

PCTIL2014050477-seq1-000001-EN
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

<400> 1

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

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

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

Ser Pro Ala Met Glu Ala Lys Gly Lys Phe Gly Gly Gly Gly Ala Asp
85 90 95

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

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
145 150 155 160

Lys Pro Ala Thr Gln Pro Ala Pro Asp Gly Leu Val Pro Glu Pro Phe
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165

170

175

His Thr Val Asp Gln Ile Ile Ala 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

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

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

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
 275 280 285

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

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

Lys Pro Ile Pro Gly Asn Gly Pro Phe Ser Phe Phe Pro Pro Gly Lys
 325 330 335

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Leu Val Thr Leu Pro Gly Pro Ala Thr Ser Val Ala Arg Ile Pro Pro
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His Lys Ala
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 <211> 462
 <212> PRT
 <213> Mycobacterium tuberculosis H37Rv

<400> 2

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

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Leu Val₃₅ Leu Pro Gly Pro Phe Val₄₀ Pro Ile Asp Ser Ile₄₅ Asp Asp Glu
 Pro Ser₅₀ Leu Tyr Arg Phe His₅₅ Arg Arg Leu Ala Ser₆₀ Phe Ser Arg Val
 Ile₆₅ Arg Leu Asp His Arg₇₀ Gly Val Gly Leu Ser₇₅ Ser Arg Leu Ala Ala₈₀
 Ile Thr Thr Leu Gly₈₅ Pro Lys Phe Trp Ala₉₀ Gln Asp Ala Ile Ala₉₅ Val
 Met Asp Ala Val₁₀₀ Gly Cys Glu Gln Ala₁₀₅ Thr Ile Phe Ala Pro₁₁₀ Ser Phe
 His Ala Met₁₁₅ Asn Gly Leu Val Leu₁₂₀ Ala Ala Asp Tyr Pro₁₂₅ Glu Arg Val
 Arg Ser₁₃₀ Leu Ile Val Val Asn₁₃₅ Gly Ser Ala Arg Pro₁₄₀ Leu Trp Ala Pro
 Asp₁₄₅ Tyr Pro Val Gly Ala₁₅₀ Gln Val Arg Arg Ala₁₅₅ Asp Pro Phe Leu Thr₁₆₀
 Val Ala Leu Glu Pro₁₆₅ Asp Ala Val Glu Arg₁₇₀ Gly Phe Asp Val Leu₁₇₅ Ser
 Ile Val Ala Pro₁₈₀ Thr Val Ala Gly Asp₁₈₅ Asp Val Phe Arg Ala₁₉₀ Trp Trp
 Asp Leu Ala₁₉₅ Gly Asn Arg Ala Gly₂₀₀ Pro Pro Ser Ile Ala₂₀₅ Arg Ala Val
 Ser Lys₂₁₀ Val Ile Ala Glu Ala₂₁₅ Asp Val Arg Asp Val₂₂₀ Leu Gly His Ile
 Glu Ala Pro Thr Leu Ile₂₃₀ Leu His Arg Val Gly₂₃₅ Ser Thr Tyr Ile Pro₂₄₀
 Val Gly His Gly Arg₂₄₅ Tyr Leu Ala Glu His₂₅₀ Ile Ala Gly Ser Arg₂₅₅ Leu
 Val Glu Leu Pro₂₆₀ Gly Thr Asp Thr Leu₂₆₅ Tyr Trp Val Gly Asp₂₇₀ Thr Gly
 Pro Met Leu₂₇₅ Asp Glu Ile Glu Glu₂₈₀ Phe Ile Thr Gly Val₂₈₅ Arg Gly Gly
 Ala Asp Ala Glu Arg Met Leu₂₉₅ Ala Thr Ile Met Phe₃₀₀ Thr Asp Ile Val

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Gly Ser Thr Gln His Ala Ala Ala Leu Gly Asp Asp Arg Trp Arg Asp
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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 tuberculosis H37Rv

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 <212> PRT
 <213> Mycobacterium bovis AF2122/97

<400> 4

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

Val Ala Leu Glu Pro Asp Ala Val Glu Gln 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

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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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Arg Leu Cys Val Leu Met Arg Asp Asp Ala Thr Arg Thr Arg
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<213> Mycobacterium bovis AF2122/97

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1389

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 <213> Mycobacterium bovis BCG str. Pasteur 1173P2
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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

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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
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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<212> DNA
<213> Mycobacterium bovis BCG str. Pasteur 1173P2

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 <212> PRT
 <213> Mycobacterium bovis BCG str. Tokyo 172

<400> 8

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 35 40 45

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

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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
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

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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
435 440 445

Arg Leu Cys Val Leu Met Arg Asp Asp Ala Thr Arg Thr Arg
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<213> Mycobacterium bovis BCG str. Tokyo 172

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<213> Mycobacterium tuberculosis H37Ra
<400> 10

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Asp Met Asp Ile Ala Tyr Gln Val Leu Gly Asp Gly Pro Thr Asp Leu
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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

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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 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
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 gcctaccagg tgctgggtga cgggtccgacg gatctgctgg tgttgccggg gccgttcgtg 120
 ccgatcgact cgatcgacga cgagccatcg ctgtaccgtt tccatcgccg tcttgcgta 180
 ttcagcaggg tgatccgcct cgaccatcgt ggggtcggcc tgtcgtcacg gtcgcccgcg 240
 ataaccacgc tggggccgaa gttctgggcc caggacgcga tcgcggtgat ggacgcggtc 300
 ggatgcgagc aggcgacaat tttcgcgccc agtttccacg ccatgaacgg acttggtctc 360
 gccgccgact accccgagcg ggtgcgcagc ctgatcgctg tcaacggctc ggcgcgcca 420
 ctatgggagc ccgactaccg ggtaggcgcc cagggttcgtc gagctgacct gttcctgacg 480
 gtggcgctgg aaccggatgc cgtcgagcgg ggcttcgacg tgctgagcat cgtggctcct 540
 accgtggccg gagatgacgt gtttcgagcc tgggtgggac tcgccggcaa ccgtgccgga 600
 ccgccgagca ttgcccgctg cgtttcaaag gtcatacgcc aggccgacgt acgagatgtc 660
 ttgggacaca tcgaggctcc aacactgatc ttgcaccgtg tcggatcgac gtacatcccg 720
 gtgggacatg gtcgctacct cgccgagcac atcgctggat cccgcttggt cgaactaccg 780
 ggcaccgata ccctgtactg ggttggcgac accggggcga tgctcgatga aatcgaggaa 840
 ttcatacccg gcgtgcgcgg cggcgctgac gccgagcgca tgcttgccac catcatgttt 900
 accgacatcg tcggctcgac ccagcacgcc gccgcgctcg gcgacgaccg atggcgcgac 960
 ctgttgagca accacgacac catcgtgtgc cagcaaatcc agcgggttcg cggtcgcgaa 1020
 gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080
 tgcgcggacg acatcgtcga cgcggtcgcc gcgctgggta ttgaggtccg gatcgggtatt 1140
 catgcgggag aggtcgaggt gcgcatgcc tcgcacggta ccgacgtcgc cggcgaggcc 1200
 gtgcatatcg gtgcgcgcgt ctgcgcgctg gccggaccca gtgaggtgct ggtgtcctcg 1260
 accgtgcgag acatcgtcgc cggatcacgg caccggttcg ccgagcgtgg tgagcaggaa 1320
 ctcaagggcg taccgggagc 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

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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
ccggtatgcgc tcggcccag gttctgggcc gaggatgcga ttgcggtgat ggacgcggcc 300
ggatgccagc aagccacgat tcttgccctc gggttcaccg cgacgaccgc cctggtgctg 360
gccgccgact atcccagcgc ggtgcgcagc ctggtgctca tcaacgcctc cgcgcggaca 420

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ctgcatgctg	ccgactacga	actgggcatc	aggtccaaca	ccgccgaacc	attcctcacc	480
ctcgggaaccg	atccccgacgc	ggtcgagcag	gggttcgacg	tgctgctcat	catggcgccc	540
agtgtggccc	atgacgacgc	gttccgccac	tggtgggacg	tgcccgaaa	ccgggcggcc	600
tcgcccagca	cgccgctgct	cttcatcaac	gcggttcaag	cctcggtatg	gcgcgactcg	660
ctgccccaca	tcaccgctgc	gacgctgac	ctgcatcggg	tgggcaccaa	gttcgttccg	720
gtcgcgacgc	gccgctatct	ggccgagcac	attgccgggt	cgcgcttggt	cgagcttccc	780
ggttccgatt	ccttgtattg	ggtcggcgac	accgccgcgt	tgctcgacga	ggtcgaggag	840
ttcatcaccg	gcgtccgggg	cggcttcgtc	accgagcggg	tactgaccgc	ggcatgttcc	900
accggcatcg	tcggctcgac	ccagcgcgcg	gccaccgtgg	gtgacctgct	ctggcgcgac	960
ctgctcgata	accacgacaa	cctggctccg	cacgagatcc	agcggttcgg	tgggcgcgag	1020
gtcaataaccg	cgccgctgac	gttcgctcgc	acgttcagca	gcccagatgc	ggcaatcaac	1080
tgccgagcgc	ccgtcgtcga	cgccgctcgc	gtgctcggca	tcgaggtccg	ggtaggggatt	1140
catgccggcg	aggtcgaggt	gcggggggcc	gacgtcgccg	acctggccgt	acacatcggt	1200
gcccgggtct	gtgcgctggc	cggctccagt	gaggtgctgg	tgctcctcgc	ggtagcgtgc	1260
atcgtcaccg	gtcgcagcca	cagattcgcc	gagcgcggcg	aacacgaact	caagggcggtg	1320
ccggggccgat	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		

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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

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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

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 tcggcccag gttctgggccc gaggatgcga ttgcgggtgat ggacgcggcc	300
ggatgccagg aagccacgat tcttgccctc gggttcaccg cgacgaccgc cctggtgctg	360
gccgccgact atcccagcg ggtgcgcagc ctggtgctca tcaacgcctc cgcgcgga	420
ctgcatgctc ccgactacga actgggcatc aggtccaaca ccgccgaacc attcctcacc	480
ctcggaaacc atcccagcg ggtcgagcag gggttcgacg tgctgcgcat catggcgccc	540
agcgtggccc atgacgagc gttccgcgac tgggtgggatc tggccggaaa ccgggcggcc	600
tcgcccagca cggcgcgctc cttcatcaac gcggttcaag cctcggatgc gcgcgactcg	660
ctgccccaca tcaccgcgcc gacgtgatc ctgcatcggg tgggcaccaa gttcgttccg	720
gtcgagcagc gccgctatct ggccgagcac attgccgggt cgcgcttggt cgagcttccc	780
ggttccgatt cttgtattg ggtcggcgac accgccgcgt tgctcgacga ggtcgaggag	840
ttcatcaccg gcgtccgggg cggcttcgtc accgagcggg tactgaccac ggtcatgttc	900
accgacatcg tcggctcgac ccagcgcgca gccaccgtgg gtgacctgcg ctggcgcgac	960
ctgctcgata accacgaaa 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 tgcctcgac 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

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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

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gcctaccagg tgctgggtga cgggtccgacg gatctgctgg tggtagccggg gccgttcgtg 120
ccgatcgact cgatcgacga cgagccatcg ctgtaccgtt tccatcgccg tcttgcgta 180
ttcagcaggg tgatccgcct cgaccatcgt ggggtcggcc tgcgtcacg gctcgccgag 240
ataaccacgc tggggccgaa gttctgggcc caggacgcga tcgcggtgat ggacgcggtc 300
ggatgcgagc aggcgacaat tttcgcgccc agtttccacg ccatgaacgg acttgttctc 360
gccgccgact accccgagcg ggtgcgcagc ctgatcgctg tcaacggctc ggcgcgccc 420
ctatgggagc ccgactaccc ggtaggcgcc cagggttcgtc gagctgacct gttcctgacg 480
gtggcgctgg aaccggatgc cgtcgagcgg ggcttcgacg tgctgagcat cgtggctcct 540
accgtggccg gagatgacgt gtttcgagcc tgggtgggatc tcgccggcaa ccgtgccgga 600
ccgccgagca tggcccgctg cgtttcaaag gtcatacgcc aggccgacgt acgagatgtc 660
ttgggacaca tcgaggtcc aacactgatc ttgcaccgtg tcggatcgac gtacatcccc 720
gtgggacatg gtcgctacct cgccgagcac atcgctggat 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 cacgaaatcc agcggttcgg cggtcgcgaa 1020
gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080
tgcgcggacg acatcgctga cgcggtcgcc gcgctgggta ttgaggtccg gatcggtatt 1140
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gtgcatatcg gtgcgcgctg ctgcgcgctg gccggaccca gtgaggtgct ggtgtcctcg 1260
accgtgcgag acatcgctgc cggatcacgg caccggttcg ccgagcgtgg tgagcaggaa 1320
ctcaagggcg taccgggcag atggcggtta tgcgtgctca tgcgcgacga cgccacccgc 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

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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
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

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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
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ccgatcgact cgatcgacga cgagccatcg ctgtaccgtt tccatcgccg tcttgctgta 180
ttcagcaggg tgatccgcct cgaccatcgt ggggtcggcc tgtcgtcacg gtcgcccgcg 240
ataaccacgc tggggccgaa gttctgggcc caggacgcga tcgcggtgat ggacgcggtc 300
ggatgcgagc aggcgacaat tttcgcgcc agtttccacg ccatgaacgg acttgttctc 360
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ctatgggcgc ccgactaccc ggtaggcgcc caggttcgtc gagctgacct gttcctgacg 480
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ccgccgagca tggcccgtgc cgtttcaaag gtcatagccg aggccgacgt acgagatgtc 660
ttgggacaca tcgaggctcc aacactgatc ttgcaccgtg tcggatcgac gtacatcccg 720
gtgggacatg gtcgctacct cgccgagcac atcgtggat cccgcttggc cgaactaccc 780
ggcaccgata ccctgtactg ggttggcgac accgggcccga tgctcgatga aatcgaggaa 840

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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
tgcgcgga acatcgctga cgcggtcgcc gcgctgggta ttgaggtccg gatcggtatt	1140
catgcgggag aggtcgaggt gcgcgatgcc tcgcacggta ccgacgtcgc cggcgtggcc	1200
gtgcatatcg gtgcgcgctg ctgcgcgctg gccggaccca gtgaggtgct ggtgtcctcg	1260
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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

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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
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ctctccgtcg ccctgaccct ccaggtcacc caagctgccc cgaacctcga caagcgcgtc 120
gcttgccccg acggcgtgca caccgcctcc aacgcggcgt gctgtgcatg gttcccggtc 180

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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
cacggcgtca cccgtggcga cttcatcgca ttcgctggtg ccgtcggcgt gagcaactgc 480
ccggggcgcg cgagatgca gttcttccct 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 gcggtaccg cattccctgg caagactggt 780
atccagggca ccgtcatgtc cccgctcaag ggcgagatgc gtctgcagac ggaccacttg 840
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ccgacgtca tcaccgcccc cggtcctctt gcgtccgtcg ctgcacccc cccgccgccg 1140
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cgcacggtta tctcgcgttt gcatcatgta tacctgctcg tggaatatac aaagtgtct 1260
atc 1263

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

<400> 22

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

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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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ggcgtgctg 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 caccggtcgt 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

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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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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
cctcgacgag atcgtgcgcc tgcagaagcc cttcgtccag aagcacggcg tcacccccgg 600
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
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aatcgactcc agccattcca ttgcggctgc gaacgacgtc gacccgacca cccaggtctt 960
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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

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gctcctctag tgcgccgaga cgcccttccc gactctctcg accctccccg gcccgcaaac 1500
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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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 cctcgttcac aggcaaggta cgcgcttttt tcattggctg cgggtggccag ggagtctgct 180
 atcgagggca cacggcgcg cgagggcatc ggcagaggcg gagggtagtg caggccagag 240
 cggataaaa acgcaaacag gcaggccacc ctctctccag gacactcgca gtcttctgtg 300
 cgctcagctt aacagtcatg gctcttaagc aactcgctgc tgccgtcgct ctcgcactct 360

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cgacgcgtcg	tcgtgcgctt	ggtttgacgt	tctcgacgac	atccagcaga	acctcttcaa	540
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ttcgggtctag	agcctactca	ccgcgtctac	agtgtcttcc	acgacgccat	cgctatctcg	660
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gtcgtgagt	gtagcatagt	ggtggaggcg	ctgatggctc	cattatcctc	ttcgacgata	780
tcgagaccaa	ctttcacccc	aacattggcc	ttgacgagat	tgtcaacctg	cagaagccct	840
tcattccagaa	gcacggcggt	actcctggcg	atttcattgc	ctttgctggc	gccgtcgcca	900
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gttgagcacc	ccagcgtgga	atcagtctga	cacttgtcct	gcagctactc	aggccgctcc	1020
agacggcctc	gttcccagagc	cattccgtac	gtcagctgca	cagatacgca	tatacacccg	1080
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gtttgacgag	cttgagctcg	tctggatgct	gtctgcgtaa	gttgcaatcc	ggctgttcta	1200
cactgacaga	gctgaccaca	cgccacagtc	actccgtcgc	tgcggcgaac	gatgtcgatc	1260
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aaggcactaa	cgggtccattg	cagccaghcc	tcctccgggt	gcttaaattg	tattcatcac	1920
ggtcatcacg	ttcacggtac	tactacgtct	ggattgcgtc	gccttggtg	cctttgtagg	1980
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gcac						2104