

SEQUENCE LISTING

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<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
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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
Page 1

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
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 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
 Ser His Ser Asp Ile Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Ser
 340 345 350
 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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<210> 2
 <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

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
 Ile 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
 Asp 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 Ala Trp Trp₁₉₀
 Asp Leu Ala 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
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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
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
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<212> DNA
<213> Mycobacterium tuberculosis H37Rv

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ccgatcgact cgatcgacga cgagccatcg ctgtaccggt tccatcgccg tcttgcgta 180
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 <212> PRT
 <213> Mycobacterium bovis AF2122/97

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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
 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 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
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 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
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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 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

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
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<213> Mycobacterium bovis BCG str. Pasteur 1173P2

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<213> Mycobacterium bovis BCG str. Tokyo 172

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Leu Val Leu Pro Gly Pro Phe Val Pro Ile Asp Ser Ile Asp Asp Glu
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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

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. Tokyo 172

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

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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 tcgcggtgat ggacgcgggtc 300
 ggatgcgagc aggcgacaat tttcgcgccc agtttccacg ccatgaacgg acttggtctc 360
 gccgccgact accccgagcg ggtgcgcagc ctgatcgctg tcaacggctc ggcgcgccc 420
 ctatgggagc ccgactaccc ggtaggcgccc cagggttcgtc gagctgaccc 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 gtacatccc 720
 gtgggacatg gtcgctacct cgccgagcac atcgttgat cccgcttggt cgaactaccc 780
 ggcaccgata ccctgtactg ggttggcgac accgggcccga tgctcgatga aatcgaggaa 840
 ttcatacccg gcgtgcgcgg cggcgctgac gccgagcgca tgcttgccac catcatgttt 900
 accgacatcg tcggctcgac ccagcacgcc gccgcgctcg gcgacgaccg atggcgcgac 960
 ctgttgagca accacgacac catcgtgtgc cagcaaacc agcggttcgg cggtcgcgaa 1020
 gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080
 tgcgcggacg acatcgtcga cgcggtcgcc gcgctgggta ttgaggtccg gatcggtatt 1140
 catgcgggag aggtcgaggt gcgcatgcc tcgcacggta ccgacgtcgc cggcgaggcc 1200
 gtgcatatcg gtgcgcgcgt ctgcgcgctg gccggaccca gtgaggtgct ggtgtcctcg 1260
 accgtgcgag acatcgtcgc cggatcacgg caccggttcg ccgagcgtgg tgagcaggaa 1320
 ctcaagggcg taccgggagc atggcggtta tgcgtgctca tgcgcgacga cgccaccgac 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
 ccggtatgcgc tcggcccag gttctgggcc gaggatgcga ttgcggtgat ggacgcggcc 300
 ggatgccagc aagccacgat tcttgctcctc gggttcaccg cgacgaccgc cctggtgctg 360
 gccgccgact atcccagcgc ggtgcgcagc ctggtgctca tcaacgcctc cgcgcggaca 420

ctgcatgcg c cgactacga actgggcatc aggtccaaca ccgccgaacc attcctcacc 480
 ctcggaaccg atccccgacgc ggtcgagcag gggttcgacg tgctgcgcat catggcgccc 540
 agtgtggccc atgacgacgc gttccgccac tgggtgggatc tggccgga aa ccgggcggcc 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 accgccgcgt tgctcgacga ggtcgaggag 840
 ttcatacccg gcgtccgggg cggcttcgtc accgagcggg tactgaccgc ggtcatgttc 900
 accggcatcg tcggctcgac ccagcgcgcg gccaccgtgg gtgacctgcg ctggcgcgac 960
 ctgctcgata accacgacaa cctgggtccgc cagcagatcc agcggttcgg tgggcgcgag 1020
 gtcaataaccg cgggcgacgg gttcgtcgcg acgttcagca gcccgagtgc ggcaatcaac 1080
 tgcgcggacg ccgtcgtcga cgccgtcgcg gtgctcggca tcgaggtccg ggtggggatt 1140
 catgccggcg aggtcgaggt gcggggggcc gacgtcgccg acctggccgt acacatcggt 1200
 gcccggggtct gtgcgctggc cggctccagt gaggtgctgg tgcctcgac ggtgcgtgac 1260
 atcgtcaccg gtcgagcca cagattcgcc gagcgcggcg aacacgaact caagggcggtg 1320
 ccgggccgat 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

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 atcccagcgc ggtgcgcagc ctggtgctca tcaacgcctc cgcgcgga	420
ctgcatgctc ccgactacga actgggcatc aggtccaaca ccgccgaacc attcctcacc	480
ctcggaaacc atcccagcgc ggtcgagcag gggttcgacg tgctgcgcac catggcgccc	540
agcgtggccc atgacgacgc 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 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 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 gctcgccgcg 240
ataaccacgc tggggccgaa gttctgggcc caggacgcga tcgcggtgat ggacgcggtc 300
ggatgcgagc aggcgacaat tttcgcgccc agtttccacg ccatgaacgg acttgttctc 360
gccgccgact accccgagcg ggtgcgcagc ctgatcgtcg tcaacggctc ggcgcgccc 420
ctatgggagc ccgactaccc ggtaggcgcc caggttcgtc gagctgacct gttcctgacg 480
gtggcgctgg aaccggatgc cgtcgagcgg ggcttcgacg tgctgagcat cgtggctcct 540
accgtggccg gagatgacgt gtttcgagcc tgggtgggatc tcgccggcaa ccgtgccgga 600
ccgccgagca tggcccgatgc cgtttcaaag gtcatacgcc aggccgacgt acgagatgtc 660
ttgggacaca tcgaggctcc 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
ctgttggaca accacgacac catcgtgtgc cacgaaatcc agcggttcgg cggtcgcgaa 1020
gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080
tgcgcggacg acatcgctga cgcggtcgcc gcgctgggta ttgaggtccg gatcggtatt 1140
catgcgggag aggtcgaggt gcgcatgcc tcgcacggta ccgacgtcgc cggcgtggcc 1200
gtgcatatcg gtgcgcgcgt 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

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 tcttgctgca 180
ttcagcaggg tgatccgcct cgaccatcgt ggggtcggcc tgtcgtcacg gtcgcccgcg 240
ataaccacgc tggggccgaa gttctgggcc caggacgcga tcgcggtgat ggacgcggtc 300
ggatgcgagc aggcgacaat tttcgcgcc agtttccacg ccatgaacgg acttgttctc 360
gccgccgact accccgagcg ggtgcgcagc ctgatcgtcg 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 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 cagaaatcc agcggttcgg cggtcgcgaa 1020
 gtgaacacgg ccggtgacgg tttcgtcgcg acgttcacca gtccgagtgc cgcgatcgcg 1080
 tgcgcggacg acatcgtcga cgcggtcgcc gcgctgggta ttgaggtccg gatcggtatt 1140
 catgcgggcg aggtcgaggt gcgcatgcc tcgcacggta ccgacgtcgc cggcgtggcc 1200
 gtgcatatcg gtgcgcgctg ctgcgcgctg gccggacca 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

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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 gttcttctt ggccgccccg aggcaacgca ggccgcccc      540
gacggtctcg tgcccagacc cttccacacc atcgatcagg ttctcgctcg catgcttgac      600
gctggtggct tcgacgagat cgagactgtc tggctgctct ctgcccactc catcgcggtt      660
gcgaacgacg tcgaccgcac 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 cctgcgcata cacgccgttc     1080
ccgacgtca tcaccgcccc cggtcctctt gcgtccgtcg ctgcataccc 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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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 ctgccctggt gctccgcaga tgaacttctt caccggctcg 480
gctcctgcta ctcaggccgc tccagacggc ctcgttcccg agccattcca cactgtcgac 540
cagatcatct ctcgctcaa cgacgtggc gagtttgacg agcttgagct cgtctggatg 600
ctgtctgctc actccgtcgc tgcggcgaac gatgtcgatc cgacgatcca ggggcttgcg 660
ttcgactcta ccccggtgtg 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
 aggtcactct cagcctctca gactcttctc cagtcgccct agctcagaca tggctttcaa 60
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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
 cgacttcatc gccttcgctg gcgcgggttg cctgtccaac tgccccggtg cccgcgagat 660
 gaacttcttc accggccgtg ctcccgccac ccaggccgcc cccgatggtc ttgtccccga 720
 gcccttccgt gagttattcc gcccacatat gtcgaccgta gcgaactgac agcactcgtg 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 ctgcgagttc ttcgtcgaga cccagctcgc 1020
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 gcctacagct ccgcgaacaa ccagggcgag gtcacgtccc cgcttgcggg cgagatgcgc 1140
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gcgcccgca acacccccgg attctctttc ttccccgccg gcaagaccat ggctgacgtc 1380
gagcaggctg tgcgtgaatt catgtttgag cgcataatg tggctggcaa gctgacgaac 1440
gctcctctag tgcgccgaga cgcccttccc gactctctcg accctccccg gcccgcaaac 1500
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ggcacaggca gctaagctta gacttaaccc cagaaggttc agatgtagaa actgctcgct 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

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
ttcgggtctag	agcctactca	ccgcgtctac	agtgtcttcc	acgacgccat	cgctatctcg	660
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tcgagaccaa	ctttcacccc	aacattggcc	ttgacgagat	tgtcaacctg	cagaagccct	840
tcattccagaa	gcacggcggt	actcctggcg	atttcattgc	ctttgctggc	gccgtcgcca	900
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gacaagcaat	tcttcgattg	tggctcgcac	gccgcccgtg	gcacatagct	cctatgtagt	2100
gcac						2104