

eolf-seql
SEQUENCE LISTING

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<120> MODIFIED MENINGOCOCCAL FHBP POLYPEPTIDES

<130> VN56307 WO

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<150> EP 14177564.3

<151> 2014-07-17

<160> 60

<170> PatentIn version 3.5

<210> 1

<211> 274

<212> PRT

<213> Neisseria meningitidis

<400> 1

Met Asn Arg Thr Ala Phe Cys Cys Leu Ser Leu Thr Thr Ala Leu Ile
1 5 10 15

Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
20 25 30

Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
35 40 45

Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
50 55 60

Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
65 70 75 80

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
85 90 95

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

Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe
115 120 125

Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala
130 135 140

Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe
145 150 155 160

Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe
165 170 175

Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
180 185 190

Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu
195 200 205

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

Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser
225 230 235 240

Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser
245 250 255

Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala
260 265 270

Lys Gln

eolf-seql

<210> 2

<211> 273

<212> PRT

<213> Neisseria meningitidis

<400> 2

Met Asn Arg Thr Ala Phe Cys Cys Leu Ser Leu Thr Ala Ala Leu Ile
1 5 10 15

Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
20 25 30

Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
35 40 45

Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
50 55 60

Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
65 70 75 80

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
85 90 95

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

Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu
115 120 125

Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn
130 135 140

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

Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser
165 170 175

eolf-seql

Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
180 185 190

Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn
195 200 205

Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala
210 215 220

Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr
225 230 235 240

His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala
245 250 255

Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys
260 265 270

Gln

<210> 3

<211> 281

<212> PRT

<213> Neisseria meningitidis

<400> 3

Met Asn Arg Thr Ala Phe Cys Cys Leu Ser Leu Thr Thr Ala Leu Ile
1 5 10 15

Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val
20 25 30

Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu
35 40 45

eolf-seq1

Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile
50 55 60

Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr
65 70 75 80

Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys
85 90 95

Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp
100 105 110

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

Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro
130 135 140

Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly
145 150 155 160

Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala
165 170 175

Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu
180 185 190

His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile Glu
195 200 205

His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu
210 215 220

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

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

Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val
260 265 270

His Glu Ile Gly Ile Ala Gly Lys Gln
275 280

<210> 4

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 4

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
85 90 95

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

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
115 120 125

eolf-seql

Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
130 135 140

Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145 150 155 160

Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
165 170 175

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
180 185 190

Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
195 200 205

Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
210 215 220

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

Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 5

<211> 247

<212> PRT

<213> Neisseria meningitidis

<400> 5

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

eolf-seql

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
210 215 220

eolf-seql

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
245

<210> 6

<211> 488

<212> PRT

<213> Neisseria meningitidis

<400> 6

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

Ala Cys Gly Gly Gly Gly Gly Gly Ser Pro Asp Val Lys Ser Ala Asp
20 25 30

Thr Leu Ser Lys Pro Ala Ala Pro Val Val Ser Glu Lys Glu Thr Glu
35 40 45

Ala Lys Glu Asp Ala Pro Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro
50 55 60

Ser Ala Gln Gly Ser Gln Asp Met Ala Ala Val Ser Glu Glu Asn Thr
65 70 75 80

Gly Asn Gly Gly Ala Val Thr Ala Asp Asn Pro Lys Asn Glu Asp Glu
85 90 95

Val Ala Gln Asn Asp Met Pro Gln Asn Ala Ala Gly Thr Asp Ser Ser
100 105 110

Thr Pro Asn His Thr Pro Asp Pro Asn Met Leu Ala Gly Asn Met Glu
115 120 125

Asn Gln Ala Thr Asp Ala Gly Glu Ser Ser Gln Pro Ala Asn Gln Pro
130 135 140

eolf-seql

Asp Met Ala Asn Ala Ala Asp Gly Met Gln Gly Asp Asp Pro Ser Ala
145 150 155 160

Gly Gly Gln Asn Ala Gly Asn Thr Ala Ala Gln Gly Ala Asn Gln Ala
165 170 175

Gly Asn Asn Gln Ala Ala Gly Ser Ser Asp Pro Ile Pro Ala Ser Asn
180 185 190

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

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

Cys Lys Gly Asp Ser Cys Ser Gly Asn Asn Phe Leu Asp Glu Glu Val
225 230 235 240

Gln Leu Lys Ser Glu Phe Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser
245 250 255

Asn Tyr Lys Lys Asp Gly Lys Asn Asp Lys Phe Val Gly Leu Val Ala
260 265 270

Asp Ser Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys
275 280 285

Pro Lys Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg
290 295 300

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

Thr Leu Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly
325 330 335

eolf-seql

Asn Ile Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu Thr Tyr Gly Ala
 340 345 350

Glu Lys Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val Gln Gly Glu Pro
 355 360 365

Ala Lys Gly Glu Met Leu Ala Gly Ala Ala Val Tyr Asn Gly Glu Val
 370 375 380

Leu His Phe His Thr Glu Asn Gly Arg Pro Tyr Pro Thr Arg Gly Arg
 385 390 395 400

Phe Ala Ala Lys Val Asp Phe Gly Ser Lys Ser Val Asp Gly Ile Ile
 405 410 415

Asp Ser Gly Asp Asp Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala
 420 425 430

Ile Asp Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Ser Gly
 435 440 445

Asp Val Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly
 450 455 460

Lys Tyr Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val
 465 470 475 480

Phe Ala Gly Lys Lys Glu Gln Asp
 485

<210> 7

<211> 364

<212> PRT

<213> Neisseria meningitidis

<400> 7

eolf-seql

Met	Ser	Met	Lys	His	Phe	Pro	Ser	Lys	Val	Leu	Thr	Thr	Ala	Ile	Leu
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Ala	Thr	Phe	Cys	Ser	Gly	Ala	Leu	Ala	Ala	Thr	Ser	Asp	Asp	Asp	Val
			20					25					30		
Lys	Lys	Ala	Ala	Thr	Val	Ala	Ile	Val	Ala	Ala	Tyr	Asn	Asn	Gly	Gln
		35					40					45			
Glu	Ile	Asn	Gly	Phe	Lys	Ala	Gly	Glu	Thr	Ile	Tyr	Asp	Ile	Gly	Glu
	50					55					60				
Asp	Gly	Thr	Ile	Thr	Gln	Lys	Asp	Ala	Thr	Ala	Ala	Asp	Val	Glu	Ala
65					70					75					80
Asp	Asp	Phe	Lys	Gly	Leu	Gly	Leu	Lys	Lys	Val	Val	Thr	Asn	Leu	Thr
				85					90					95	
Lys	Thr	Val	Asn	Glu	Asn	Lys	Gln	Asn	Val	Asp	Ala	Lys	Val	Lys	Ala
			100					105					110		
Ala	Glu	Ser	Glu	Ile	Glu	Lys	Leu	Thr	Thr	Lys	Leu	Ala	Asp	Thr	Asp
		115					120					125			
Ala	Ala	Leu	Ala	Asp	Thr	Asp	Ala	Ala	Leu	Asp	Glu	Thr	Thr	Asn	Ala
	130					135					140				
Leu	Asn	Lys	Leu	Gly	Glu	Asn	Ile	Thr	Thr	Phe	Ala	Glu	Glu	Thr	Lys
145					150					155					160
Thr	Asn	Ile	Val	Lys	Ile	Asp	Glu	Lys	Leu	Glu	Ala	Val	Ala	Asp	Thr
				165					170					175	
Val	Asp	Lys	His	Ala	Glu	Ala	Phe	Asn	Asp	Ile	Ala	Asp	Ser	Leu	Asp
			180					185					190		

eolf-seql

Glu Thr Asn Thr Lys Ala Asp Glu Ala Val Lys Thr Ala Asn Glu Ala
195 200 205

Lys Gln Thr Ala Glu Glu Thr Lys Gln Asn Val Asp Ala Lys Val Lys
210 215 220

Ala Ala Glu Thr Ala Ala Gly Lys Ala Glu Ala Ala Ala Gly Thr Ala
225 230 235 240

Asn Thr Ala Ala Asp Lys Ala Glu Ala Val Ala Ala Lys Val Thr Asp
245 250 255

Ile Lys Ala Asp Ile Ala Thr Asn Lys Ala Asp Ile Ala Lys Asn Ser
260 265 270

Ala Arg Ile Asp Ser Leu Asp Lys Asn Val Ala Asn Leu Arg Lys Glu
275 280 285

Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu Phe Gln
290 295 300

Pro Tyr Asn Val Gly Arg Phe Asn Val Thr Ala Ala Val Gly Gly Tyr
305 310 315 320

Lys Ser Glu Ser Ala Val Ala Ile Gly Thr Gly Phe Arg Phe Thr Glu
325 330 335

Asn Phe Ala Ala Lys Ala Gly Val Ala Val Gly Thr Ser Ser Gly Ser
340 345 350

Ser Ala Ala Tyr His Val Gly Val Asn Tyr Glu Trp
355 360

<210> 8

<211> 174

<212> PRT

<213> Neisseria meningitidis

eolf-seql

<400> 8

Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala
1 5 10 15

Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala
20 25 30

His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro
35 40 45

Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp
50 55 60

Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu
65 70 75 80

Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
85 90 95

Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
100 105 110

Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly
115 120 125

Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
130 135 140

Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
145 150 155 160

Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe
165 170

<210> 9

<211> 792

eolf-seql

<212> PRT

<213> Neisseria meningitidis

<400> 9

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

Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30

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

Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60

Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80

Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95

Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Val Lys
130 135 140

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

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Asp Asp Arg Gln
165 170 175

eolf-seql

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Asn
210 215 220

Arg Gly Tyr Ala Val Glu Gly Glu Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240

Ser Ala Arg Gly Ile Pro Asp Ser Ser Lys His Lys Tyr Asn His His
245 250 255

Ala Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly
260 265 270

Ala Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser
275 280 285

Tyr Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg
290 295 300

Arg Arg Asn Ala Asn Leu Phe Tyr Glu Trp Met Pro Asp Ser Asn Trp
305 310 315 320

Leu Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Lys Thr Lys Val Ala
325 330 335

Ala Val Asn Asn Lys Gly Ser Phe Pro Met Asp Tyr Ser Thr Trp Thr
340 345 350

Arg Asn Tyr Asn Gln Lys Asp Leu Asp Glu Ile Tyr Asn Arg Ser Met
355 360 365

eolf-seq1

Asp Thr Arg Phe Lys Arg Phe Thr Leu Arg Leu Asp Ser His Pro Leu
370 375 380

Gln Leu Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Val Ser
385 390 395 400

Arg Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly
405 410 415

Arg Val Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr
420 425 430

Asn Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe
435 440 445

Ser Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln
450 455 460

Glu Leu Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala
465 470 475 480

Asn Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu
485 490 495

Asn Gln Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val
500 505 510

Pro Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn
515 520 525

Trp Leu Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr
530 535 540

Leu Ser Leu Gln Gly Arg Ser Glu Lys Gly Met Leu Asp Ala Asn Leu
545 550 555 560

eolf-seq1

Tyr Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr
565 570 575

Thr Ser Gly Thr Pro Gly Cys Thr Glu Glu Asn Ala Tyr Tyr Gly Ile
580 585 590

Cys Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile
595 600 605

Asp Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val
610 615 620

Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser
625 630 635 640

Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser
645 650 655

Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser
660 665 670

Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys
675 680 685

Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr
690 695 700

Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala
705 710 715 720

Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr
725 730 735

Leu Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp
740 745 750

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Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp
755 760 765

Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr
770 775 780

Ala Val Ser Leu Glu Trp Lys Phe
785 790

<210> 10

<211> 591

<212> PRT

<213> Neisseria meningitidis

<400> 10

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

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
35 40 45

Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
50 55 60

Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly
65 70 75 80

Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
85 90 95

Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
100 105 110

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

eolf-seql

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
130 135 140

Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145 150 155 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
165 170 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
180 185 190

Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
195 200 205

Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
210 215 220

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

Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
245 250 255

Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
260 265 270

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

Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
290 295 300

Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
305 310 315 320

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Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
325 330 335

Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
340 345 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
355 360 365

Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
370 375 380

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

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
405 410 415

Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
420 425 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
435 440 445

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
450 455 460

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

Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
485 490 495

Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
500 505 510

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Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
515 520 525

Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
530 535 540

Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
545 550 555 560

Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
565 570 575

Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
580 585 590

<210> 11
<211> 1457
<212> PRT
<213> Neisseria meningitidis

<400> 11
Met Lys Thr Thr Asp Lys Arg Thr Thr Glu Thr His Arg Lys Ala Pro
1 5 10 15

Lys Thr Gly Arg Ile Arg Phe Ser Pro Ala Tyr Leu Ala Ile Cys Leu
20 25 30

Ser Phe Gly Ile Leu Pro Gln Ala Trp Ala Gly His Thr Tyr Phe Gly
35 40 45

Ile Asn Tyr Gln Tyr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Lys Phe
50 55 60

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

eolf-seql

Val Gly Lys Ser Met Thr Lys Ala Pro Met Ile Asp Phe Ser Val Val
85 90 95

Ser Arg Asn Gly Val Ala Ala Leu Val Gly Asp Gln Tyr Ile Val Ser
100 105 110

Val Ala His Asn Gly Gly Tyr Asn Asn Val Asp Phe Gly Ala Glu Gly
115 120 125

Arg Asn Pro Asp Gln His Arg Phe Thr Tyr Lys Ile Val Lys Arg Asn
130 135 140

Asn Tyr Lys Ala Gly Thr Lys Gly His Pro Tyr Gly Gly Asp Tyr His
145 150 155 160

Met Pro Arg Leu His Lys Phe Val Thr Asp Ala Glu Pro Val Glu Met
165 170 175

Thr Ser Tyr Met Asp Gly Arg Lys Tyr Ile Asp Gln Asn Asn Tyr Pro
180 185 190

Asp Arg Val Arg Ile Gly Ala Gly Arg Gln Tyr Trp Arg Ser Asp Glu
195 200 205

Asp Glu Pro Asn Asn Arg Glu Ser Ser Tyr His Ile Ala Ser Ala Tyr
210 215 220

Ser Trp Leu Val Gly Gly Asn Thr Phe Ala Gln Asn Gly Ser Gly Gly
225 230 235 240

Gly Thr Val Asn Leu Gly Ser Glu Lys Ile Lys His Ser Pro Tyr Gly
245 250 255

Phe Leu Pro Thr Gly Gly Ser Phe Gly Asp Ser Gly Ser Pro Met Phe
260 265 270

eolf-seql

Ile Tyr Asp Ala Gln Lys Gln Lys Trp Leu Ile Asn Gly Val Leu Gln
275 280 285

Thr Gly Asn Pro Tyr Ile Gly Lys Ser Asn Gly Phe Gln Leu Val Arg
290 295 300

Lys Asp Trp Phe Tyr Asp Glu Ile Phe Ala Gly Asp Thr His Ser Val
305 310 315 320

Phe Tyr Glu Pro Arg Gln Asn Gly Lys Tyr Ser Phe Asn Asp Asp Asn
325 330 335

Asn Gly Thr Gly Lys Ile Asn Ala Lys His Glu His Asn Ser Leu Pro
340 345 350

Asn Arg Leu Lys Thr Arg Thr Val Gln Leu Phe Asn Val Ser Leu Ser
355 360 365

Glu Thr Ala Arg Glu Pro Val Tyr His Ala Ala Gly Gly Val Asn Ser
370 375 380

Tyr Arg Pro Arg Leu Asn Asn Gly Glu Asn Ile Ser Phe Ile Asp Glu
385 390 395 400

Gly Lys Gly Glu Leu Ile Leu Thr Ser Asn Ile Asn Gln Gly Ala Gly
405 410 415

Gly Leu Tyr Phe Gln Gly Asp Phe Thr Val Ser Pro Glu Asn Asn Glu
420 425 430

Thr Trp Gln Gly Ala Gly Val His Ile Ser Glu Asp Ser Thr Val Thr
435 440 445

Trp Lys Val Asn Gly Val Ala Asn Asp Arg Leu Ser Lys Ile Gly Lys
450 455 460

eolf-seql

Gly Thr Leu His Val Gln Ala Lys Gly Glu Asn Gln Gly Ser Ile Ser
465 470 475 480

Val Gly Asp Gly Thr Val Ile Leu Asp Gln Gln Ala Asp Asp Lys Gly
485 490 495

Lys Lys Gln Ala Phe Ser Glu Ile Gly Leu Val Ser Gly Arg Gly Thr
500 505 510

Val Gln Leu Asn Ala Asp Asn Gln Phe Asn Pro Asp Lys Leu Tyr Phe
515 520 525

Gly Phe Arg Gly Gly Arg Leu Asp Leu Asn Gly His Ser Leu Ser Phe
530 535 540

His Arg Ile Gln Asn Thr Asp Glu Gly Ala Met Ile Val Asn His Asn
545 550 555 560

Gln Asp Lys Glu Ser Thr Val Thr Ile Thr Gly Asn Lys Asp Ile Ala
565 570 575

Thr Thr Gly Asn Asn Asn Ser Leu Asp Ser Lys Lys Glu Ile Ala Tyr
580 585 590

Asn Gly Trp Phe Gly Glu Lys Asp Thr Thr Lys Thr Asn Gly Arg Leu
595 600 605

Asn Leu Val Tyr Gln Pro Ala Ala Glu Asp Arg Thr Leu Leu Leu Ser
610 615 620

Gly Gly Thr Asn Leu Asn Gly Asn Ile Thr Gln Thr Asn Gly Lys Leu
625 630 635 640

Phe Phe Ser Gly Arg Pro Thr Pro His Ala Tyr Asn His Leu Asn Asp
645 650 655

eolf-seq1

His Trp Ser Gln Lys Glu Gly Ile Pro Arg Gly Glu Ile Val Trp Asp
660 665 670

Asn Asp Trp Ile Asn Arg Thr Phe Lys Ala Glu Asn Phe Gln Ile Lys
675 680 685

Gly Gly Gln Ala Val Val Ser Arg Asn Val Ala Lys Val Lys Gly Asp
690 695 700

Trp His Leu Ser Asn His Ala Gln Ala Val Phe Gly Val Ala Pro His
705 710 715 720

Gln Ser His Thr Ile Cys Thr Arg Ser Asp Trp Thr Gly Leu Thr Asn
725 730 735

Cys Val Glu Lys Thr Ile Thr Asp Asp Lys Val Ile Ala Ser Leu Thr
740 745 750

Lys Thr Asp Ile Ser Gly Asn Val Asp Leu Ala Asp His Ala His Leu
755 760 765

Asn Leu Thr Gly Leu Ala Thr Leu Asn Gly Asn Leu Ser Ala Asn Gly
770 775 780

Asp Thr Arg Tyr Thr Val Ser His Asn Ala Thr Gln Asn Gly Asn Leu
785 790 795 800

Ser Leu Val Gly Asn Ala Gln Ala Thr Phe Asn Gln Ala Thr Leu Asn
805 810 815

Gly Asn Thr Ser Ala Ser Gly Asn Ala Ser Phe Asn Leu Ser Asp His
820 825 830

Ala Val Gln Asn Gly Ser Leu Thr Leu Ser Gly Asn Ala Lys Ala Asn
835 840 845

eolf-seql

Val Ser His Ser Ala Leu Asn Gly Asn Val Ser Leu Ala Asp Lys Ala
850 855 860

Val Phe His Phe Glu Ser Ser Arg Phe Thr Gly Gln Ile Ser Gly Gly
865 870 875 880

Lys Asp Thr Ala Leu His Leu Lys Asp Ser Glu Trp Thr Leu Pro Ser
885 890 895

Gly Thr Glu Leu Gly Asn Leu Asn Leu Asp Asn Ala Thr Ile Thr Leu
900 905 910

Asn Ser Ala Tyr Arg His Asp Ala Ala Gly Ala Gln Thr Gly Ser Ala
915 920 925

Thr Asp Ala Pro Arg Arg Arg Ser Arg Arg Ser Arg Arg Ser Leu Leu
930 935 940

Ser Val Thr Pro Pro Thr Ser Val Glu Ser Arg Phe Asn Thr Leu Thr
945 950 955 960

Val Asn Gly Lys Leu Asn Gly Gln Gly Thr Phe Arg Phe Met Ser Glu
965 970 975

Leu Phe Gly Tyr Arg Ser Asp Lys Leu Lys Leu Ala Glu Ser Ser Glu
980 985 990

Gly Thr Tyr Thr Leu Ala Val Asn Asn Thr Gly Asn Glu Pro Ala Ser
995 1000 1005

Leu Glu Gln Leu Thr Val Val Glu Gly Lys Asp Asn Lys Pro Leu
1010 1015 1020

Ser Glu Asn Leu Asn Phe Thr Leu Gln Asn Glu His Val Asp Ala
1025 1030 1035

eolf-seql

Gly	Ala	Trp	Arg	Tyr	Gln	Leu	Ile	Arg	Lys	Asp	Gly	Glu	Phe	Arg
1040						1045					1050			
Leu	His	Asn	Pro	Val	Lys	Glu	Gln	Glu	Leu	Ser	Asp	Lys	Leu	Gly
1055						1060					1065			
Lys	Ala	Glu	Ala	Lys	Lys	Gln	Ala	Glu	Lys	Asp	Asn	Ala	Gln	Ser
1070						1075					1080			
Leu	Asp	Ala	Leu	Ile	Ala	Ala	Gly	Arg	Asp	Ala	Val	Glu	Lys	Thr
1085						1090					1095			
Glu	Ser	Val	Ala	Glu	Pro	Ala	Arg	Gln	Ala	Gly	Gly	Glu	Asn	Val
1100						1105					1110			
Gly	Ile	Met	Gln	Ala	Glu	Glu	Glu	Lys	Lys	Arg	Val	Gln	Ala	Asp
1115						1120					1125			
Lys	Asp	Thr	Ala	Leu	Ala	Lys	Gln	Arg	Glu	Ala	Glu	Thr	Arg	Pro
1130						1135					1140			
Ala	Thr	Thr	Ala	Phe	Pro	Arg	Ala	Arg	Arg	Ala	Arg	Arg	Asp	Leu
1145						1150					1155			
Pro	Gln	Leu	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	Arg	Asp	Leu
1160						1165					1170			
Ile	Ser	Arg	Tyr	Ala	Asn	Ser	Gly	Leu	Ser	Glu	Phe	Ser	Ala	Thr
1175						1180					1185			
Leu	Asn	Ser	Val	Phe	Ala	Val	Gln	Asp	Glu	Leu	Asp	Arg	Val	Phe
1190						1195					1200			
Ala	Glu	Asp	Arg	Arg	Asn	Ala	Val	Trp	Thr	Ser	Gly	Ile	Arg	Asp
1205						1210					1215			

eolf-seql

Thr	Lys	His	Tyr	Arg	Ser	Gln	Asp	Phe	Arg	Ala	Tyr	Arg	Gln	Gln
	1220					1225					1230			
Thr	Asp	Leu	Arg	Gln	Ile	Gly	Met	Gln	Lys	Asn	Leu	Gly	Ser	Gly
	1235					1240					1245			
Arg	Val	Gly	Ile	Leu	Phe	Ser	His	Asn	Arg	Thr	Glu	Asn	Thr	Phe
	1250					1255					1260			
Asp	Asp	Gly	Ile	Gly	Asn	Ser	Ala	Arg	Leu	Ala	His	Gly	Ala	Val
	1265					1270					1275			
Phe	Gly	Gln	Tyr	Gly	Ile	Asp	Arg	Phe	Tyr	Ile	Gly	Ile	Ser	Ala
	1280					1285					1290			
Gly	Ala	Gly	Phe	Ser	Ser	Gly	Ser	Leu	Ser	Asp	Gly	Ile	Gly	Gly
	1295					1300					1305			
Lys	Ile	Arg	Arg	Arg	Val	Leu	His	Tyr	Gly	Ile	Gln	Ala	Arg	Tyr
	1310					1315					1320			
Arg	Ala	Gly	Phe	Gly	Gly	Phe	Gly	Ile	Glu	Pro	His	Ile	Gly	Ala
	1325					1330					1335			
Thr	Arg	Tyr	Phe	Val	Gln	Lys	Ala	Asp	Tyr	Arg	Tyr	Glu	Asn	Val
	1340					1345					1350			
Asn	Ile	Ala	Thr	Pro	Gly	Leu	Ala	Phe	Asn	Arg	Tyr	Arg	Ala	Gly
	1355					1360					1365			
Ile	Lys	Ala	Asp	Tyr	Ser	Phe	Lys	Pro	Ala	Gln	His	Ile	Ser	Ile
	1370					1375					1380			
Thr	Pro	Tyr	Leu	Ser	Leu	Ser	Tyr	Thr	Asp	Ala	Ala	Ser	Gly	Lys
	1385					1390					1395			

eolf-seql

Val Arg Thr Arg Val Asn Thr Ala Val Leu Ala Gln Asp Phe Gly
1400 1405 1410

Lys Thr Arg Ser Ala Glu Trp Gly Val Asn Ala Glu Ile Lys Gly
1415 1420 1425

Phe Thr Leu Ser Leu His Ala Ala Ala Ala Lys Gly Pro Gln Leu
1430 1435 1440

Glu Ala Gln His Ser Ala Gly Ile Lys Leu Gly Tyr Arg Trp
1445 1450 1455

<210> 12

<211> 797

<212> PRT

<213> Neisseria meningitidis

<400> 12

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

Pro Leu Ala Leu Ala Asp Phe Thr Ile Gln Asp Ile Arg Val Glu Gly
20 25 30

Leu Gln Arg Thr Glu Pro Ser Thr Val Phe Asn Tyr Leu Pro Val Lys
35 40 45

Val Gly Asp Thr Tyr Asn Asp Thr His Gly Ser Ala Ile Ile Lys Ser
50 55 60

Leu Tyr Ala Thr Gly Phe Phe Asp Asp Val Arg Val Glu Thr Ala Asp
65 70 75 80

Gly Gln Leu Leu Leu Thr Val Ile Glu Arg Pro Thr Ile Gly Ser Leu
85 90 95

Asn Ile Thr Gly Ala Lys Met Leu Gln Asn Asp Ala Ile Lys Lys Asn
100 105 110

eolf-seql

Leu Glu Ser Phe Gly Leu Ala Gln Ser Gln Tyr Phe Asn Gln Ala Thr
115 120 125

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

Lys Leu Asn Ile Gln Ile Thr Pro Lys Val Thr Lys Leu Ala Arg Asn
145 150 155 160

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

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

Met Arg Gln Met Ser Leu Thr Glu Gly Gly Ile Trp Thr Trp Leu Thr
195 200 205

Arg Ser Asn Gln Phe Asn Glu Gln Lys Phe Ala Gln Asp Met Glu Lys
210 215 220

Val Thr Asp Phe Tyr Gln Asn Asn Gly Tyr Phe Asp Phe Arg Ile Leu
225 230 235 240

Asp Thr Asp Ile Gln Thr Asn Glu Asp Lys Thr Lys Gln Thr Ile Lys
245 250 255

Ile Thr Val His Glu Gly Gly Arg Phe Arg Trp Gly Lys Val Ser Ile
260 265 270

Glu Gly Asp Thr Asn Glu Val Pro Lys Ala Glu Leu Glu Lys Leu Leu
275 280 285

Thr Met Lys Pro Gly Lys Trp Tyr Glu Arg Gln Gln Met Thr Ala Val
290 295 300

eolf-seql

Leu Gly Glu Ile Gln Asn Arg Met Gly Ser Ala Gly Tyr Ala Tyr Ser
305 310 315 320

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

Phe Val Leu His Ile Glu Pro Gly Arg Lys Ile Tyr Val Asn Glu Ile
340 345 350

His Ile Thr Gly Asn Asn Lys Thr Arg Asp Glu Val Val Arg Arg Glu
355 360 365

Leu Arg Gln Met Glu Ser Ala Pro Tyr Asp Thr Ser Lys Leu Gln Arg
370 375 380

Ser Lys Glu Arg Val Glu Leu Leu Gly Tyr Phe Asp Asn Val Gln Phe
385 390 395 400

Asp Ala Val Pro Leu Ala Gly Thr Pro Asp Lys Val Asp Leu Asn Met
405 410 415

Ser Leu Thr Glu Arg Ser Thr Gly Ser Leu Asp Leu Ser Ala Gly Trp
420 425 430

Val Gln Asp Thr Gly Leu Val Met Ser Ala Gly Val Ser Gln Asp Asn
435 440 445

Leu Phe Gly Thr Gly Lys Ser Ala Ala Leu Arg Ala Ser Arg Ser Lys
450 455 460

Thr Thr Leu Asn Gly Ser Leu Ser Phe Thr Asp Pro Tyr Phe Thr Ala
465 470 475 480

Asp Gly Val Ser Leu Gly Tyr Asp Val Tyr Gly Lys Ala Phe Asp Pro
485 490 495

eolf-seql

Arg Lys Ala Ser Thr Ser Ile Lys Gln Tyr Lys Thr Thr Thr Ala Gly
500 505 510

Ala Gly Ile Arg Met Ser Val Pro Val Thr Glu Tyr Asp Arg Val Asn
515 520 525

Phe Gly Leu Val Ala Glu His Leu Thr Val Asn Thr Tyr Asn Lys Ala
530 535 540

Pro Lys His Tyr Ala Asp Phe Ile Lys Lys Tyr Gly Lys Thr Asp Gly
545 550 555 560

Thr Asp Gly Ser Phe Lys Gly Trp Leu Tyr Lys Gly Thr Val Gly Trp
565 570 575

Gly Arg Asn Lys Thr Asp Ser Ala Leu Trp Pro Thr Arg Gly Tyr Leu
580 585 590

Thr Gly Val Asn Ala Glu Ile Ala Leu Pro Gly Ser Lys Leu Gln Tyr
595 600 605

Tyr Ser Ala Thr His Asn Gln Thr Trp Phe Phe Pro Leu Ser Lys Thr
610 615 620

Phe Thr Leu Met Leu Gly Gly Glu Val Gly Ile Ala Gly Gly Tyr Gly
625 630 635 640

Arg Thr Lys Glu Ile Pro Phe Phe Glu Asn Phe Tyr Gly Gly Gly Leu
645 650 655

Gly Ser Val Arg Gly Tyr Glu Ser Gly Thr Leu Gly Pro Lys Val Tyr
660 665 670

Asp Glu Tyr Gly Glu Lys Ile Ser Tyr Gly Gly Asn Lys Lys Ala Asn
675 680 685

eolf-seql

Val Ser Ala Glu Leu Leu Phe Pro Met Pro Gly Ala Lys Asp Ala Arg
690 695 700

Thr Val Arg Leu Ser Leu Phe Ala Asp Ala Gly Ser Val Trp Asp Gly
705 710 715 720

Lys Thr Tyr Asp Asp Asn Ser Ser Ser Ala Thr Gly Gly Arg Val Gln
725 730 735

Asn Ile Tyr Gly Ala Gly Asn Thr His Lys Ser Thr Phe Thr Asn Glu
740 745 750

Leu Arg Tyr Ser Ala Gly Gly Ala Val Thr Trp Leu Ser Pro Leu Gly
755 760 765

Pro Met Lys Phe Ser Tyr Ala Tyr Pro Leu Lys Lys Lys Pro Glu Asp
770 775 780

Glu Ile Gln Arg Phe Gln Phe Gln Leu Gly Thr Thr Phe
785 790 795

<210> 13

<211> 180

<212> PRT

<213> Neisseria meningitidis

<400> 13

Met Val Ser Ala Val Ile Gly Ser Ala Ala Val Gly Ala Lys Ser Ala
1 5 10 15

Val Asp Arg Arg Thr Thr Gly Ala Gln Thr Asp Asp Asn Val Met Ala
20 25 30

Leu Arg Ile Glu Thr Thr Ala Arg Ser Tyr Leu Arg Gln Asn Asn Gln
35 40 45

eolf-seql

Thr Lys Gly Tyr Thr Pro Gln Ile Ser Val Val Gly Tyr Asp Arg His
50 55 60

Leu Leu Leu Leu Gly Gln Val Ala Thr Glu Gly Glu Lys Gln Phe Val
65 70 75 80

Gly Gln Ile Ala Arg Ser Glu Gln Ala Ala Glu Gly Val Tyr Asn Tyr
85 90 95

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

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

Ala Thr Arg Ala Arg Val Lys Ile Val Thr Tyr Gly Asn Val Thr Tyr
130 135 140

Val Met Gly Ile Leu Thr Pro Glu Glu Gln Ala Gln Ile Thr Gln Lys
145 150 155 160

Val Ser Thr Thr Val Gly Val Gln Lys Val Ile Thr Leu Tyr Gln Asn
165 170 175

Tyr Val Gln Arg
180

<210> 14

<211> 644

<212> PRT

<213> Neisseria meningitidis

<400> 14

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

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

eolf-seql

Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro Ser Ala Gln Gly Gly Gln
35 40 45

Asp Met Ala Ala Val Ser Glu Glu Asn Thr Gly Asn Gly Gly Ala Ala
50 55 60

Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu Gly Ala Gln Asn Asp Met
65 70 75 80

Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu Thr Pro Asn His Thr Pro
85 90 95

Ala Ser Asn Met Pro Ala Gly Asn Met Glu Asn Gln Ala Pro Asp Ala
100 105 110

Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro Asp Met Ala Asn Thr Ala
115 120 125

Asp Gly Met Gln Gly Asp Asp Pro Ser Ala Gly Gly Glu Asn Ala Gly
130 135 140

Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala Glu Asn Asn Gln Thr Ala
145 150 155 160

Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn Pro Ser Ala Thr Asn Ser
165 170 175

Gly Gly Asp Phe Gly Arg Thr Asn Val Gly Asn Ser Val Val Ile Asp
180 185 190

Gly Pro Ser Gln Asn Ile Thr Leu Thr His Cys Lys Gly Asp Ser Cys
195 200 205

Ser Gly Asn Asn Phe Leu Asp Glu Glu Val Gln Leu Lys Ser Glu Phe
210 215 220

eolf-seql

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

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

Val Gln Met Lys Gly Ile Asn Gln Tyr Ile Ile Phe Tyr Lys Pro Lys
260 265 270

Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser Ala Arg Ser Arg Arg Ser
275 280 285

Leu Pro Ala Glu Met Pro Leu Ile Pro Val Asn Gln Ala Asp Thr Leu
290 295 300

Ile Val Asp Gly Glu Ala Val Ser Leu Thr Gly His Ser Gly Asn Ile
305 310 315 320

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

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

Gly Glu Met Leu Ala Gly Thr Ala Val Tyr Asn Gly Glu Val Leu His
355 360 365

Phe His Thr Glu Asn Gly Arg Pro Ser Pro Ser Arg Gly Arg Phe Ala
370 375 380

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

Gly Asp Gly Leu His Met Gly Thr Gln Lys Phe Lys Ala Ala Ile Asp
405 410 415

eolf-seql

Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu Asn Gly Gly Gly Asp Val
420 425 430

Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu Glu Val Ala Gly Lys Tyr
435 440 445

Ser Tyr Arg Pro Thr Asp Ala Glu Lys Gly Gly Phe Gly Val Phe Ala
450 455 460

Gly Lys Lys Glu Gln Asp Gly Ser Gly Gly Gly Gly Ala Thr Tyr Lys
465 470 475 480

Val Asp Glu Tyr His Ala Asn Ala Arg Phe Ala Ile Asp His Phe Asn
485 490 495

Thr Ser Thr Asn Val Gly Gly Phe Tyr Gly Leu Thr Gly Ser Val Glu
500 505 510

Phe Asp Gln Ala Lys Arg Asp Gly Lys Ile Asp Ile Thr Ile Pro Val
515 520 525

Ala Asn Leu Gln Ser Gly Ser Gln His Phe Thr Asp His Leu Lys Ser
530 535 540

Ala Asp Ile Phe Asp Ala Ala Gln Tyr Pro Asp Ile Arg Phe Val Ser
545 550 555 560

Thr Lys Phe Asn Phe Asn Gly Lys Lys Leu Val Ser Val Asp Gly Asn
565 570 575

Leu Thr Met His Gly Lys Thr Ala Pro Val Lys Leu Lys Ala Glu Lys
580 585 590

Phe Asn Cys Tyr Gln Ser Pro Met Ala Lys Thr Glu Val Cys Gly Gly
595 600 605

eolf-seql

Asp Phe Ser Thr Thr Ile Asp Arg Thr Lys Trp Gly Val Asp Tyr Leu
610 615 620

Val Asn Val Gly Met Thr Lys Ser Val Arg Ile Asp Ile Gln Ile Glu
625 630 635 640

Ala Ala Lys Gln

<210> 15

<211> 327

<212> PRT

<213> Neisseria meningitidis

<400> 15

Ala Thr Asn Asp Asp Asp Val Lys Lys Ala Ala Thr Val Ala Ile Ala
1 5 10 15

Ala Ala Tyr Asn Asn Gly Gln Glu Ile Asn Gly Phe Lys Ala Gly Glu
20 25 30

Thr Ile Tyr Asp Ile Asp Glu Asp Gly Thr Ile Thr Lys Lys Asp Ala
35 40 45

Thr Ala Ala Asp Val Glu Ala Asp Asp Phe Lys Gly Leu Gly Leu Lys
50 55 60

Lys Val Val Thr Asn Leu Thr Lys Thr Val Asn Glu Asn Lys Gln Asn
65 70 75 80

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

Thr Lys Leu Ala Asp Thr Asp Ala Ala Leu Ala Asp Thr Asp Ala Ala
100 105 110

eolf-seq1

Leu Asp Ala Thr Thr Asn Ala Leu Asn Lys Leu Gly Glu Asn Ile Thr
 115 120 125

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

Leu Glu Ala Val Ala Asp Thr Val Asp Lys His Ala Glu Ala Phe Asn
 145 150 155 160

Asp Ile Ala Asp Ser Leu Asp Glu Thr Asn Thr Lys Ala Asp Glu Ala
 165 170 175

Val Lys Thr Ala Asn Glu Ala Lys Gln Thr Ala Glu Glu Thr Lys Gln
 180 185 190

Asn Val Asp Ala Lys Val Lys Ala Ala Glu Thr Ala Ala Gly Lys Ala
 195 200 205

Glu Ala Ala Ala Gly Thr Ala Asn Thr Ala Ala Asp Lys Ala Glu Ala
 210 215 220

Val Ala Ala Lys Val Thr Asp Ile Lys Ala Asp Ile Ala Thr Asn Lys
 225 230 235 240

Asp Asn Ile Ala Lys Lys Ala Asn Ser Ala Asp Val Tyr Thr Arg Glu
 245 250 255

Glu Ser Asp Ser Lys Phe Val Arg Ile Asp Gly Leu Asn Ala Thr Thr
 260 265 270

Glu Lys Leu Asp Thr Arg Leu Ala Ser Ala Glu Lys Ser Ile Ala Asp
 275 280 285

His Asp Thr Arg Leu Asn Gly Leu Asp Lys Thr Val Ser Asp Leu Arg
 290 295 300

eolf-seql

Lys Glu Thr Arg Gln Gly Leu Ala Glu Gln Ala Ala Leu Ser Gly Leu
 305 310 315 320

Phe Gln Pro Tyr Asn Val Gly
 325

<210> 16
 <211> 248
 <212> PRT
 <213> Neisseria meningitidis

<400> 16
 Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
 1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
 20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
 35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
 50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
 85 90 95

Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
 100 105 110

Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
 115 120 125

Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
 130 135 140

eolf-seql

Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
145 150 155 160

Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
165 170 175

Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
180 185 190

Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
195 200 205

Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
210 215 220

Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
225 230 235 240

His Ile Gly Leu Ala Ala Lys Gln
245

<210> 17

<211> 250

<212> PRT

<213> Neisseria meningitidis

<400> 17

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

eolf-seq1

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
85 90 95

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
100 105 110

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser
115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
225 230 235 240

Val His Glu Ile Gly Ile Ala Gly Lys Gln eolf-seql
245 250

<210> 18
<211> 776
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 18
Met Gly Pro Asp Ser Asp Arg Leu Gln Gln Arg Arg Val Ala Ala Asp
1 5 10 15

Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
20 25 30

Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn
35 40 45

Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn
50 55 60

Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg
65 70 75 80

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

Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val
100 105 110

Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu
115 120 125

Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr

eolf-seql

130

135

140

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

Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe
165 170 175

Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu
180 185 190

Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser
195 200 205

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

Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly
225 230 235 240

Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala
245 250 255

Gly Lys Gln Gly Ser Gly Pro Asp Ser Asp Arg Leu Gln Gln Arg Arg
260 265 270

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
275 280 285

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser
290 295 300

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
305 310 315 320

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu

eolf-seql

325

330

335

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
 340 345 350

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
 355 360 365

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
 370 375 380

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser
 385 390 395 400

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
 405 410 415

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
 420 425 430

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
 435 440 445

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
 450 455 460

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
 465 470 475 480

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
 485 490 495

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
 500 505 510

Val His Glu Ile Gly Ile Ala Gly Lys Gln Gly Ser Gly Gly Gly Gly

eolf-seql

515

520

525

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
 530 535 540

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
 545 550 555 560

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
 565 570 575

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
 580 585 590

Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
 595 600 605

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
 610 615 620

Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
 625 630 635 640

Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
 645 650 655

Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
 660 665 670

Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
 675 680 685

Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
 690 695 700

Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys

eolf-seql

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
85 90 95

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

Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu
115 120 125

Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn
130 135 140

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

Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser
165 170 175

Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
180 185 190

Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn
195 200 205

Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala
210 215 220

Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr
225 230 235 240

His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala
245 250 255

Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys
260 265 270

eolf-seql

Gln

<210> 20

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 20

Gly Ser Gly Gly Gly Gly

1 5

<210> 21

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 21

Gly Pro Asp Ser Asp Arg Leu Gln Gln Arg Arg

1 5 10

<210> 22

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 22

Gly Ser Gly Pro Asp Ser Asp Arg Leu Gln Gln Arg Arg

		eolf-seql
1	5	10

<210> 23
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23
 Gly Lys Gly Pro Asp Ser Asp Arg Leu Gln Gln Arg Arg
 1 5 10

<210> 24
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 24
 Met Gly Pro Asp Ser Asp Arg Leu Gln Gln Arg Arg
 1 5 10

<210> 25
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 25
 Met Ala Ser
 1

eolf-seql

<210> 26

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 26

Leu Glu His His His His His His

1 5

<210> 27

<211> 769

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 27

Met Gly Pro Asp Ser Asp Arg Leu Gln Gln Arg Arg Val Ala Ala Asp

1 5 10 15

Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys

20 25 30

Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Val Val Arg Lys Asn

35 40 45

Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn

50 55 60

Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg

65 70 75 80

Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu

85 90 95

eolf-seql

Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val
100 105 110

Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu
115 120 125

Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly Gly Glu His Thr
130 135 140

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

Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe
165 170 175

Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu
180 185 190

Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser
195 200 205

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

Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly
225 230 235 240

Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Ala Ile Gly Ile Ala
245 250 255

Gly Lys Gln Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Thr
260 265 270

Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly
275 280 285

eolf-seql

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

Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala Gly Asp Lys
305 310 315 320

Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg
325 330 335

Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu
340 345 350

Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val
355 360 365

Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Thr Asp Ser Leu
370 375 380

Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly Gly Glu His Thr
385 390 395 400

Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala
405 410 415

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

Thr Lys Lys Gln Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Leu Glu
435 440 445

Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser
450 455 460

His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly
465 470 475 480

eolf-seql

Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly
485 490 495

Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Ala Ile Gly Ile Ala
500 505 510

Gly Lys Gln Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala
515 520 525

Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly
530 535 540

Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Ser Lys Asn Glu Lys Leu
545 550 555 560

Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser
565 570 575

Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe
580 585 590

Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly
595 600 605

Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln
610 615 620

Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys
625 630 635 640

Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp
645 650 655

Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly
660 665 670

eolf-seql

Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
675 680 685

Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn
690 695 700

Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala
705 710 715 720

Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr
725 730 735

Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala
740 745 750

Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys
755 760 765

Gln

<210> 28

<211> 757

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 28

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Val
20 25 30

eolf-seql

Val	Arg	Lys	Asn	Glu	Lys	Leu	Lys	Leu	Ala	Ala	Gln	Gly	Ala	Glu	Lys
		35					40					45			
Thr	Tyr	Gly	Asn	Gly	Asp	Ser	Leu	Asn	Thr	Gly	Lys	Leu	Lys	Asn	Asp
	50					55					60				
Lys	Val	Ser	Arg	Phe	Asp	Phe	Ile	Arg	Gln	Ile	Glu	Val	Asp	Gly	Gln
65					70					75					80
Leu	Ile	Thr	Leu	Glu	Ser	Gly	Glu	Phe	Gln	Ile	Tyr	Lys	Gln	Asp	His
				85					90					95	
Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Glu	Lys	Ile	Asn	Asn	Pro	Asp	Lys
			100					105						110	
Ile	Asp	Ser	Leu	Ile	Asn	Gln	Arg	Ser	Phe	Arg	Val	Ser	Gly	Leu	Gly
		115					120						125		
Gly	Glu	His	Thr	Ala	Phe	Asn	Gln	Leu	Pro	Asp	Gly	Lys	Ala	Glu	Tyr
	130						135				140				
His	Gly	Lys	Ala	Phe	Ser	Ser	Asp	Asp	Ala	Gly	Gly	Lys	Leu	Thr	Tyr
145					150					155					160
Thr	Ile	Asp	Phe	Ala	Ala	Lys	Gln	Gly	His	Gly	Lys	Ile	Glu	His	Leu
				165					170					175	
Lys	Thr	Pro	Glu	Gln	Asn	Val	Glu	Leu	Ala	Ala	Ala	Glu	Leu	Lys	Ala
			180					185					190		
Asp	Glu	Lys	Ser	His	Ala	Val	Ile	Leu	Gly	Asp	Thr	Arg	Tyr	Gly	Ser
		195					200					205			
Glu	Glu	Lys	Gly	Thr	Tyr	His	Leu	Ala	Leu	Phe	Gly	Asp	Arg	Ala	Gln
	210					215					220				

eolf-seql

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Ala
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln Gly Ser Gly Gly Gly Gly Val Ala Ala
245 250 255

Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His
260 265 270

Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Val Ile Pro Gln
275 280 285

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

Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
305 310 315 320

Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln
325 330 335

Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His
340 345 350

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
355 360 365

Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly
370 375 380

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr
385 390 395 400

His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr
405 410 415

eolf-seql

Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile Glu His Leu
420 425 430

Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
435 440 445

Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser
450 455 460

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
465 470 475 480

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Ala
485 490 495

Ile Gly Ile Ala Gly Lys Gln Gly Ser Gly Gly Gly Gly Val Ala Ala
500 505 510

Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His
515 520 525

Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Ser Lys
530 535 540

Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly
545 550 555 560

Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser
565 570 575

Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr
580 585 590

Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu
595 600 605

eolf-seql

Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys
610 615 620

Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His
625 630 635 640

Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly
645 650 655

Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
660 665 670

Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser
675 680 685

Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly
690 695 700

Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu
705 710 715 720

Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val
725 730 735

Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly
740 745 750

Leu Ala Ala Lys Gln
755

<210> 29

<211> 769

<212> PRT

<213> Artificial Sequence

<220>

<221> source

eolf-seql

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 29

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

Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
20 25 30

Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Val Val Arg Lys Asn
35 40 45

Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn
50 55 60

Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg
65 70 75 80

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

Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val
100 105 110

Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu
115 120 125

Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly Gly Glu His Thr
130 135 140

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

Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe
165 170 175

eolf-seq1

Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu
180 185 190

Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser
195 200 205

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

Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly
225 230 235 240

Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala
245 250 255

Gly Lys Gln Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Thr
260 265 270

Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly
275 280 285

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

Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala Gly Asp Lys
305 310 315 320

Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg
325 330 335

Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu
340 345 350

Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val
355 360 365

eolf-seql

Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Thr Asp Ser Leu
370 375 380

Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly Gly Glu His Thr
385 390 395 400

Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala
405 410 415

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

Thr Lys Lys Gln Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Leu Glu
435 440 445

Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser
450 455 460

His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly
465 470 475 480

Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly
485 490 495

Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala
500 505 510

Gly Lys Gln Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala
515 520 525

Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly
530 535 540

Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Ser Lys Asn Glu Lys Leu
545 550 555 560

eolf-seq1

Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser
565 570 575

Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe
580 585 590

Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly
595 600 605

Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe Gln
610 615 620

Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys
625 630 635 640

Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp
645 650 655

Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly
660 665 670

Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
675 680 685

Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn
690 695 700

Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala
705 710 715 720

Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr
725 730 735

Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala
740 745 750

eolf-seql

Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys
 755 760 765

Gln

<210> 30

<211> 757

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 30

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
 1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Val
 20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
 35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
 50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
 85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
 100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly

eolf-seql

115

120

125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
 130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
 145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
 180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
 210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
 225 230 235 240

Ile Gly Ile Ala Gly Lys Gln Gly Ser Gly Gly Gly Gly Val Ala Ala
 245 250 255

Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His
 260 265 270

Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Val Ile Pro Gln
 275 280 285

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

Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp

eolf-seql

305		310		315		320							
Lys	Ile	Ser	Arg	Phe	Asp	Gln	Lys	Ile	Glu	Val	Asp	Gly	Gln
				325			330					335	
Thr	Ile	Thr	Leu	Ala	Ser	Gly	Glu	Phe	Gln	Ile	Tyr	Lys	Gln
			340				345					350	Asn His
Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Glu	Lys	Ile	Asn	Asn	Pro
		355					360				365	Asp	Lys
Thr	Asp	Ser	Leu	Ile	Asn	Gln	Arg	Ser	Phe	Arg	Val	Ser	Gly
	370					375					380	Leu	Gly
Gly	Glu	His	Thr	Ala	Phe	Asn	Gln	Leu	Pro	Gly	Gly	Lys	Ala
385					390				395				Glu Tyr
His	Gly	Lys	Ala	Phe	Ser	Ser	Asp	Asp	Pro	Asn	Gly	Arg	Leu
			405				410						His Tyr
Ser	Ile	Asp	Phe	Thr	Lys	Lys	Gln	Gly	Tyr	Gly	Arg	Ile	Glu
			420				425					430	His Leu
Lys	Thr	Leu	Glu	Gln	Asn	Val	Glu	Leu	Ala	Ala	Ala	Glu	Leu
		435					440					445	Lys Ala
Asp	Glu	Lys	Ser	His	Ala	Val	Ile	Leu	Gly	Asp	Thr	Arg	Tyr
	450					455					460		Gly Ser
Glu	Glu	Lys	Gly	Thr	Tyr	His	Leu	Ala	Leu	Phe	Gly	Asp	Arg
465					470				475				Ala Gln
Glu	Ile	Ala	Gly	Ser	Ala	Thr	Val	Lys	Ile	Gly	Glu	Lys	Val
			485					490					His Glu
Ile	Gly	Ile	Ala	Gly	Lys	Gln	Gly	Ser	Gly	Gly	Gly	Val	Ala
													Ala

eolf-seq1

500

505

510

Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His
 515 520 525

Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Ser Lys
 530 535 540

Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly
 545 550 555 560

Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser
 565 570 575

Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr
 580 585 590

Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu
 595 600 605

Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys
 610 615 620

Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His
 625 630 635 640

Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly
 645 650 655

Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 660 665 670

Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser
 675 680 685

Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly

eolf-seql

690

695

700

Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu
705 710 715 720

Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val
725 730 735

Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly
740 745 750

Leu Ala Ala Lys Gln
755

<210> 31

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> MOD_RES

<222> (32)..(32)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (123)..(123)

<223> Any amino acid except Leu

<400> 31

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Xaa
20 25 30

eolf-seql

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Xaa Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
210 215 220

eolf-seql

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
245

<210> 32
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (32)..(32)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Any amino acid except Leu

<400> 32
Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Xaa
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val

eolf-seql

65		70		75		80									
Asp	Gly	Gln	Thr	Ile	Thr	Leu	Ala	Ser	Gly	Glu	Phe	Gln	Ile	Tyr	Lys
				85					90					95	
Gln	Asn	His	Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Glu	Lys	Ile	Asn	Asn
			100					105					110		
Pro	Asp	Lys	Thr	Asp	Ser	Leu	Ile	Asn	Gln	Arg	Ser	Phe	Xaa	Val	Ser
		115					120					125			
Gly	Leu	Gly	Gly	Glu	His	Thr	Ala	Phe	Asn	Gln	Leu	Pro	Gly	Gly	Lys
	130					135					140				
Ala	Glu	Tyr	His	Gly	Lys	Ala	Phe	Ser	Ser	Asp	Asp	Pro	Asn	Gly	Arg
145					150					155					160
Leu	His	Tyr	Ser	Ile	Asp	Phe	Thr	Lys	Lys	Gln	Gly	Tyr	Gly	Arg	Ile
				165					170					175	
Glu	His	Leu	Lys	Thr	Leu	Glu	Gln	Asn	Val	Glu	Leu	Ala	Ala	Ala	Glu
			180					185					190		
Leu	Lys	Ala	Asp	Glu	Lys	Ser	His	Ala	Val	Ile	Leu	Gly	Asp	Thr	Arg
		195					200					205			
Tyr	Gly	Ser	Glu	Glu	Lys	Gly	Thr	Tyr	His	Leu	Ala	Leu	Phe	Gly	Asp
	210					215					220				
Arg	Ala	Gln	Glu	Ile	Ala	Gly	Ser	Ala	Thr	Val	Lys	Ile	Gly	Glu	Lys
225					230					235					240
Val	His	Glu	Ile	Gly	Ile	Ala	Gly	Lys	Gln						
				245					250						

<210> 33

eolf-seql

<211> 273

<212> PRT

<213> Neisseria meningitidis

<400> 33

Met Asn Arg Thr Ala Phe Cys Cys Leu Ser Leu Thr Thr Ala Leu Ile
1 5 10 15

Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
20 25 30

Ala Arg Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
35 40 45

Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
50 55 60

Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
65 70 75 80

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
85 90 95

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

Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu
115 120 125

Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn
130 135 140

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

Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser
165 170 175

eolf-seql

Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
180 185 190

Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn
195 200 205

Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala
210 215 220

Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr
225 230 235 240

His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala
245 250 255

Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys
260 265 270

Gln

<210> 34

<211> 247

<212> PRT

<213> Neisseria meningitidis

<400> 34

Val Ala Ala Asp Ile Gly Ala Arg Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp

eolf-seql

50

55

60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln

eolf-seql

245

<210> 35

<211> 247

<212> PRT

<213> Neisseria meningitidis

<400> 35

Val Ala Ala Asp Ile Gly Ala Arg Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

eolf-seql

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
245

<210> 36

<211> 248

<212> PRT

<213> Neisseria meningitidis

<400> 36

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Lys

eolf-seql

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> MOD_RES

<222> (32)..(32)

<223> Any amino acid except Ser

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Any amino acid except Leu

<400> 37

Val	Ala	Ala	Asp	Ile	Gly	Thr	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro
1				5				10					15		

Leu	Asp	His	Lys	Asp	Lys	Gly	Leu	Lys	Ser	Leu	Thr	Leu	Glu	Asp	Xaa
			20				25						30		

Ile	Pro	Gln	Asn	Gly	Thr	Leu	Thr	Leu	Ser	Ala	Gln	Gly	Ala	Glu	Lys
		35				40						45			

Thr	Phe	Lys	Ala	Gly	Asp	Lys	Asp	Asn	Ser	Leu	Asn	Thr	Gly	Lys	Leu
	50					55					60				

Lys	Asn	Asp	Lys	Ile	Ser	Arg	Phe	Asp	Phe	Val	Gln	Lys	Ile	Glu	Val
65				70					75					80	

Asp	Gly	Gln	Thr	Ile	Thr	Leu	Ala	Ser	Gly	Glu	Phe	Gln	Ile	Tyr	Lys
			85					90						95	

Gln	Asn	His	Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Glu	Lys	Ile	Asn	Asn
			100				105						110		

eolf-seql

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Xaa Val Ser
115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
225 230 235 240

Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 38

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

eolf-seql

<220>

<221> MOD_RES

<222> (32)..(32)

<223> Any amino acid except Ser

<220>

<221> MOD_RES

<222> (123)..(123)

<223> Any amino acid except Leu

<220>

<221> MOD_RES

<222> (240)..(240)

<223> Any amino acid except Glu

<400> 38

Val	Ala	Ala	Asp	Ile	Gly	Ala	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro
1				5				10						15	

Leu	Asp	His	Lys	Asp	Lys	Ser	Leu	Gln	Ser	Leu	Thr	Leu	Asp	Gln	Xaa
			20					25						30	

Val	Arg	Lys	Asn	Glu	Lys	Leu	Lys	Leu	Ala	Ala	Gln	Gly	Ala	Glu	Lys
		35					40					45			

Thr	Tyr	Gly	Asn	Gly	Asp	Ser	Leu	Asn	Thr	Gly	Lys	Leu	Lys	Asn	Asp
	50					55					60				

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

Leu	Ile	Thr	Leu	Glu	Ser	Gly	Glu	Phe	Gln	Ile	Tyr	Lys	Gln	Asp	His
			85						90					95	

Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Glu	Lys	Ile	Asn	Asn	Pro	Asp	Lys
			100					105					110		

Ile	Asp	Ser	Leu	Ile	Asn	Gln	Arg	Ser	Phe	Xaa	Val	Ser	Gly	Leu	Gly
			115				120					125			

eolf-seql

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
 130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
 145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
 180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
 210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Xaa
 225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
 245

<210> 39

<211> 262

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<220>

<221> MOD_RES

<222> (32)..(32)

<223> Any amino acid except Ser

eolf-seql

<220>

<221> MOD_RES

<222> (123)..(123)

<223> Any amino acid except Leu

<220>

<221> MOD_RES

<222> (240)..(240)

<223> Any amino acid except Glu

<400> 39

Cys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Ala Ala Asp
1 5 10 15

Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Xaa
20 25 30

Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Pro Gln Asn
35 40 45

Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala
50 55 60

Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
65 70 75 80

Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr
85 90 95

Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser
100 105 110

Ala Val Val Ala Leu Gln Ile Glu Lys Ile Xaa Asn Pro Asp Lys Thr
115 120 125

Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly
130 135 140

Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His

eolf-seql

Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala
50 55 60

Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
65 70 75 80

Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr
85 90 95

Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser
100 105 110

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

Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly
130 135 140

Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His
145 150 155 160

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

Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile Glu His Leu Lys
180 185 190

Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp
195 200 205

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

Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu
225 230 235 240

eolf-seql

Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile
245 250 255

Gly Ile Ala Gly Lys Gln
260

<210> 41

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 41

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
85 90 95

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
100 105 110

eolf-seql

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser
115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
225 230 235 240

Val His Ala Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 42

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 42

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro

eolf-seql

1	5	10	15
Leu Asp His	Lys Asp Lys Gly Leu	Lys Ser Leu Thr Leu	Glu Asp Val
	20	25	30
Ile Pro Gln	Asn Gly Thr Leu Thr	Leu Ser Ala Gln Gly	Ala Glu Lys
	35	40	45
Thr Phe Lys	Ala Gly Asp Lys Asp Asn Ser	Leu Asn Thr Gly	Lys Leu
	50	55	60
Lys Asn Asp	Lys Ile Ser Arg Phe Asp	Phe Val Gln Lys Ile	Glu Val
65	70	75	80
Asp Gly Gln	Thr Ile Thr Leu Ala Ser	Gly Glu Phe Gln Ile	Tyr Lys
	85	90	95
Gln Asn His	Ser Ala Val Val Ala Leu	Gln Ile Glu Lys Ile	Asn Asn
	100	105	110
Pro Asp Lys	Thr Asp Ser Leu Ile Asn	Gln Arg Ser Phe Leu	Val Ser
	115	120	125
Gly Leu Gly	Gly Glu His Thr Ala Phe	Asn Gln Leu Pro	Gly Gly Lys
	130	135	140
Ala Glu Tyr	His Gly Lys Ala Phe Ser	Ser Asp Asp Pro	Asn Gly Arg
145	150	155	160
Leu His Tyr	Ser Ile Asp Phe Thr Lys	Lys Gln Gly Tyr	Gly Arg Ile
	165	170	175
Glu His Leu	Lys Thr Leu Glu Gln Asn	Val Glu Leu Ala	Ala Ala Glu
	180	185	190
Leu Lys Ala	Asp Glu Lys Ser His Ala	Val Ile Leu Gly	Asp Thr Arg

eolf-seql

195

200

205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
225 230 235 240

Val His Ala Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 43

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 43

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Val
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
85 90 95

eolf-seql

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
 100 105 110

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser
 115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
 130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
 145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
 165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
 180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
 195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
 210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
 225 230 235 240

Val His Ala Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 44

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

eolf-seql

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 44

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Val
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
85 90 95

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
100 105 110

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser
115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
165 170 175

eolf-seql

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
225 230 235 240

Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 45

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 45

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Val
20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

eolf-seq1

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
245

eolf-seql

<210> 46

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 46

Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
1 5 10 15

Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
20 25 30

Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
35 40 45

Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
50 55 60

Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65 70 75 80

Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
85 90 95

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

Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
115 120 125

Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
130 135 140

Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
145 150 155 160

Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
165 170 175

eolf-seql

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

Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile
195 200 205

Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
210 215 220

Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
225 230 235 240

Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
245 250 255

<210> 47

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> MOD_RES

<222> (32)..(32)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (123)..(123)

<223> Any amino acid except Leu

<220>

<221> MOD_RES

<222> (240)..(240)

<223> Any amino acid except Glu

eolf-seql

<400> 47

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Xaa
20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Xaa Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

eolf-seql

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
 210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Xaa
 225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
 245

<210> 48
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> MOD_RES
 <222> (32)..(32)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (126)..(126)
 <223> Any amino acid except Leu

<220>
 <221> MOD_RES
 <222> (243)..(243)
 <223> Any amino acid except Glu

<400> 48
 Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
 1 5 10 15

eolf-seq1

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Xaa
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
85 90 95

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
100 105 110

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Xaa Val Ser
115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
195 200 205

eolf-seql

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
225 230 235 240

Val His Xaa Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 49

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> MOD_RES

<222> (34)..(34)

<223> Any amino acid except Arg

<400> 49

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

Val Xaa Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

eolf-seql

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
85 90 95

Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
100 105 110

Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
115 120 125

Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
130 135 140

Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
145 150 155 160

Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
165 170 175

Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
180 185 190

Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
195 200 205

Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
210 215 220

Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
225 230 235 240

His Ile Gly Leu Ala Ala Lys Gln
245

<210> 50

<211> 247

<212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 50

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Val
20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

eolf-seql

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Ala
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
245

<210> 51

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 51

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Val
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu

eolf-seql

50

55

60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
 65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
 85 90 95

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
 100 105 110

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser
 115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
 130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
 145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
 165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
 180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
 195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
 210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
 225 230 235 240

Val His Ala Ile Gly Ile Ala Gly Lys Gln

245

eolf-seql
250

<210> 52

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 52

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

Val Ser Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
85 90 95

Ser Ala Leu Thr Ala Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His
100 105 110

Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala
115 120 125

Gly Glu His Thr Ser Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr
130 135 140

eolf-seql

Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
145 150 155 160

Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His
165 170 175

Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys
180 185 190

Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
195 200 205

Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala
210 215 220

Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg
225 230 235 240

His Ile Gly Leu Ala Ala Lys Gln
245

<210> 53

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 53

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

eolf-seql

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly
115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
210 215 220

eolf-seql

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Ala
225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
245

<210> 54

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 54

Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser
20 25 30

Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
35 40 45

Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
50 55 60

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

Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
85 90 95

Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
100 105 110

eolf-seql

Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser Gly Leu Gly
 115 120 125

Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
 130 135 140

His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
 145 150 155 160

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

Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala
 180 185 190

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

Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
 210 215 220

Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu
 225 230 235 240

Ile Gly Ile Ala Gly Lys Gln
 245

<210> 55

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 55

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro

eolf-seql

1	5	10	15
Leu Asp His	Lys Asp Lys Gly Leu	Lys Ser Leu Thr Leu	Glu Asp Ser
	20	25	30
Ile Pro Gln	Asn Gly Thr Leu Thr	Leu Ser Ala Gln Gly	Ala Glu Lys
	35	40	45
Thr Phe Lys	Ala Gly Asp Lys Asp	Asn Ser Leu Asn Thr	Gly Lys Leu
	50	55	60
Lys Asn Asp	Lys Ile Ser Arg Phe Asp	Phe Val Gln Lys Ile	Glu Val
65	70	75	80
Asp Gly Gln	Thr Ile Thr Leu Ala Ser	Gly Glu Phe Gln Ile	Tyr Lys
	85	90	95
Gln Asn His	Ser Ala Val Val Ala	Leu Gln Ile Glu Lys	Ile Asn Asn
	100	105	110
Pro Asp Lys	Thr Asp Ser Leu Ile Asn	Gln Arg Ser Phe Arg	Val Ser
	115	120	125
Gly Leu Gly	Gly Glu His Thr Ala	Phe Asn Gln Leu Pro	Gly Gly Lys
	130	135	140
Ala Glu Tyr	His Gly Lys Ala Phe Ser	Ser Asp Asp Pro Asn	Gly Arg
145	150	155	160
Leu His Tyr	Ser Ile Asp Phe Thr Lys	Lys Gln Gly Tyr Gly	Arg Ile
	165	170	175
Glu His Leu	Lys Thr Leu Glu Gln Asn	Val Glu Leu Ala Ala	Ala Glu
	180	185	190
Leu Lys Ala	Asp Glu Lys Ser His Ala	Val Ile Leu Gly Asp	Thr Arg

eolf-seql

195

200

205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
225 230 235 240

Val His Ala Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 56

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 56

Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser
20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
85 90 95

eolf-seql

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
 100 105 110

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Arg Val Ser
 115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
 130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
 145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
 165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
 180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
 195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
 210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
 225 230 235 240

Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 57

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

eolf-seql

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> MOD_RES
 <222> (32)..(32)
 <223> Any amino acid except Ser

<220>
 <221> MOD_RES
 <222> (126)..(126)
 <223> Any amino acid except Leu

<220>
 <221> MOD_RES
 <222> (243)..(243)
 <223> Any amino acid except Glu

<400> 57
 Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro
 1 5 10 15

Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Xaa
 20 25 30

Ile Pro Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys
 35 40 45

Thr Phe Lys Ala Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
 50 55 60

Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val
 65 70 75 80

Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys
 85 90 95

Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn
 100 105 110

eolf-seql

Pro Asp Lys Thr Asp Ser Leu Ile Asn Gln Arg Ser Phe Xaa Val Ser
 115 120 125

Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Gly Gly Lys
 130 135 140

Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg
 145 150 155 160

Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile
 165 170 175

Glu His Leu Lys Thr Leu Glu Gln Asn Val Glu Leu Ala Ala Ala Glu
 180 185 190

Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg
 195 200 205

Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp
 210 215 220

Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys
 225 230 235 240

Val His Xaa Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 58

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

eolf-seql

<220>
<221> VARIANT
<222> (3)..(10)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(10)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 58
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10

<210> 59
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> VARIANT
<222> (3)..(10)
<223> /replace=" "

<220>
<221> misc_feature
<222> (1)..(10)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 59
His His His His His His His His His His
1 5 10

<210> 60
<211> 10
<212> PRT

eolf-seql

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>

<221> VARIANT

<222> (4)..(10)

<223> /replace=" "

<220>

<221> misc_feature

<222> (1)..(10)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 60

His His His His His His His His His His
1 5 10