1020 |
| gtcaataacc cgggcgacgg gttcgtcgcg acgttcagca gcccagatgc ggcaatcaac    | 1080 |
| tgcgcgagc ccgtcgtcga cgccgtcgcc gtgctcggca tcgaggtccg ggtggggatt     | 1140 |
| catgccggcg aggtcgaggt gcggggggcc gacgtcgccg gcctggccgt acacatcggt    | 1200 |
| gcccgggtct gtgcgctggc cggctccagt gaggtgctgg tgtcctcgac ggtgcgtgac    | 1260 |

atcgtcaccg gctcgagcca cagattcgcc gagcgcggcg aacacgaact caagggcgtg 1320  
ccggggccgat ggcggctttg tgcgctggtc cgggagcacc tcacgggcca gcggtag 1377

<210> 16  
<211> 462  
<212> PRT  
<213> Mycobacterium tuberculosis KZN 1435

<400> 16

Met Ala Gln Ala Pro His Ile His Arg Thr Arg Tyr Ala Lys Cys Gly  
1 5 10 15

Asp Met Asp Ile Ala Tyr Gln Val Leu Gly Asp Gly Pro Thr Asp Leu  
20 25 30

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

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

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

Ile Thr Thr Leu Gly Pro Lys Phe Trp Ala Gln Asp Ala Ile Ala Val  
85 90 95

Met Asp Ala Val Gly Cys Glu Gln Ala Thr Ile Phe Ala Pro Ser Phe  
100 105 110

His Ala Met Asn Gly Leu Val Leu Ala Ala Asp Tyr Pro Glu Arg Val  
115 120 125

Arg Ser Leu Ile Val Val Asn Gly Ser Ala Arg Pro Leu Trp Ala Pro  
130 135 140

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

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

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

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

Ser Lys Val Ile Ala Glu Ala Asp Val Arg Asp Val Leu Gly His Ile  
210 215 220

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

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

Val Glu Leu Pro Gly Thr Asp Thr Leu Tyr Trp Val Gly Asp Thr Gly  
260 265 270

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

Ala Asp Ala Glu Arg Met Leu Ala Thr Ile Met Phe Thr Asp Ile Val  
290 295 300

Gly Ser Thr Gln His Ala Ala Ala Leu Gly Asp Asp Arg Trp Arg Asp  
305 310 315 320

Leu Leu Asp Asn His Asp Thr Ile Val Cys His Glu Ile Gln Arg Phe  
325 330 335

Gly Gly Arg Glu Val Asn Thr Ala Gly Asp Gly Phe Val Ala Thr Phe  
340 345 350

Thr Ser Pro Ser Ala Ala Ile Ala Cys Ala Asp Asp Ile Val Asp Ala  
355 360 365

Val Ala Ala Leu Gly Ile Glu Val Arg Ile Gly Ile His Ala Gly Glu  
370 375 380

Val Glu Val Arg Asp Ala Ser His Gly Thr Asp Val Ala Gly Val Ala  
385 390 395 400

Val His Ile Gly Ala Arg Val Cys Ala Leu Ala Gly Pro Ser Glu Val  
405 410 415

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

Phe Ala Glu Arg Gly Glu Gln Glu Leu Lys Gly Val Pro Gly Arg Trp  
435 440 445

Arg Leu Cys Val Leu Met Arg Asp Asp Ala Thr Arg Thr Arg  
450 455 460

<210> 17  
<211> 1389  
<212> DNA  
<213> Mycobacterium tuberculosis KZN 1435

<400> 17  
gtggcgagg ctccacat tcacaggacc cgctacgcaa aatgcggcga catggatatc

60

gcctaccagg tgctgggtga cgggtccgacg gatctgctgg tgttgccggg gccgttcgtg 120  
ccgatcgact cgatcgacga cgagccatcg ctgtaccgtt tccatcgccg tcttgcgta 180  
ttcagcaggg tgatccgcct cgaccatcgt ggggtcggcc tgcgtcacg gctcgccgag 240  
ataaccacgc tggggccgaa gttctgggcc caggacgca tgcggtgat ggacgcggtc 300  
ggatgcgagc aggcgacaat tttcgcgcc agtttccacg ccatgaacgg acttgttctc 360  
gccgccgact accccgagcg ggtgcgcagc ctgatcgtcg tcaacggctc ggcgcgcca 420  
ctatgggagc ccgactaccc ggtaggcgcc caggttcgtc gagctgacct gttcctgacg 480  
gtggcgctgg aaccggatgc cgtcgagcgg ggcttcgacg tgctgagcat cgtggctcct 540  
accgtggccg gagatgacgt gtttcgagcc tggtgggacg tcgccggcaa ccgtgccgga 600  
ccgccgagca tggcccgatgc cgtttcaaag gtcatacgcc aggccgacgt acgagatgac 660  
ttgggacaca tcgaggtcc aacactgatc ttgcaccgtg tcggatcgac gtacatcccc 720  
gtgggacatg gtcgctacct cgccgagcac atcgctggat cccgcttggc cgaactaccc 780  
ggcaccgata ccctgtactg ggttggcgac accgggcca tgctcgatga aatcgaggaa 840  
ttcatcaccg gcgtgcgcgg cggcgctgac gccgagcga tgcttgccac catcatgttt 900  
accgacatcg tcggctcgac ccagcacgcc gccgcgctcg gcgacgaccg atggcgcgac 960  
ctgttgga accacgacac catcgtgtgc cagaaatcc agcggttcgg cggtcgcgaa 1020  
gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080  
tgcgcggacg acatcgctga cgcggtcgcc gcgctgggta ttgaggtccg gatcggtatt 1140  
catgcgggag aggtcgaggt gcgcatgcc tcgcacggta ccgacgtcgc cggcgaggcc 1200  
gtgcatatcg gtgcgcgctg ctgcgcgctg gccggacca gtgaggtgct ggtgtcctcg 1260  
accgtgcgag acatcgctgc cggatcacgg caccggttcg ccgagcgtgg tgagcaggaa 1320  
ctcaagggcg taccgggcag atggcggtta tgcgtgctca tgcgcgacga cgccaccgac 1380  
acgcgctaa 1389

<210> 18  
<211> 462  
<212> PRT  
<213> Mycobacterium tuberculosis F11

<400> 18

Met Ala Gln Ala Pro His Ile His Arg Thr Arg Tyr Ala Lys Cys Gly  
1 5 10 15

Asp Met Asp Ile Ala Tyr Gln Val Leu Gly Asp Gly Pro Thr Asp Leu  
20 25 30

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

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

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

Ile Thr Thr Leu Gly Pro Lys Phe Trp Ala Gln Asp Ala Ile Ala Val  
85 90 95

Met Asp Ala Val Gly Cys Glu Gln Ala Thr Ile Phe Ala Pro Ser Phe  
100 105 110

His Ala Met Asn Gly Leu Val Leu Ala Ala Asp Tyr Pro Glu Arg Val  
115 120 125

Arg Ser Leu Ile Val Val Asn Gly Ser Ala Arg Pro Leu Trp Ala Pro  
130 135 140

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

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

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

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

Ser Lys Val Ile Ala Glu Ala Asp Val Arg Asp Val Leu Gly His Ile  
210 215 220

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

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

Val Glu Leu Pro Gly Thr Asp Thr Leu Tyr Trp Val Gly Asp Thr Gly  
260 265 270

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

Ala Asp Ala Glu Arg Met Leu Ala Thr Ile Met Phe Thr Asp Ile Val  
290 295 300

Gly Ser Thr Gln His Ala Ala Ala Leu Gly Asp Asp Arg Trp Arg Asp  
305 310 315 320

Leu Leu Asp Asn His Asp Thr Ile Val Cys His Glu Ile Gln Arg Phe  
325 330 335

Gly Gly Arg Glu Val Asn Thr Ala Gly Asp Gly Phe Val Ala Thr Phe  
340 345 350

Thr Ser Pro Ser Ala Ala Ile Ala Cys Ala Asp Asp Ile Val Asp Ala  
355 360 365

Val Ala Ala Leu Gly Ile Glu Val Arg Ile Gly Ile His Ala Gly Glu  
370 375 380

Val Glu Val Arg Asp Ala Ser His Gly Thr Asp Val Ala Gly Val Ala  
385 390 395 400

Val His Ile Gly Ala Arg Val Cys Ala Leu Ala Gly Pro Ser Glu Val  
405 410 415

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

Phe Ala Glu Arg Gly Glu Gln Glu Leu Lys Gly Val Pro Gly Arg Trp  
435 440 445

Arg Leu Cys Val Leu Met Arg Asp Asp Ala Thr Arg Thr Arg  
450 455 460

<210> 19  
<211> 1389  
<212> DNA  
<213> Mycobacterium tuberculosis F11

<400> 19  
gtggcgcagg ctccccacat tcacaggacc cgctacgcaa aatgcggcga catggatatc 60  
gcctaccagg tgctgggtga cgggccgacg gatctgctgg tgttgccggg gccgttcgtg 120  
ccgatcgact cgatcgacga cgagccatcg ctgtaccgtt tccatcgccg tcttgcgta 180  
ttcagcaggg tgatccgcct cgaccatcgt ggggctcggcc tgtcgtcacg gtcgcccgcg 240  
ataaccacgc tggggccgaa gttctgggcc caggacgcga tcgcggtgat ggacgcggtc 300  
ggatgcgagc aggcgacaat tttcgcgcc agtttccacg ccatgaacgg acttgttctc 360  
gccgccgact accccgagcg ggtgcgcagc ctgatcgctc tcaacggctc ggcgcgccca 420  
ctatgggcgc ccgactaccc ggtaggcgcc caggttcgtc gagctgacct gttcctgacg 480  
gtggcgctgg aaccggatgc cgtcgagcgg ggcttcgacg tgctgagcat cgtggctcct 540  
accgtggccg gagatgacgt gtttcgagcc tgggtgggatc tcgccggcaa ccgtgccgga 600  
ccgccgagca tggcccgtgc cgtttcaaag gtcatagccg aggccgacgt acgagatgtc 660  
ttgggacaca tcgaggctcc aacactgatc ttgcaccgtg tcggatcgac gtacatcccg 720  
gtgggacatg gtcgctacct cgccgagcac atcgttgat cccgcttggc cgaactaccc 780  
ggcaccgata ccctgtactg ggttggcgac accgggcccga tgctcgatga aatcgaggaa 840

ttcatcaccg gcgtgcgcgg cggcgctgac gccgagcgca tgcttgccac catcatgttt 900  
 accgacatcg tcggctcgac ccagcacgcc gccgcgctcg gcgacgaccg atggcgcgac 960  
 ctgttgga accacgacac catcgtgtgc cagaaatcc agcggttcgg cggtcgcgaa 1020  
 gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080  
 tgcgcggacg acatcgtcga cgcggtcgcc gcgctgggta ttgaggtccg gatcgggtatt 1140  
 catgcgggcg aggtcgaggt gcgcgatgcc tcgcacggta ccgacgtcgc cggcgtggcc 1200  
 gtgcatatcg gtgcgcgctg ctgcgcgctg gccggaccca gtgaggtgct ggtgtcctcg 1260  
 accgtgcgag acatcgtcgc cggatcacgg caccggttcg ccgagcgtgg tgagcaggaa 1320  
 ctcaagggcg taccgggcag atggcggcta tgcgtgctca tgcgcgacga cgccaccgcg 1380  
 acgcgctaa 1389

<210> 20  
 <211> 372  
 <212> PRT  
 <213> *Phanerochaete chrysosporium*

<400> 20

Met Ala Phe Lys Gln Leu Leu Ala Ala Leu Ser Val Ala Leu Thr Leu  
1 5 10 15

Gln Val Thr Gln Ala Ala Pro Asn Leu Asp Lys Arg Val Ala Cys Pro  
20 25 30

Asp Gly Val His Thr Ala Ser Asn Ala Ala Cys Cys Ala Trp Phe Pro  
35 40 45

Val Leu Asp Asp Ile Gln Gln Asn Leu Phe His Gly Gly Gln Cys Gly  
50 55 60

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

Ile Ser Pro Lys Leu Gln Ser Gln Gly Lys Phe Gly Gly Gly Gly Ala  
85 90 95

Asp Gly Ser Ile Ile Thr Phe Ser Ser Ile Glu Thr Thr Tyr His Pro  
100 105 110

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

Lys His Gly Val Thr Arg Gly Asp Phe Ile Ala Phe Ala Gly Ala Val  
130 135 140

Gly Val Ser Asn Cys Pro Gly Ala Pro Gln Met Gln Phe Phe Leu Gly  
145 150 155 160

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

<210> 21  
 <211> 1263  
 <212> DNA  
 <213> Phanerochaete chrysosporium

<400> 21  
 gctacagctc accgtccggt ctcagcagca gcaatggcgt tcaagcagct cctcgcagcc 60  
 ctctccgtcg ccctgaccct ccaggtcacc caagctgccc cgaacctcga caagcgcgtc 120  
 gcttgccccg acggcgtgca caccgcctcc aacgcggcgt gctgtgcatg gttcccggtc 180

```

ctcgatgata tccagcagaa cctcttccac ggtggccagt gcggtgccga ggcccacgag      240
gcccttcgta tgggtcttcca cgactccatc gctatctcgc ccaagcttca gtcgcagggc      300
aagtttggcg gcggcgggcg ggacggctcg atcattacct tctcctcgat cgagaccacg      360
taccacccga acatcggcct cgacgaggtc gtcgccatcc agaagccgtt catcgcgaag      420
cacggcggtca cccgtggcga cttcatcgca ttcgctggtg ccgtcggcgt gagcaactgc      480
ccggggcgcg cgagatgca gttcttctt ggccgccccg aggcaacgca ggccgcccc      540
gacggtctcg tgcccagacc cttccacacc atcgatcagg ttctcgctcg catgcttgac      600
gctggtggct tcgacgagat cgagactgtc tggctgctct ctgccactc catcgcggt      660
gcgaacgacg tcgacccgac catctccggc ctgccgttcg actccactcc cggccagttc      720
gactcccagt tcttcgtcga gacgcagctc cgcggtaccg cattccctgg caagactggt      780
atccagggca ccgtcatgtc cccgctcaag ggcgagatgc gtctgcagac ggaccacttg      840
ttcgcgcgtg actcgcgcac ggcatgagag tggcagtcct tcgtcaacaa ccagacgaag      900
ctgcaggagg acttccagtt catcttcacg gcgctctcga cgctcggcca cgacatgaac      960
gccatgatcg actgctccga ggtcatcccc gcgcccaagc ccgtcaactt cggcccgtcg     1020
ttcttccccg ccgtaagac gcacgccgac atcgagcagg cctgcgcatc cacgccgttc     1080
ccgacgtca tcaccgcccc cggtcctctt gcgtccgtcg ctcgcatccc cccgccgccg     1140
tcccccaact aagctatgtc tatgctggac atgctctcgg ttctacctcg tcggtatcgt     1200
cgcacggtta tctcgcgttt gcatcatgta tacctgctcg tggaatatac aaagtgtgtc     1260
atc                                                                    1263

```

```

<210> 22
<211> 372
<212> PRT
<213> Phanerochaete chrysosporium

```

```
<400> 22
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```
Met Ala Leu Lys Gln Leu Ala Ala Ala Val Ala Leu Ala Leu Ser Ile
1          5          10          15
```

```
Gln Ala Ala Gln Gly Ala Ala Val Lys Glu Lys Arg Ala Thr Cys Ser
          20          25          30
```

```
Asn Gly Ala Thr Val Gly Asp Ala Ser Ser Cys Ala Trp Phe Asp Val
          35          40          45
```

```
Leu Asp Asp Ile Gln Gln Asn Leu Phe Asn Gly Ala Gln Cys Gly Ala
          50          55          60
```

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

```
Ser Pro Ala Leu Glu Ser Gln Gly Lys Phe Gly Gly Gly Gly Ala Asp
          85          90          95
```

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

Pro Pro Gly Ala  
370

<210> 23  
<211> 1119  
<212> DNA  
<213> Phanerochaete chrysosporium

<400> 23  
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ggcgtctgtg tgaaggagaa gcgcgccacc tgctccaacg gcgcgactgt cggcgacgcg 120  
tcgtcgtgcg cctggtttga cgttctcgac gacatccagc agaacctctt caacggcgcc 180  
cagtgtggtg ctgaggctca cgagtccatt cgtcttgtct tccacgacgc catcgctatc 240  
tcgcctgccc ttgagtctca aggcaaattc ggtggtggag gcgctgatgg ctccattatc 300  
ctcttcgacg atatcgagac caactttcac cccaacattg gccttgacga gattgtcaac 360  
ctgcagaagc cttcatcca gaagcacggc gttactcctg gcgatttcat tgcctttgct 420  
ggcgccgtcg ccatgagcaa ctgccctggg gctccgcaga tgaacttctt caccggctcg 480  
gctcctgcta ctcaggccgc tccagacggc ctcgttcccg agccattcca cactgtcgac 540  
cagatcatct ctcggtcaa cgacgtggc gagtttgacg agcttgagct cgtctggatg 600  
ctgtctgctc actccgtcgc tgcggcgaac gatgtcgatc cgacgatcca ggggcttgcg 660  
ttcgactcta ccccggtgtt cttcgactcg cagttcttcg ttgagacaca gcttcgcggc 720  
acggcgttcc ccggctcggg tggcaaccag ggtgaggttg aatcccctct ccccggtgag 780  
atgcgcctcc agtccgactc ctcgatcgcc cgcgactcgc gcacggcggtg cgagtggcag 840  
tccttcgtca acaaccagtc gaagctcggt agcgacttcc agttcatctt cctcgccctt 900  
accagctcg gcgagaacct ggatgctatg accgactgct cagacgtgat cccgatctcg 960  
aagccggtcc ccaacaacgt cccgttctcg ttcttcccgg ctggcaagac catggctgat 1020  
gttgagcagg cgtgtgctga gacgcccttc ccgactctga cgacgcttcc tggccccgag 1080  
acctcgggtg agcgcatcca gcctcctccg ggtgcttaa 1119

<210> 24  
<211> 372  
<212> PRT  
<213> Phanerochaete sordida

<400> 24

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

Gly Ala Val Gln Gly Val Ala Val Glu Lys Arg Ala Thr Cys Ser Asn  
20 25 30

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

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

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

Pro Ala Met Glu Ala Ala Gly Gln Phe Gly Gly Gly Gly Ala Asp Gly  
85 90 95

Ser Ile Met Ile Phe Asp Glu Ile Glu Thr Asn Phe His Pro Asn Ile  
100 105 110

Gly Leu Asp Glu Ile Val Arg Leu Gln Lys Pro Phe Val Gln Lys His  
115 120 125

Gly Val Thr Pro Gly Asp Phe Ile Ala Phe Ala Gly Ala Val Ala Leu  
130 135 140

Ser Asn Cys Pro Gly Ala Pro Gln Met Asn Phe Phe Thr Gly Arg Ala  
145 150 155 160

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

Thr Val Asp Gln Ile Ile Asp Arg Val Gly Asp Ala Gly Glu Phe Asp  
180 185 190

Glu Leu Glu Leu Val Trp Met Leu Ser Ala His Ser Ile Ala Ala Ala  
195 200 205

Asn Asp Val Asp Pro Thr Thr Gln Gly Leu Pro Phe Asp Ser Thr Pro  
210 215 220

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

Gly Phe Pro Ala Ser Ala Asn Asn Gln Gly Glu Val Thr Ser Pro Leu  
245 250 255

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

Arg Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Ser Lys Leu  
275 280 285

Val Ser Asp Phe Gln Phe Ile Phe Leu Ala Leu Thr Gln Leu Gly Gln  
290 295 300

Asp Pro Thr Val Met Thr Asp Cys Ser Asp Val Ile Pro Ile Ser Lys  
305 310 315 320

Pro Ala Pro Ala Asn Thr Pro Gly Phe Ser Phe Phe Pro Ala Gly Lys  
325 330 335

Thr Met Ala Asp Val Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Thr  
340 345 350

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

Pro Pro Gly Ala  
370

<210> 25  
<211> 1727  
<212> DNA  
<213> Phanerochaete sordida

<400> 25  
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gaggctcctc gctgtttctca ccgccgccat ctccctcggc gccgtccagg gtacgtccta 120  
cgcttcccca ctttaccgca ggacactgac agcggcgcct aggtgtcgct gttgagaagc 180  
gcgccacctg ctccaacggc aagacgggtca gcgcgtcgtc gtgctgcgcc tggttcaatg 240  
tcctctcgga catccaggag aacctcttca acggcggcca gtgcggcgct gaggcccatg 300  
agtccatccg cctgtaagca tcaccctctg tccctagcgt tcttgactg atctcgtcgc 360  
agtgtcttcc acgactccat cgccatctcg cctgctatgg aggccgctgg tcagtttggg 420  
tatgtagacg tggcctccgc ttctgcacaa tcctgacaga gcacaatata gcggcggcgg 480  
tgctgacggc tccatcatga tcttcgacga gatcgagacc aacttccacc ccaacatcgg 540  
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cgacttcata gccttcgctg gcgcgggttg cctgtccaac tgccccggtg cccgcgagat 660  
gaacttcttc accggccgtg ctcccgccac ccaggccgcc cccgatggtc ttgtccccga 720  
gcccttccgt gagttattcc gccacatat gtcgaccgta gcgaactgac agcactcgta 780  
gacactgtcg accagattat cgaccgtgtc ggcgacgccg gcgagttcga tgagctcgag 840  
ctcgtctgga tgctttccgc gtacggcttc gttctcactg ccggctatcg catactgatc 900  
aatcgactcc agccattcca ttgcggctgc gaacgacgtc gacccgacca cccaggtctt 960  
tcccttcgac tccacccccg gtatcttcga ctgcagttc ttcgtcgaga cccagctcgc 1020  
cggcactggc ttccccgct acgtctctc gtctttccct ctttctgcgc tgctcaccac 1080  
gcctacagct ccgcgaacaa ccagggcgag gtcacgtccc cgcttgcggg cgagatgcgc 1140  
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gtcaacaacc agtcgaagct cgtgtccgac ttccagttca tcttcctcgc cctcacgcag 1260  
ctcggccagg acccgaccgt catgaccgac tgctcggacg ttattcccat ctccaagccc 1320

gcgcccgcgga acacccccgg attctctttc ttccccgccg gcaagaccat ggctgacgtc 1380  
gagcaggctg tgcgtgaatt catgtttgag cgcataatg tggctggcaa gctgacgaac 1440  
gctcctctag tgcgccgaga cgcccttccc gactctctcg accctccccg gcccgcaaac 1500  
ctcggtcgtc cgcatgttcg tactaaaatt caatcatatc cggggggccag ctgacaatgt 1560  
tttcttacag ccaacccccct cccggtgctt aaatagccac cacaacccgg ttctctcccc 1620  
ggcacaggca gctaagctta gacttaaccc cagaaggttc agatgtagaa actgctcgtc 1680  
ttgtctcaat accgcttttg aagcaaatac acgtgtatta ctggccc 1727

<210> 26

<211> 371

<212> PRT

<213> Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)

<400> 26

Met Ala Leu Lys Gln Leu Ala Ala Ala Val Ala Leu Ala Leu Ser Ile  
1 5 10 15

Gln Ala Ala Gln Gly Ala Ala Val Lys Glu Lys Arg Ala Thr Cys Ser  
20 25 30

Asn Gly Ala Thr Val Gly Asp Ala Ser Ser Cys Ala Trp Phe Asp Val  
35 40 45

Leu Asp Asp Ile Gln Gln Asn Leu Phe Asn Gly Ala Gln Cys Gly Ala  
50 55 60

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

Ser Pro Ala Leu Glu Ser Gln Gly Lys Phe Gly Gly Gly Gly Ala Asp  
85 90 95

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

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

His Gly Val Thr Pro Gly Asp Phe Ile Ala Phe Ala Gly Ala Val Ala  
130 135 140

Met Ser Asn Cys Pro Gly Ala Pro Gln Met Asn Phe Phe Thr Gly Arg  
145 150 155 160

Ala Pro Ala Thr Gln Ala Ala Pro Asp Gly Leu Val Pro Glu Pro Phe  
165 170 175

His Thr Val Asp Gln Ile Ile Ser Arg Val Asn Asp Ala Gly Glu Phe  
180 185 190

Asp Glu Leu Glu Leu Val Trp Met Leu Ser Ala His Ser Val Ala Ala  
195 200 205

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

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

Thr Ala Phe Pro Gly Ser Gly Gly Asn Gln Gly Glu Val Glu Ser Pro  
245 250 255

Leu Pro Gly Glu Met Arg Leu Gln Ser Asp Ser Ser Ile Ala Arg Asp  
260 265 270

Ser Arg Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Ser Lys  
275 280 285

Leu Val Ser Asp Phe Gln Phe Ile Phe Leu Ala Leu Thr Gln Leu Gly  
290 295 300

Glu Asn Pro Asp Ala Met Thr Asp Cys Ser Asp Val Ile Pro Ile Ser  
305 310 315 320

Lys Pro Val Pro Asn Asn Val Pro Phe Ser Phe Phe Pro Ala Gly Lys  
325 330 335

Thr Met Ala Asp Val Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Thr  
340 345 350

Leu Thr Thr Leu Pro Gly Pro Glu Thr Ser Val Gln Arg Ile Pro Pro  
355 360 365

Pro Gly Ala  
370

<210> 27  
<211> 2104  
<212> DNA  
<213> Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)

<400> 27  
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gccgccgttg ctcgaccac gactacaatg ccgtctgtcg agcatctact cccgaccgat 120  
cctcgttcac aggcaaggta cgcgcttttt tcattggctg cgggtggccag ggagtctgct 180  
atcgagggca cacggcgcg cgagggcatc ggcagaggcg gagggtagtg caggccagag 240  
cggtataaaa acgcaaacag gcaggccacc ctctctccag gacactcgca gtcttctgtg 300  
cgctcagctt aacagtcatg gctcttaagc aactcgctgc tgccgtcgct ctcgcactct 360

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| cgatccaggc  | tgcccaaggt  | gcggcatcta | ctccatatcc | ttgtccccc  | gtactgacct | 420  |
| cgatgcaggc  | gctgctgtga  | aggagaagcg | cgccacctgc | tccaacggcg | cgactgtcgg | 480  |
| cgacgcgtcg  | tcgtgcgctt  | ggtttgacgt | tctcgacgac | atccagcaga | acctcttcaa | 540  |
| cggcgcccag  | tgtggtgctg  | aggctcacga | gtccattcgt | ctgtaagtgc | ctccgcttgt | 600  |
| ttcggctctag | agcctactca  | ccgcgtctac | agtgtcttcc | acgacgccat | cgctatctcg | 660  |
| cctgcccttg  | agtctcaagg  | caaattcggg | tcgcgtcctc | tctccgtttg | actgcagggg | 720  |
| gtcgtgagt   | gtagcatagt  | ggtggaggcg | ctgatggctc | cattatcctc | ttcgacgata | 780  |
| tcgagaccaa  | ctttcacccc  | aacattggcc | ttgacgagat | tgtcaacctg | cagaagccct | 840  |
| tcattccagaa | gcacggcggt  | actcctggcg | atttcattgc | ctttgctggc | gccgtcgcca | 900  |
| tgagcaactg  | ccctggtgct  | ccgcagatga | acttcttcac | cggtcgtgct | cctggtatgt | 960  |
| gttgagcacc  | ccagcgtgga  | atcagtctga | cacttgtcct | gcagctactc | aggccgctcc | 1020 |
| agacggcctc  | gttcccagag  | cattccgtac | gtcagctgca | cagatacgca | tatacacccg | 1080 |
| ctgaccaact  | cttacagaca  | ctgtcgacca | gatcatctct | cgcgtaacg  | acgctggcga | 1140 |
| gtttgacgag  | cttgagctcg  | tctggatgct | gtctgcgtaa | gttgcaatcc | ggctgttcta | 1200 |
| cactgacaga  | gctgaccaca  | cgccacagtc | actccgtcgc | tgcggcgaac | gatgtcgatc | 1260 |
| cgacgatcca  | ggggcttgcg  | ttcgactcta | ccccgggtgt | cttcgactcg | cagttcttcg | 1320 |
| ttgagacaca  | gcttcgcggc  | acggcgttcc | ccggctcggg | tggcaaccag | ggtgaggttg | 1380 |
| aatccccctc  | ccccggtgag  | atgcgccctc | agtccgactc | ctcgatcgcc | cgcgactcgc | 1440 |
| gcacggcgtg  | cgagtggcag  | tccttcgtca | gtgcgtatta | catgtgcatc | ctagggcgag | 1500 |
| tggtcagacg  | ctgagtttgc  | gccgtagaca | accagtcgaa | gctcgttagc | gacttccagt | 1560 |
| tcattcttcct | cgcccttacc  | cagctcggcg | agaaccggga | tgctatgacc | gactgctcag | 1620 |
| acgtgatccc  | gatctcgaag  | ccggtcccca | acaacgtccc | gttctcgttc | ttcccggctg | 1680 |
| gcaagaccat  | ggctgatgtt  | gagcaggcgg | tgcgtagcaa | ctcacgtcta | ccatattgct | 1740 |
| gcaggagcta  | acttatgcac  | agtgtgctga | gacgcccttc | ccgactctga | cgacgcttcc | 1800 |
| tggccccgag  | acctcggcgc  | agcgcatgta | agtactttct | gatgccaatg | tacaagcacc | 1860 |
| aaggcactaa  | cgggtccattg | cagccaghcc | tcctccgggt | gcttaaattg | tattcatcac | 1920 |
| ggtcatcacg  | ttcacggtac  | tactacgtct | ggattgcgtc | gccttggtg  | cctttgtagg | 1980 |
| cttatcgaat  | acacagcttt  | tctctcagtc | atgaccatga | agtgtgccat | ggtaagcgga | 2040 |
| gacaagcaat  | tcttcgattg  | tggctcgcac | gccgcccgtg | gcacatagct | cctatgtagt | 2100 |
| gcac        |             |            |            |            |            | 2104 |