

SEQUENCE LISTING

<110> Glaxo Smith Kline Biologicals SA

<120> IMMUNOGENIC COMPOSITION

<130> VB66439

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<151> 2018-02-13

<160> 32

<170> PatentIn version 3.5

<210> 1

<211> 522

<212> PRT

<213> Staphylococcus aureus

<400> 1

Ala Ser Glu Asn Ser Val Thr Gln Ser Asp Ser Ala Ser Asn Glu Ser
1 5 10 15

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

Thr Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu
35 40 45

Thr Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser
50 55 60

Ser Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr
65 70 75 80

Thr Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser
85 90 95

Asn Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr
100 105 110

Phe Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser
115 120 125

Thr Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala
130 135 140

Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn
145 150 155 160

Lys Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg
165 170 175

Ala Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Ala Ala Gly Thr
180 185 190

Asp Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly
195 200 205

Thr Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly
210 215 220

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

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

Pro Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp
260 265 270

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

Asp Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu
290 295 300

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

Thr Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys
325 330 335

Phe Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr
340 345 350

Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn
355 360 365

Val Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser
370 375 380

Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val
385 390 395 400

Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn
405 410 415

Phe Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn
420 425 430

Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro
435 440 445

Tyr Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp
450 455 460

Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp
465 470 475 480

Arg Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly
485 490 495

Ser Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu
500 505 510

Pro Gly Glu Ile Glu Pro Ile Pro Glu Asp
515 520

<210> 2
<211> 340
<212> PRT
<213> Staphylococcus aureus

<400> 2

Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu

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

Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn
225 230 235 240

Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe
245 250 255

Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn
260 265 270

Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr
275 280 285

Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp
290 295 300

Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp
305 310 315 320

Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro
325 330 335

Ile Pro Glu Asp
340

<210> 3
<211> 293
<212> PRT
<213> Staphylococcus aureus

<400> 3

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

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

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
115 120 125

Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140

Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175

Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190

Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205

Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
210 215 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
245 250 255

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
260 265 270

Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285

Glu Glu Met Thr Asn
290

<210> 4
<211> 516
<212> PRT
<213> Staphylococcus aureus

<400> 4

Met Lys Lys Lys Asn Ile Tyr Ser Ile Arg Lys Leu Gly Val Gly Ile
1 5 10 15

Ala Ser Val Thr Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro
20 25 30

Ala Ala Asn Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr
35 40 45

Gln Val Leu Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe
50 55 60

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly
65 70 75 80

Glu Ala Gln Lys Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln
85 90 95

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

Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser
115 120 125

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

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

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
165 170 175

Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
180 185 190

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

Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
210 215 220

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
225 230 235 240

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
245 250 255

Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
260 265 270

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
275 280 285

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

Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu
305 310 315 320

Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys
325 330 335

Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys
340 345 350

Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys
355 360 365

Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys

370

375

380

Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys
 385 390 395 400

Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys
 405 410 415

Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly Asp Thr Val Asn
 420 425 430

Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys Ile Ala Ala Asp
 435 440 445

Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly Gln Glu Leu Val
 450 455 460

Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala Asn Lys Ala Gln
 465 470 475 480

Ala Leu Pro Glu Thr Gly Glu Glu Asn Pro Phe Ile Gly Thr Thr Val
 485 490 495

Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu Leu Ala Gly Arg
 500 505 510

Arg Arg Glu Leu
 515

<210> 5

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> ClfA N2N3 P116S/Y118A

<400> 5

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

Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His

20

25

30

Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser
 35 40 45

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

Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly
 65 70 75 80

Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile
 85 90 95

Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr
 100 105 110

Leu Thr Met Ser Ala Ala Ile Asp Pro Glu Asn Val Lys Lys Thr Gly
 115 120 125

Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr
 130 135 140

Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile
 145 150 155 160

Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln
 165 170 175

Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu
 180 185 190

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

Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu
 210 215 220

Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn
 225 230 235 240

Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe
245 250 255

Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn
260 265 270

Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr
275 280 285

Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp
290 295 300

Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp
305 310 315 320

Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro
325 330 335

Ile Pro Glu Asp
340

<210> 6
<211> 346
<212> PRT
<213> Artificial Sequence

<220>
<223> ClfA N2N3 P116S/Y118A with PglB

<400> 6

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

Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His
20 25 30

Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser
35 40 45

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

Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly
65 70 75 80

Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile
85 90 95

Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr
100 105 110

Leu Thr Met Ser Ala Ala Ile Asp Pro Glu Asn Val Lys Lys Thr Gly
115 120 125

Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr
130 135 140

Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile
145 150 155 160

Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln
165 170 175

Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu
180 185 190

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

Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu
210 215 220

Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn
225 230 235 240

Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe
245 250 255

Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn
260 265 270

Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr

275

280

285

Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp
 290 295 300

Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp
 305 310 315 320

Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro
 325 330 335

Lys Asp Gln Asn Ala Thr Lys Pro Glu Asp
 340 345

<210> 7

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> ClfA N2N3 P116S/Y118A

<400> 7

Ser Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln
 1 5 10 15

Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro
 20 25 30

His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn
 35 40 45

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

Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala
 65 70 75 80

Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val
 85 90 95

Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala

100

105

110

Thr Leu Thr Met Ser Ala Ala Ile Asp Pro Glu Asn Val Lys Lys Thr
 115 120 125

Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys
 130 135 140

Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser
 145 150 155 160

Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg
 165 170 175

Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val
 180 185 190

Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp
 195 200 205

Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp
 210 215 220

Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr
 225 230 235 240

Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu
 245 250 255

Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val
 260 265 270

Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser
 275 280 285

Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp
 290 295 300

Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile
 305 310 315 320

Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu
325 330 335

Pro Lys Asp Gln Asn Ala Thr Lys Pro Glu Asp
340 345

<210> 8
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Mature Hla H35L

<400> 8

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

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

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
115 120 125

Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140

Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175

Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190

Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205

Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
210 215 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
245 250 255

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
260 265 270

Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285

Glu Glu Met Thr Asn
290

<210> 9

<211> 299

<212> PRT

<213> Artificial Sequence

<220>

<223> Mature Hla H35L with PglB consensus sequence substituted for
residue K131

<400> 9

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

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

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
115 120 125

Thr Gly Lys Asp Gln Asn Arg Thr Lys Ile Gly Gly Leu Ile Gly Ala
130 135 140

Asn Val Ser Ile Gly His Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys
145 150 155 160

Thr Ile Leu Glu Ser Pro Thr Asp Lys Lys Val Gly Trp Lys Val Ile
165 170 175

Phe Asn Asn Met Val Asn Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser
180 185 190

Trp Asn Pro Val Tyr Gly Asn Gln Leu Phe Met Lys Thr Arg Asn Gly
195 200 205

Ser Met Lys Ala Ala Asp Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser
210 215 220

Leu Leu Ser Ser Gly Phe Ser Pro Asp Phe Ala Thr Val Ile Thr Met
225 230 235 240

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

Arg Val Arg Asp Asp Tyr Gln Leu His Trp Thr Ser Thr Asn Trp Lys
260 265 270

Gly Thr Asn Thr Lys Asp Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr
275 280 285

Lys Ile Asp Trp Glu Lys Glu Glu Met Thr Asn
290 295

<210> 10
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Mature Hla H35L/H48C/G122C

<400> 10

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn Cys
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

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

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

Met Ser Thr Leu Thr Tyr Gly Phe Asn Cys Asn Val Thr Gly Asp Asp
115 120 125

Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140

Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175

Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190

Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205

Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
210 215 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
245 250 255

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
260 265 270

Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285

Glu Glu Met Thr Asn
290

<210> 11
<211> 299

<212> PRT
<213> Artificial Sequence

<220>

<223> Mature Hla H35L/H48C/G122C with PglB consensus sequence substituted for residue K131

<400> 11

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn Cys
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

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

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

Met Ser Thr Leu Thr Tyr Gly Phe Asn Cys Asn Val Thr Gly Asp Asp
115 120 125

Thr Gly Lys Asp Gln Asn Arg Thr Lys Ile Gly Gly Leu Ile Gly Ala
130 135 140

Asn Val Ser Ile Gly His Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys
145 150 155 160

Thr Ile Leu Glu Ser Pro Thr Asp Lys Lys Val Gly Trp Lys Val Ile
165 170 175

Phe Asn Asn Met Val Asn Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser

180

185

190

Trp Asn Pro Val Tyr Gly Asn Gln Leu Phe Met Lys Thr Arg Asn Gly
 195 200 205

Ser Met Lys Ala Ala Asp Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser
 210 215 220

Leu Leu Ser Ser Gly Phe Ser Pro Asp Phe Ala Thr Val Ile Thr Met
 225 230 235 240

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

Arg Val Arg Asp Asp Tyr Gln Leu His Trp Thr Ser Thr Asn Trp Lys
 260 265 270

Gly Thr Asn Thr Lys Asp Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr
 275 280 285

Lys Ile Asp Trp Glu Lys Glu Glu Met Thr Asn
 290 295

<210> 12

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> H1a H35L/H48C/G122C with N-terminal S, C-terminal GSHRHR, and
 KDQNRTK substituted for residue K131

<400> 12

Ser Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly
 1 5 10 15

Ser Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu
 20 25 30

Asn Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn
 35 40 45

Cys Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly
50 55 60

Gln Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala
65 70 75 80

Trp Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val
85 90 95

Ala Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu
100 105 110

Tyr Met Ser Thr Leu Thr Tyr Gly Phe Asn Cys Asn Val Thr Gly Asp
115 120 125

Asp Thr Gly Lys Asp Gln Asn Arg Thr Lys Ile Gly Gly Leu Ile Gly
130 135 140

Ala Asn Val Ser Ile Gly His Thr Leu Lys Tyr Val Gln Pro Asp Phe
145 150 155 160

Lys Thr Ile Leu Glu Ser Pro Thr Asp Lys Lys Val Gly Trp Lys Val
165 170 175

Ile Phe Asn Asn Met Val Asn Gln Asn Trp Gly Pro Tyr Asp Arg Asp
180 185 190

Ser Trp Asn Pro Val Tyr Gly Asn Gln Leu Phe Met Lys Thr Arg Asn
195 200 205

Gly Ser Met Lys Ala Ala Asp Asn Phe Leu Asp Pro Asn Lys Ala Ser
210 215 220

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

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

Glu Arg Val Arg Asp Asp Tyr Gln Leu His Trp Thr Ser Thr Asn Trp
260 265 270

Lys Gly Thr Asn Thr Lys Asp Lys Trp Ile Asp Arg Ser Ser Glu Arg
275 280 285

Tyr Lys Ile Asp Trp Glu Lys Glu Glu Met Thr Asn Gly Ser His Arg
290 295 300

His Arg
305

<210> 13
<211> 291
<212> PRT
<213> Staphylococcus aureus

<400> 13

Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn
1 5 10 15

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
20 25 30

Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
35 40 45

Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe
50 55 60

Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn
65 70 75 80

Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp
85 90 95

Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
100 105 110

Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn
115 120 125

Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg

130

135

140

Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
 145 150 155 160

Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala
 165 170 175

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
 180 185 190

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
 195 200 205

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
 210 215 220

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys
 225 230 235 240

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr
 245 250 255

Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
 260 265 270

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

Ala Pro Lys
 290

<210> 14
 <211> 56
 <212> PRT
 <213> Staphylococcus aureus

<400> 14

Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn
 1 5 10 15

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
20 25 30

Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
35 40 45

Leu Asn Asp Ser Gln Ala Pro Lys
50 55

<210> 15
<211> 61
<212> PRT
<213> Staphylococcus aureus

<400> 15

Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe
1 5 10 15

Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly
20 25 30

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu
35 40 45

Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55 60

<210> 16
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 16

Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala
35 40 45

Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55

<210> 17
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 17

Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala
35 40 45

Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55

<210> 18
<211> 58
<212> PRT
<213> Staphylococcus aureus

<400> 18

Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
50 55

<210> 19
<211> 56
<212> PRT
<213> Artificial Sequence

<220>

<223> SpA E domain with QQ-KK substitutions at positions 7 and 8 and DD-AA substitutions at positions 34 and 35

<400> 19

Ala Gln His Asp Glu Ala Lys Lys Asn Ala Phe Tyr Gln Val Leu Asn
1 5 10 15

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
20 25 30

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

Leu Asn Asp Ser Gln Ala Pro Lys
50 55

<210> 20

<211> 61

<212> PRT

<213> Artificial Sequence

<220>

<223> SpA D domain with QQ-KK substitutions at positions 12 and 13 and DD-AA substitutions at positions 39 and 40

<400> 20

Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Lys Lys Ser Ala Phe
1 5 10 15

Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly
20 25 30

Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser Gln Ser Thr Asn Val Leu
35 40 45

Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55 60

<210> 21

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> SpA A domain with QQ-KK substitutions at positions 9 and 108 and DD-AA substitutions at positions 36 and 37

<400> 21

Ala Asp Asn Asn Phe Asn Lys Glu Lys Lys Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala
35 40 45

Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55

<210> 22

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> SpA B domain with QQ-KK substitutions at positions 9 and 10 and DD-AA substitutions at positions 36 and 37

<400> 22

Ala Asp Asn Lys Phe Asn Lys Glu Lys Lys Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

Ser Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
50 55

<210> 23

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> SpA C domain with QQ-KK substitutions at positions 9 and 10 and DD-AA substitutions at positions 36 and 37

<400> 23

Ala Asp Asn Lys Phe Asn Lys Glu Lys Lys Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln
20 25 30

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

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
50 55

<210> 24

<211> 61

<212> PRT

<213> Artificial Sequence

<220>

<223> SpA D domain with QQ-KR substitutions at positions 4 and 5, QQ-KK substitutions at positions 12 and 13 and DD-AA substitutions at positions 39 and 40

<400> 24

Ala Asp Ala Lys Arg Asn Asn Phe Asn Lys Asp Lys Lys Ser Ala Phe
1 5 10 15

Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly
20 25 30

Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser Gln Ser Thr Asn Val Leu
35 40 45

Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55 60

<210> 25

<211> 61

<212> PRT

<213> Artificial Sequence

<220>

<223> SpA D domain with QQ-KR substitutions at positions 4 and 5

<400> 25

Ala Asp Ala Lys Arg Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe
1 5 10 15

Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly
20 25 30

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu
35 40 45

Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
50 55 60

<210> 26

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> SpA IgG binding portion with the substitutions of SEQ ID NOs
19-23

<400> 26

Ala Gln His Asp Glu Ala Lys Lys Asn Ala Phe Tyr Gln Val Leu Asn
1 5 10 15

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
20 25 30

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

Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe
50 55 60

Asn Lys Asp Lys Lys Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn
65 70 75 80

Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala
85 90 95

Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
100 105 110

Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Lys Lys Asn
115 120 125

Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg
130 135 140

Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn
145 150 155 160

Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala
165 170 175

Asp Asn Lys Phe Asn Lys Glu Lys Lys Asn Ala Phe Tyr Glu Ile Leu
180 185 190

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
195 200 205

Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
210 215 220

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys
225 230 235 240

Glu Lys Lys Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr
245 250 255

Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser
260 265 270

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

Ala Pro Lys
290

<210> 27
<211> 291
<212> PRT
<213> Artificial Sequence

<220>
<223> SpA IgG binding portion with the substitutions of SEQ ID NOs 19
and 21 24

<400> 27

Ala Gln His Asp Glu Ala Lys Lys Asn Ala Phe Tyr Gln Val Leu Asn
1 5 10 15

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
20 25 30

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

Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Lys Arg Asn Asn Phe
50 55 60

Asn Lys Asp Lys Lys Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn
65 70 75 80

Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala
85 90 95

Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
100 105 110

Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Lys Lys Asn
115 120 125

Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg
130 135 140

Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn
145 150 155 160

Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala

165

170

175

Asp Asn Lys Phe Asn Lys Glu Lys Lys Asn Ala Phe Tyr Glu Ile Leu
 180 185 190

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
 195 200 205

Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
 210 215 220

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys
 225 230 235 240

Glu Lys Lys Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr
 245 250 255

Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser
 260 265 270

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

Ala Pro Lys
 290

<210> 28
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PglB consensus sequence

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa = Asp or Glu

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Xaa can be any naturally occurring amino acid except proline

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid except proline

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = Ser or Thr

<400> 28

Xaa Xaa Asn Xaa Xaa
1 5

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PglB consensus sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = Asp or Glu

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid except proline

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid except proline

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa = Ser or Thr

<400> 29

Lys Xaa Xaa Asn Xaa Xaa Lys
1 5

<210> 30
<211> 7
<212> PRT

<213> Artificial Sequence

<220>

<223> PglB consensus sequence

<400> 30

Lys Asp Gln Asn Arg Thr Lys
1 5

<210> 31

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> PglB consensus sequence

<400> 31

Lys Asp Gln Asn Ala Thr Lys
1 5

<210> 32

<211> 349

<212> PRT

<213> Artificial Sequence

<220>

<223> ClfAN2N3P116S/Y118A at I337, N-terminal S, C-terminal GS

<400> 32

Ser Val Ala Ala Asp Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln
1 5 10 15

Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro
20 25 30

His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn
35 40 45

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

Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala
65 70 75 80

Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val
85 90 95

Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala
100 105 110

Thr Leu Thr Met Ser Ala Ala Ile Asp Pro Glu Asn Val Lys Lys Thr
115 120 125

Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys
130 135 140

Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser
145 150 155 160

Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg
165 170 175

Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val
180 185 190

Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp
195 200 205

Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp
210 215 220

Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr
225 230 235 240

Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu
245 250 255

Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val
260 265 270

Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser
275 280 285

Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp

290

295

300

Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile
305 310 315 320

Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu
325 330 335

Pro Lys Asp Gln Asn Ala Thr Lys Pro Glu Asp Gly Ser
340 345