

eolf-seql
SEQUENCE LISTING

<110> HANSA MEDICAL AB

<120> CYSTEINE PROTEASE

<130> N404707W0

<160> 37

<170> PatentIn version 3.5

<210> 1

<211> 339

<212> PRT

<213> Streptococcus pyogenes

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

Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn Phe Thr Gln
50 55 60

Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln Gly Trp Tyr
65 70 75 80

Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu Cys Gly Ala
85 90 95

Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln Asn Lys Asp
100 105 110

Gln Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln Lys Ile Asn

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115

120

125

Phe Asn Gly Glu Gln Met Phe Asp Val Lys Glu Ala Ile Asp Thr Lys
130 135 140

Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys Glu Lys Ala
145 150 155 160

Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro Asp His Val
165 170 175

Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr Asn His Gly
180 185 190

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

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

His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp Leu Ile Lys
225 230 235 240

Lys Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His Thr Tyr Ala
245 250 255

Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala Asp Phe Asp
260 265 270

Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser Asp Ser Asn
275 280 285

Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn Ser Ala Gly
290 295 300

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

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Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Lys Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His
210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
275 280 285

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

Ser Trp Asn Gln Thr Asn
305 310

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 <213> Streptococcus pyogenes

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Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
 35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
 50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
 65 70 75 80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
 85 90 95

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
 115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
 130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
 145 150 155 160

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Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Lys Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His
210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
275 280 285

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

Ser Trp Asn Gln Thr Asn
305 310

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Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
20 25 30

Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65 70 75 80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
85 90 95

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Arg Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

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Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Lys Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His
210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
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290 295 300

Ser Trp Asn Gln Thr Asn
305 310

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Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
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Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln

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35

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Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
 50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
 65 70 75 80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
 85 90 95

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
 115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
 130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
 145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Lys Gly Ser Lys Asp Pro Arg Gly
 165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
 195 200 205

Leu Ile Lys Lys Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His
 210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala

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Asn Lys Asp Gln Ile Lys Arg Tyr Leu Arg Glu His Pro Glu Lys Gln
85 90 95

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

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

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

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

Ser Trp Asn Gln Thr Asn
 305 310

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Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
 20 25 30

Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
 35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
 50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
 65 70 75 80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Lys Glu His Pro Glu Lys Gln
 85 90 95

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

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Arg Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Lys Glu Leu Glu Glu Gly Lys Ala Leu Gly Leu Ser His
210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

Lys Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
275 280 285

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

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Ser Trp Asn Gln Thr Asn
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Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
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Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65 70 75 80

Asn Lys Asp Gln Ile Glu Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
85 90 95

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

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Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Glu Glu Leu Thr Lys Gly Lys Ala Leu Gly Leu Ser His
210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

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

Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65 70 75 80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Lys Glu His Pro Glu Lys Gln
85 90 95

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

Arg Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
165 170 175

Gly Ile Phe Asp Ala Val Phe Thr Arg Gly Asn Gln Ser Lys Leu Leu

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180

185

190

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Ser Glu Leu Glu Asn Gly Lys Ala Leu Gly Leu Ser His
210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

Lys Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
275 280 285

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

Ser Trp Asn Gln Thr Asn
305 310

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<213> Streptococcus pyogenes

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Asp Ser Phe Ser Ala Asn Gln Glu Ile Arg Tyr Ser Glu Val Thr Pro
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Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
20 25 30

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Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65 70 75 80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Lys Glu His Pro Glu Lys Gln
85 90 95

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

Arg Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Lys Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Lys Glu Leu Glu Glu Gly Lys Ala Leu Gly Leu Ser His
210 215 220

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Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

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

Ser Trp Asn Gln Thr Asn
305 310

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Asp Ser Phe Ser Ala Asn Gln Glu Ile Arg Tyr Ser Glu Val Thr Pro
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Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
20 25 30

Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
50 55 60

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Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65 70 75 80

Asn Lys Asp Gln Ile Glu Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
85 90 95

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Lys Gly Ser Lys Asp Pro Arg Gly
165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
195 200 205

Leu Ile Lys Glu Glu Leu Thr Lys Gly Lys Ala Leu Gly Leu Ser His
210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
245 250 255

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Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
260 265 270

Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
275 280 285

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

Ser Trp Asn Gln Thr Asn
305 310

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Asp Ser Phe Ser Ala Asn Gln Glu Ile Arg Tyr Ser Glu Val Thr Pro
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Tyr His Val Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
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Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65 70 75 80

Asn Lys Asp Gln Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
85 90 95

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
 115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
 130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
 145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
 165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
 195 200 205

Leu Ile Lys Lys Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His
 210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
 225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
 245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
 260 265 270

Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
 275 280 285

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

Ser Trp
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 <213> Streptococcus pyogenes
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Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn Phe Thr Gln Gly
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Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln Gly Trp Tyr Asp
 20 25 30

Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu Cys Gly Ala Ala
 35 40 45

Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln Asn Lys Asp Gln
 50 55 60

Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln Lys Ile Asn Phe
 65 70 75 80

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

His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys Glu Lys Ala Phe
 100 105 110

Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro Asp His Val Ile
 115 120 125

Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr Asn His Gly Pro

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130

135

140

Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly Gly Ile Phe Asp
145 150 155 160

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

Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp Leu Ile Lys Lys
180 185 190

Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His Thr Tyr Ala Asn
195 200 205

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

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

Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn Ser Ala Gly Lys
245 250 255

Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn Ile Gly Ala Gln
260 265 270

Val Leu Gly Leu Phe Thr Leu Ser Thr Gly Gln Asp Ser Trp Asn Gln
275 280 285

Thr Asn
290

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eolf-seql

<400> 14

Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn Phe Thr Gln Gly
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Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln Gly Trp Tyr Asp
20 25 30

Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu Cys Gly Ala Ala
35 40 45

Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln Asn Lys Asp Gln
50 55 60

Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys Gln Lys Ile Asn Phe
65 70 75 80

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

His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys Glu Lys Ala Phe
100 105 110

Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro Asp His Val Ile
115 120 125

Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr Asn His Gly Pro
130 135 140

Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly Gly Ile Phe Asp
145 150 155 160

Ala Val Phe Thr Arg Gly Asn Gln Ser Lys Leu Leu Thr Ser Arg His
165 170 175

Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp Leu Ile Lys Lys
180 185 190

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Glu Leu Thr Glu Gly Lys Ala Leu Gly Leu Ser His Thr Tyr Ala Asn
195 200 205

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

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

Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn Ser Ala Gly Lys
245 250 255

Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn Ile Gly Ala Gln
260 265 270

Val Leu Gly Leu Phe Thr Leu Ser Thr Gly Gln Asp Ser Trp Asn Gln
275 280 285

Thr Asn
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<212> PRT
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<400> 15

Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn Phe Thr Gln Gly
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Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln Gly Trp Tyr Asp
20 25 30

Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu Cys Gly Ala Ala
35 40 45

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Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln Asn Lys Asp Gln
50 55 60

Ile Glu Arg Tyr Leu Glu Glu His Pro Glu Lys Gln Lys Ile Asn Phe
65 70 75 80

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

His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys Glu Lys Ala Phe
100 105 110

Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro Asp His Val Ile
115 120 125

Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr Asn His Gly Pro
130 135 140

Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly Gly Ile Phe Asp
145 150 155 160

Ala Val Phe Thr Arg Gly Asn Gln Ser Lys Leu Leu Thr Ser Arg His
165 170 175

Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp Leu Ile Lys Glu
180 185 190

Glu Leu Thr Lys Gly Lys Ala Leu Gly Leu Ser His Thr Tyr Ala Asn
195 200 205

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

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

eolf-seql

Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn Ser Ala Gly Lys
245 250 255

Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn Ile Gly Ala Gln
260 265 270

Val Leu Gly Leu Phe Thr Leu Ser Thr Gly Gln Lys Ser Trp Asn Gln
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Thr Asn
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<212> PRT
<213> Streptococcus pyogenes

<400> 16

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His Gln Ile Thr Ser Val Trp Thr Lys Gly Val Thr Pro Pro Ala Asn
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Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn Gln
35 40 45

Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu Leu
50 55 60

Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp Gln
65 70 75 80

Asn Lys Asp Gln Ile Glu Arg Tyr Leu Glu Glu His Pro Glu Lys Gln
85 90 95

eolf-seq1

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

Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe Lys
 115 120 125

Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe Pro
 130 135 140

Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu Thr
 145 150 155 160

Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg Gly
 165 170 175

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

Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser Asp
 195 200 205

Leu Ile Lys Glu Glu Leu Thr Lys Gly Lys Ala Leu Gly Leu Ser His
 210 215 220

Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly Ala
 225 230 235 240

Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp Ser
 245 250 255

Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val Asn
 260 265 270

Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp Asn
 275 280 285

eolf-seql

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

Ser Trp Asn Gln Thr Asn Gly Gly Gly His His His His His His
 305 310 315

<210> 17
 <211> 320
 <212> PRT
 <213> Streptococcus pyogenes
 <400> 17

Met Asp Ser Phe Ser Ala Asn Gln Glu Ile Arg Tyr Ser Glu Val Thr
 1 5 10 15

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Asn Phe Thr Gln Gly Glu Asp Val Phe His Ala Pro Tyr Val Ala Asn
 35 40 45

Gln Gly Trp Tyr Asp Ile Thr Lys Thr Phe Asn Gly Lys Asp Asp Leu
 50 55 60

Leu Cys Gly Ala Ala Thr Ala Gly Asn Met Leu His Trp Trp Phe Asp
 65 70 75 80

Gln Asn Lys Asp Gln Ile Lys Arg Tyr Leu Glu Glu His Pro Glu Lys
 85 90 95

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

Ile Asp Thr Lys Asn His Gln Leu Asp Ser Lys Leu Phe Glu Tyr Phe
 115 120 125

Lys Glu Lys Ala Phe Pro Tyr Leu Ser Thr Lys His Leu Gly Val Phe

eolf-seql

130

135

140

Pro Asp His Val Ile Asp Met Phe Ile Asn Gly Tyr Arg Leu Ser Leu
145 150 155 160

Thr Asn His Gly Pro Thr Pro Val Lys Glu Gly Ser Lys Asp Pro Arg
165 170 175

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

Leu Thr Ser Arg His Asp Phe Lys Glu Lys Asn Leu Lys Glu Ile Ser
195 200 205

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

His Thr Tyr Ala Asn Val Arg Ile Asn His Val Ile Asn Leu Trp Gly
225 230 235 240

Ala Asp Phe Asp Ser Asn Gly Asn Leu Lys Ala Ile Tyr Val Thr Asp
245 250 255

Ser Asp Ser Asn Ala Ser Ile Gly Met Lys Lys Tyr Phe Val Gly Val
260 265 270

Asn Ser Ala Gly Lys Val Ala Ile Ser Ala Lys Glu Ile Lys Glu Asp
275 280 285

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

Asp Ser Trp Asn Gln Thr Asn Gly Gly Gly His His His His His His
305 310 315 320

<210> 18

eolf-seql

<211> 4
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 <213> Streptococcus pyogenes

<400> 18

Asn Gln Thr Asn
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<210> 19
 <211> 20
 <212> PRT
 <213> Streptococcus pyogenes

<400> 19

Asp Ser Phe Ser Ala Asn Gln Glu Ile Arg Tyr Ser Glu Val Thr Pro
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Tyr His Val Thr
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 <212> DNA
 <213> Streptococcus pyogenes

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 aaagacgatc ttctttgcgg ggctgccaca gcagggaata tgcttcactg gtggttcgat 240
 caaaacaaag accaaattaa acgttatttg gaagagcatc cagaaaagca aaaaataaac 300
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 ctaggagttt tccctgatca tgtaattgat atgttcatta acggctaccg ccttagtcta 480
 actaaccacg gtccaacgcc agtaaaagaa ggtagtaaag atccccgagg tggatatttt 540

eolf-seq1

gacgccgtat ttacaagagg tgatcaaagt aagctattga caagtcgtca tgattttaaa	600
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ctaggcctat cacacaccta cgctaacgta cgcatcaacc atgttataaa cctgtgggga	720
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gcatctattg gtatgaagaa atactttgtt ggtgttaatt ccgctggaaa agtagctatt	840
tctgctaaag aaataaaaaga agataatata ggtgctcaag tactagggtt atttacactt	900
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taa	963

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 <212> DNA
 <213> Streptococcus pyogenes

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caaaacaaag accaaattaa acgttatttg gaagagcatc cagaaaagca aaaaataaac	300
ttccgtggcg aacagatggt tgacgtaaaa gaagctatcg aactaaaaa ccaccagcta	360
gatagtaaat tatttgaata ttttaaagaa aaagctttcc cttatctatc tactaaacac	420
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gacgccgtat ttacaagagg tgatcaaagt aagctattga caagtcgtca tgattttaaa	600
gaaaaaaaaatc tcaaagaaat cagtgatctc attaagaaag agttaaccga aggcaaggct	660
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eolf-seq1

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tctgctaaag aaataaaaaga agataatata ggtgctcaag tactaggggtt atttacactt	900
tcaacagggc aagatagttg gaatcagacc aatggcggtg gccatcatca ccatcaccac	960
taa	963

<210> 22

<211> 963

<212> DNA

<213> Streptococcus pyogenes

<400> 22

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gatagtaaat tatttgaata ttttaaagaa aaagctttcc cttatctatc tactaaacac	420
ctaggagttt tccctgatca tgtaattgat atgttcatta acggctaccg ccttagtcta	480
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gacgccgtat ttacaagagg taaccaaaagt aagctattga caagtcgtca tgattttaaa	600
gaaaaaaaaatc tcaaagaaat cagtgatctc attaagaaag agttaaccga aggcaaggct	660
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eolf-seq1

taa 963

<210> 23
 <211> 963
 <212> DNA
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 caaaacaaag accaaattaa acgttatttg gaagagcatc cagaaaagca aaaaataaac 300
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 gaaaaaaatc tcaaagaaat cagtgatctc attaagaaag agttaaccga aggcaaggct 660
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 gcatctattg gtatgaagaa atactttgtt ggtgttaata aagctggaaa agtagctatt 840
 tctgctaaag aaataaaaaga agataatata ggtgctcaag tactagggtt atttacactt 900
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 taa 963

<210> 24
 <211> 963
 <212> DNA

eolf-seq1

<213> Streptococcus pyogenes

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caaaacaaag accaaattaa acgttatttg cgtgagcatc cagaaaagca aaaaataaac	300
ttcaatggcg aacagatggt tgacgtaaaa gaagctatcg acactaaaaa ccaccagcta	360
gatagtaaat tatttgaata ttttaaagaa aaagctttcc cttatctatc tactaaacac	420
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gacgccgtat ttacaagagg taaccaaagt aagctattga caagtcgtca tgattttaaa	600
gaaaaaaaaatc tcaaagaaat cagtgatctc attaagaaag agttagatga aggcaaggct	660
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gctgactttg attctaacgg gaaccttaaa gctatttatg taacagactc tgatagtaat	780
gcatctattg gtatgaagaa atactttgtt ggtgttaatt ccgctggaaa agtagctatt	840
tctgctaaag aaataaaaga agataatata ggtgctcaag tactagggtt atttacactt	900
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taa	963

<210> 25

<211> 963

<212> DNA

<213> Streptococcus pyogenes

<400> 25

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eolf-seq1

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aaagacgatc ttctttgcgg ggctgccaca gcagggaata tgcttcactg gtggttcgat	240
caaaacaaag accaaattaa acgttatttg aaagagcatc cagaaaagca aaaaataaac	300
ttcaatggcg aacagatggt tgacgtaaaa gaagctatcc gtactaaaaa ccaccagcta	360
gatatgaaat tatttgaata ttttaaagaa aaagctttcc cttatctatc tactaaacac	420
ctaggagttt tccctgatca tgtaattgat atgttcatta acggctaccg ccttagtcta	480
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gacgccgtat ttacaagagg taaccaaagt aagctattga caagtcgtca tgattttaaa	600
gaaaaaaaaatc tcaaagaaat cagtgatctc attaagaaag agttagaaga aggcaaggct	660
ctaggcctat cacacaccta cgctaacgta cgcatcaacc atgttataaa cctgtgggga	720
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gcatctattg gtatgaagaa atactttgtt ggtgttaata aagctggaaa agtagctatt	840
tctgctaaag aaataaaaaga agataatata ggtgctcaag tactagggtt atttacactt	900
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taa	963

<210> 26

<211> 963

<212> DNA

<213> Streptococcus pyogenes

<400> 26

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tttcacgctc cttatgttgc taaccaagga tggatatgata ttaccaaagc attcaatgga	180
aaagacgatc ttctttgcgg ggctgccaca gcagggaata tgcttcactg gtggttcgat	240
caaaacaaag accaaattga acgttatttg gaagagcatc cagaaaagca aaaaataaac	300
ttcaatggcg aacagatggt tgacgtaaaa gaagctatcg aactaaaaa ccaccagcta	360

eolf-seql

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ctaggagt	ttt	tccctga	tca	tgtaatt	gat	atgttc	atta	acggct	accg	ccttagt	cta	480
actaacc	acg	gtcca	acgcc	agtaaaa	gaa	ggtagt	aaag	atcccc	gagg	tggtatt	tttt	540
gacgcc	gtat	ttaca	agagg	taaccaa	aagt	aagctat	tga	caagtc	gtca	tgatttt	aaa	600
gaaaaaa	atc	tcaaaga	aat	cagtga	tctc	attaagg	aag	agttaa	accaa	aggca	aggct	660
ctaggc	ctat	cacac	accta	cgcta	acgta	cgcat	caacc	atgtt	ataaaa	cctgt	gggga	720
gctgact	tttg	attcta	acgg	gaacct	taaa	gctattt	tatg	taacag	actc	tgatag	taat	780
gcatct	tattg	gtatga	aagaa	atacttt	ggt	gtta	aatt	ccgct	ggaaa	agtag	ctatt	840
tctgct	aaa	g	aaataaaa	gaa	aaaaa	tata	ggtg	ctca	ag	tactag	gggtt	900
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<211> 963

<212> DNA

<213> Streptococcus pyogenes

<400> 27

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aaagacg	atc	ttcttt	gcgg	ggctg	ccaca	gcagg	gaata	tgcttc	actg	gtgg	ttcgat	240
caaaaca	aaag	accaa	attaa	acgtt	atttg	aaagag	catc	cagaaa	agca	aaaaa	ataaac	300
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ctaggagt	ttt	tccctga	tca	tgtaatt	gat	atgttc	atta	acggct	accg	ccttagt	cta	480
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eolf-seq1

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gctgactttg attctaacgg gaaccttaaa gctattttatg taacagactc tgatagtaat	780
gcatctattg gtatgaagaa atactttgtt ggtgttaata aagctggaaa agtagctatt	840
tctgctaaag aaataaaaaga agataatata ggtgctcaag tactagggtt atttacactt	900
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taa	963

<210> 28

<211> 963

<212> DNA

<213> Streptococcus pyogenes

<400> 28

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gaaaaaaaaatc tcaaagaaat cagtgatctc attaagaaag agttagaaga aggcaaggct	660
ctaggcctat cacacaccta cgctaacgta cgcatcaacc atgttataaa cctgtgggga	720
gctgactttg attctaacgg gaaccttaaa gctattttatg taacagactc tgatagtaat	780

eolf-seq1

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tctgctaaag aaataaaaaga agataatata ggtgctcaag tactagggtt atttacactt	900
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taa	963

<210> 29
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 <212> DNA
 <213> Streptococcus pyogenes

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caaaacaaag accaaattga acgttatttg gaagagcatc cagaaaagca aaaaataaac	300
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gatagtaa at ttttgaata ttttaaagaa aaagctttcc cttatctatc tactaaacac	420
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gacgccgtat ttacaagagg taaccaaaagt aagctattga caagtcgtca tgattttaaa	600
gaaaaaaaaatc tcaaagaaat cagtgatctc attaaggaag agttaaccaa aggcaaggct	660
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gcatctattg gtatgaagaa atactttggtt ggtgttaatt ccgctggaaa agtagctatt	840
tctgctaaag aaataaaaaga agataatata ggtgctcaag tactagggtt atttacactt	900
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eolf-seql

taa

963

<210> 30

<211> 957

<212> DNA

<213> Streptococcus pyogenes

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tttcacgctc cttatgttgc taaccaagga tggatatgata ttacaaaaac attcaatgga 180

aaagacgatc ttctttgcgg ggctgccaca gcagggaata tgcttcactg gtggttcgat 240

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<212> DNA

<213> Streptococcus pyogenes

<400> 31

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eolf-seql

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eolf-seq1

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eolf-seql

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<212> PRT

<213> Streptococcus pyogenes

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His Val Thr

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<212> PRT

<213> Streptococcus pyogenes

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<213> Streptococcus pyogenes

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eolf-seql

His Gln Ile Thr
20